

STIC-Biotech/ChemLib

160288

From: Vivlmore, Tracy
Sent: Friday, July 22, 2005 4:57 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request, application 10/698,070

Hello,

For application 10/698,070, please perform the following searches. For SEQ ID NO: 1, a score over length search with a length of 17-35 and a cutoff of 80%. For SEQ ID NO: 2, a standard search.

Thank you,

Tracy Vivlmore PhD
Remsen 2B-02, AU 1635
Mailbox: 2C-18
Tel: 571-272-2914

STAFF USE ONLY

Searcher: Noble
Searcher Phone: 2-_____
Date Searcher Picked up: ____
Date Completed: ____
Searcher Prep/Rev. Time: 6
Online Time: 40

Type of Search

NA#: 2+10 AA#: ____
Interference: ____ SPDI: ____
S/L: ✓ Oligomer: ____
Encode/Transl: ____
Structure#: ____ Text: ____
Inventor: ____ Litigation: ____

Vendors and cost where applicable

STN: ____
DIALOG: ____
QUESTEL/ORBIT: ____
LEXIS/NEXIS: ____
SEQUENCE SYSTEM: compugen
WWW/Internet: ____
Other(Specify): gcg

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 60. $\text{min len} = 17$
 $\text{max len} = 35$

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 13:10:46 ; Search time 6 Seconds
(without alignments)
3.170 Million cell updates/sec

Title: US-10-698-070-1

Perfect score: 3763

Sequence: 1 aggtggcggcgaagaatgg.....taacaaaaatatagatg 3763

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 132 seqs, 2527 residues

Total number of hits satisfying chosen parameters: 264

Minimum DB seq length: 17

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 141 summaries

Database : fetchlrni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	0.9	33	1	US-08-863-639A-29
C 2	30.4	0.8	33	1	US-09-475-947A-251
C 3	30	0.8	30	1	US-08-068-747-6
C 4	30	0.8	30	1	US-08-068-747-11
C 5	30	0.8	30	1	US-08-863-639A-30
C 6	30	0.8	30	1	US-09-135-994-4
C 7	30	0.8	30	1	US-09-684-843A-4
C 8	30	0.8	31	1	US-08-570-155-14
C 9	30	0.8	31	1	PCT-US95-02861-14
C 10	25.4	0.7	29	1	US-09-304-232-152
C 11	24	0.6	24	1	US-08-863-639A-94
C 12	21	0.6	21	1	US-08-267-803B-66
C 13	21	0.6	21	1	US-08-863-639A-28
C 14	21	0.6	21	1	US-08-863-639A-40
C 15	21	0.6	21	1	US-08-863-639A-60
C 16	21	0.6	21	1	US-08-863-639A-66
C 17	21	0.6	21	1	US-08-863-639A-69
C 18	21	0.6	21	1	US-08-863-639A-87
C 19	20.2	0.5	25	1	US-09-396-196G-74107
C 20	19	0.5	20	1	US-09-198-452A-6476
C 21	18.8	0.5	23	1	US-09-633-098-24
C 22	18.8	0.5	23	1	US-10-177-308-24
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C 27	18.4	0.5	21	1	US-08-863-639A-92
C 28	18	0.5	18	1	US-08-863-639A-17
C 29	18	0.5	18	1	US-09-205-995-48
C 30	17.8	0.5	21	1	US-08-863-639A-14
C 31	17.8	0.5	21	1	US-08-863-639A-77
C 32	17.4	0.5	19	1	US-08-410-540-5
C 33	17.4	0.5	20	1	US-08-914-961-6

1	US-09-723-368-5	Sequence 5, Appli
20	US-08-970-369A-2	Sequence 2, Appli
18	US-09-407-562-2	Sequence 2, Appli
18	US-08-628-540-8	Sequence 8, Appli
21	US-08-941-100-3	Sequence 3, Appli
20	US-09-043-303-8	Sequence 8, Appli
21	US-09-661-753-35	Sequence 35, Appli
20	US-08-863-639A-15	Sequence 15, Appli
18	US-08-863-639A-16	Sequence 16, Appli
18	US-09-487-444-11	Sequence 11, Appli
20	US-09-657-042A-39	Sequence 39, Appli
20	US-09-907-843-23	Sequence 23, Appli
19	US-09-696-791-203	Sequence 203, App
33	US-09-475-947A-251	Sequence 251, App
17	US-08-985-162-175	Sequence 175, App
17	US-08-584-040-5601	Sequence 5601, Ap
17	US-09-371-772B-2491	Sequence 2491, Ap
17	US-09-401-063-175	Sequence 175, App
17	US-09-685-664B-2491	Sequence 2491, Ap
18	US-08-758-306-519	Sequence 519, App
18	US-08-647-144-10	Sequence 10, Appli
18	US-09-255-912-14	Sequence 14, Appli
19	US-09-696-791-203	Sequence 323, App
19	US-09-696-791-324	Sequence 324, App
31	US-08-570-155-14	Sequence 14, Appli
31	PCT-US95-02861-14	Sequence 14, Appli
33	US-08-863-639A-29	Sequence 29, Appli
33	US-08-317-431A-11	Sequence 11, Appli
18	US-09-106-038A-24	Sequence 24, Appli
18	US-09-106-038A-25	Sequence 25, Appli
18	US-09-255-911-31	Sequence 31, Appli
18	US-08-961-810-60	Sequence 60, Appli
18	US-08-352-902D-60	Sequence 60, Appli
18	US-08-748-073-3	Sequence 3, Appli
18	US-08-584-040-4471	Sequence 4471, Ap
18	US-09-475-947A-340	Sequence 340, App
18	US-09-280-030-28	Sequence 28, Appli
18	US-09-265-503B-60	Sequence 60, Appli
18	US-09-371-772B-2184	Sequence 2184, Ap
18	US-09-685-664B-2184	Sequence 2184, Ap
18	US-10-272-865-14	Sequence 14, Appli
18	US-10-272-865-34	Sequence 34, Appli
17	US-08-292-620A-1659	Sequence 1659, Ap
17	US-08-860-150-9	Sequence 9, Appli
17	US-09-338-132-9	Sequence 9, Appli
17	US-09-071-845-1659	Sequence 1659, Ap
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30	US-08-863-639A-30	Sequence 30, Appli
30	US-09-135-994-4	Sequence 4, Appli
30	US-09-684-843A-4	Sequence 4, Appli
17	US-08-390-850-438	Sequence 438, App
17	US-08-373-124A-1513	Sequence 1513, Ap
17	US-08-158-352-2	Sequence 2, Appli
17	US-08-435-634-438	Sequence 438, App
17	US-08-435-634-452	Sequence 452, App
17	US-08-758-306-903	Sequence 903, App
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17	US-09-050-159-45	Sequence 45, Appli
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Sequence 1940, Ap
Sequence 1941, Ap

ALIGNMENTS

RESULT 1
US-08-863-639A-29/c
; Sequence 29, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Rampal, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muehl
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000

TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
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Query Match 0.9%; Score 32; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
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RESULT 2
US-09-475-947A-251
; Sequence 251, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 251
; LENGTH: 33
; TYPE: DNA
; ORGANISM: human
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Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 32
RESULT 3
US-08-068-747-6
; Sequence 6, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747

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; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
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Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 4
US-08-068-747-11/c
; Sequence 11, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Houseman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; NUCLEOTIDE REPEATS IN THE HUMAN GENOME
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-11
Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 5
US-08-863-639A-30
; Sequence 30, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C.T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-30
Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 6
US-09-135-994-4
; Sequence 4, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-994-4

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Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 7
US-09-684-843A-4
; Sequence 4, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Ratum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-684-843A-4

Query Match          0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 8
US-08-570-155-14
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,155
; FILING DATE: 08/214,823
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 06353/010W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14;
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/399,499
; FILING DATE: 07 March 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06353/011001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-570-155-14

Query Match          0.8%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 9
PCT-US95-02861-14
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE
; TITLE OF INVENTION: REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02861
; FILING DATE: 08 March 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 06353/010W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14;
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02861-14

Query Match          0.8%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 10
US-09-304-232-152
; Sequence 152, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated with
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-09-304-232-152

Query Match          0.7%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 11;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGCAGCAGCAGCA 1428
Db 1 CAGCAGGAACAGCAKAGCAGGAGCAGCAGCA 29

RESULT 11
US-08-863-639A-94
; Sequence 94, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
```

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; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-94

Query Match          0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGCAGCA 1434
Db 1 GCAGCAGCAGCAGCAGCAGCAGCA 24

RESULT 12
US-08-267-803B-66/c
; Sequence 66, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-267-803B-66

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db 21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 13
US-08-863-639A-28
; Sequence 28, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-28

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 1 CAGCAGCAGCAGCAGCAGCAG 21

RESULT 14
US-08-863-639A-40
; Sequence 40, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.

```

```

; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-40

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db 1 AGCAGCAGCAGCAGCAGCAGC 21

RESULT 15
US-08-863-639A-60/c
; Sequence 60, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth

```



```
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-60

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 16
US-08-863-639A-66
; Sequence 66, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-69

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db 21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 18
US-08-863-639A-87/c
; Sequence 87, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCA 1431
Db 1 GCAGCAGCAGCAGCAGCAGCA 21
```

```
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA: US/08/863,639A
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-87

Query Match          0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCGAGCAGCAGCAGCAGCA 1431
Db 21 GCAGCGAGCAGCAGCAGCAGCA 1

RESULT 19
US-09-396-196G-74107
; Sequence 74107, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-74107

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1597 GCAGCGAGCAGCAGCAACCACTCT 1621
Db 1 GCAGCGAGCAGCAGCAACCACTCT 25

RESULT 20
US-09-198-452A-6476/c
; Sequence 6476, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6476
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6476

Query Match          0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAACAGCAACAGCAAC 1472
Db 19 CAGCAACAGCAACAGCAAC 1

RESULT 21
US-09-632-098-24/c
; Sequence 24, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21.076
US-09-632-098-24

Query Match          0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1421 CAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAAC 2

RESULT 22
US-10-177-308-24/c
; Sequence 24, Application US/10177308
; Patent No. 6762044
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/177,308
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21.076
```



```
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-47
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAAACAGCAACA 1593
Db 1 CAACAACAAACAAACAACA 20

RESULT 26
US-08-863-639A-89/c
; Sequence 89, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-89
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAAACAGCAACA 1593
Db 20 CAACAACAAACAAACAACA 1

RESULT 27
```

```
US-08-863-639A-92/c
; Sequence 92, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-92
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAAACAGCAACA 1593
Db 21 CAACAACAAACAAACAACA 2

RESULT 28
US-08-863-639A-17/c
; Sequence 17, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
```

```
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-17

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 29
US-09-205-995-48/c
; Sequence 48, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
; APPLICANT: Xu, Minzhen
; APPLICANT: Humphreys, Robert
; TITLE OF INVENTION: CANCER CELL VACCINE
; FILE REFERENCE: U.S. Application 09/205,995, (CIP)
; CURRENT APPLICATION NUMBER: US/09/205,995
; CURRENT FILING DATE: 1998-12-04
; PRIOR FILING DATE: 09/036,746
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 08/661,627
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide corresponding to a specific region
; OTHER INFORMATION: of the mouse II gene.
US-09-205-995-48

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 30
US-08-863-639A-14
; Sequence 14, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
```

```
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-14

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1572 AGCAACAACAACAACAACAAC 1592
Db 1 AACAAACAACAACAACAACAAC 21

RESULT 31
US-08-863-639A-77/c
; Sequence 77, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-77

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1572 AGCAACACACACACACAC 1592
Db 21 AACCAACACACACACACAC 1

RESULT 32
US-08-410-540-5
; Sequence 5, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong
; APPLICANT: Straus III, Jerome F.
; TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,540
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-410-540-5

Query Match      0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 31;
```

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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCAGCAGCAGCAGCAGCAG 19

RESULT 33
US-08-914-961-6/C
; Sequence 6, Application US/08914961
; Patent No. 6018042
; GENERAL INFORMATION:
; APPLICANT: Mett, Helmut
; APPLICANT: Haner, Robert
; APPLICANT: Deap, Nicholas Mark
; TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,961
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,753
; FILING DATE: 09-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-20047/P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; POSITION IN GENOME:
; MAP POSITION: 979
; UNITS: bp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..20
; OTHER INFORMATION: /note= "All nucleotides are of the
; OTHER INFORMATION: phosphorothioate type"
; US-08-914-961-6

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1545 AGCAGCAGCAGCAGCAGCA 1563
Db 19 AGRAGCAGCAGCAGCAGCA 1

RESULT 34
US-09-723-368-5
; Sequence 5, Application US/09723368
```

Patent No. 6641818
GENERAL INFORMATION:
APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARNER, Morgyn S.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: EISENBERG, Roselyn J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: KROMENACHER, Claude
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290.0050/2U1
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer PRR2A8
US-09-723-368-5

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 973 GATGAGCAGCAGCAGCAG 991
Db 2 GAAGCAGCAGCAGCAGCAG 20

RESULT 35
US-08-970-269A-2
Sequence 2, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: No. 5976803ember 14, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-08-970-269A-2
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 255 GGGAGAATCTCTCTGCA 271
Db 1 GGGAGAATCTCTCTGCA 17
RESULT 36
US-09-407-562-2
Sequence 2, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334ember 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-2
Query Match 0.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 GGGAGAACTCTCTGCA 271
Db 1 GGGAGAACTCTCTGCA 17

RESULT 37

US-08-628-540-8/c
; Sequence 8, Application US/08628540
; Patent No. 6022951
; GENERAL INFORMATION:
; APPLICANT: SANO, Takeshi
; APPLICANT: CANTOR, Charles R.
; APPLICANT: VAJDA, Sandor
; APPLICANT: REZNIK, Gabriel O.
; APPLICANT: SMITH, Cassandra L.
; APPLICANT: PANDORI, Mark W.
; TITLE OF INVENTION: STREPTAVIDIN MUTANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,540
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/420,010
; FILING DATE: 11-APR-1995
; APPLICATION NUMBER: 60/003,687
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 016865-0244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-628-540-8

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

, RESULT 38

US-08-941-100-3/c
; Sequence 3, Application US/08941100B
; Patent No. 6207390
; GENERAL INFORMATION:
; APPLICANT: Cantor, Charles R.
; APPLICANT: Sano, Takeshi
; TITLE OF INVENTION: Reduced Affinity Streptavidin
; FILE REFERENCE: BU-03165
; CURRENT APPLICATION NUMBER: US/08/941,100B
; CURRENT FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 08/469,353
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/420,010
; PRIOR FILING DATE: 1995-04-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Streptomyces avidinii
US-08-941-100-3

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

RESULT 39

US-09-043-303-8
; Sequence 8, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazujiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-043-303-8

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1448 CAGCAGCAGCAGCAACA 1467
Db 1 CACCACCAGCAACAACA 20

RESULT 40

US-09-661-753-35
; Sequence 35, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498

; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-35

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 90.4%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGC 1430
Db 1 GTAGCAGCAGCGGCAGC 20

RESULT 41
US-08-863-639A-15
; Sequence 15, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-15

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1576 ACAACAACAGCAACAA 1593
Db 1 ACAACAACAGCAACAA 18

RESULT 42
US-08-863-639A-16
; Sequence 16, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-16

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAA 1591
Db 1 CAACAACAACAGCAACAA 18

RESULT 43
US-09-487-444-11
; Sequence 11, Application US/09487444
; Patent No. 6159697
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION
; FILE REFERENCE: RTS-0133
; CURRENT APPLICATION NUMBER: US/09/487,444
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-444-11

```
Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1406 CAACAGCAGCAGCAGCAG 1423
Db 1 CGACAGCAGCAGCAGCAG 18

RESULT 44
US-09-657-042A-39/c
; Sequence 39, Application US/09657042A
; Patent No. 6329203
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTS-0148
; CURRENT APPLICATION NUMBER: US/09/657,042A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-042A-39

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 976 GCAGCAGCAGCAGCAGCA 993
Db 19 GCAGCAGCTCCAGCAGCA 2

RESULT 45
US-09-907-843-23/c
; Sequence 23, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-23

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAAC 1442
Db 17 CAGCAGCAGCAGCAAC 2

RESULT 46
US-09-696-791-203/c
; Sequence 203, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
```

```
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk2 ribozyme binding site
US-09-696-791-203

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACACAGATAGC 948
Db 19 AGCAGCTGGACACAGATAGC 1

RESULT 47
US-09-475-947A-251/c
; Sequence 251, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 251
; LENGTH: 33
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-251

Query Match      0.4%; Score 15.6; DB 1; Length 33;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1925 CAGCACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTACTGCTGCTGCTGCTGCTGCTG 1

RESULT 48
US-08-985-162-175
; Sequence 175, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
```

```

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985.162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036.476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-175

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 38;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3633 GAGAACCTAGAAAACAT 3649
Db 1 GAGAACCUAGAAAUCAU 17
|||||:|||||:|

RESULT 49
US-08-584-040-5601/c
; Sequence 5601, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584.040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005.974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5601

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
|||||:|||||:|

RESULT 50
US-09-371-772B-2491/c
; Sequence 2491, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
; US-09-371-772B-2491

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
|||||:|||||:|

RESULT 51
US-09-401-063-175
; Sequence 175, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT

```

```

, TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
,
, TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
,
, TITLE OF INVENTION: FACTOR RECEPTORS
,
, NUMBER OF SEQUENCES: 1877
,
, CORRESPONDENCE ADDRESS:
,
, ADDRESSEE: Lyon & Lyon
,
, STREET: 633 West Fifth Street
,
, STREET: Suite 4700
,
, CITY: Los Angeles
,
, STATE: California
,
, COUNTRY: U.S.A.
,
, ZIP: 90071-2066
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: 3.5" diskette, 1.44 Mb
,
, MEDIUM TYPE: storage
,
, COMPUTER: IBM Compatible
,
, OPERATING SYSTEM: IBM P.C. DOS 5.0
,
, SOFTWARE: FastSeq for Windows 2.0
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/09/401,063
,
, FILING DATE:
,
, CLASSIFICATION:
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: 08/985,162
,
, FILING DATE: 04 December 1997
,
, APPLICATION NUMBER: 60/036,476
,
, FILING DATE: 31 January 1997
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Warburg, Richard J.
,
, REGISTRATION NUMBER: 32,327
,
, REFERENCE/DOCKET NUMBER: 230/107
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: (213) 489-1600
,
, TELEFAX: (213) 955-0440
,
, TELEX: 67-3510
,
, INFORMATION FOR SEQ ID NO: 175:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 17 base pairs
,
, TYPE: nucleic acid
,
, STRANDEDNESS: single
,
, TOPOLOGY: linear
,
, US-09-401-063-175

```

```
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2491

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred.No.38;
Matches 16; Conservative 0; Mismatches 1; Indels

QY      326 TTGCTATGAGCCCAAGC 342
DB      17 TTGCTGTGAGCCAAGC 1

RESULT 53
US-08-758-306-519
; Sequence 519, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 519:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-519

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred.No.47;
Matches 15; Conservative 1; Mismatches 1; Indels

QY      993 AGCACCGCCTTACCAAC 1009
```

Db 1 AGCCCCAGCCUACCAAC 17

RESULT 54
US-08-647-144-10/c
; Sequence 10, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Di Padova, Franco
; APPLICANT: Barclay, George R.
; APPLICANT: Poxtan, Ian R.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5858728th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,144
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,046
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: EP 92/00380
; FILING DATE: 22-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: YES
US-08-647-144-10

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 593 AGTGCCTTGACCTGGA 609
Db 17 AGTGCCTTGACCTGGA 1

RESULT 55
US-09-255-912-14/c
; Sequence 14, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-912-14

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAACGACGCGGAGGAGA 89
Db 18 GGAGCAGCGGAGGAGA 2

RESULT 56
US-09-696-791-323
; Sequence 323, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk3 ribozyme binding site
US-09-696-791-323

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTGACTTCTCTCAGCCA 2958
Db 3 TTGAGTTCTCTCAGCCA 19

RESULT 57
US-09-696-791-324
; Sequence 324, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk3 ribozyme binding site
US-09-696-791-324

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTTCAGTCTCTCAGCCA 2958
Db 2 TTTCAGTCTCTCAGCCA 18

RESULT 58
US-08-570-155-14/c
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.155
; FILING DATE: 17 March 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/399,499
; FILING DATE: 07 March 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06353/011001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02861-14

Query Match 0.4%; Score 15; DB 1; Length 31;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 59
PCT-US95-02861-14/c
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: REPEATS

; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02861
; FILING DATE: 08 March 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 06353/010W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02861-14

Query Match 0.4%; Score 15; DB 1; Length 31;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 60
US-08-863-639A-29
; Sequence 29, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:

```

; TOPOLOGY: linear
; US-08-317-431A-11
;
; Query Match 0.4%; Score 14.8; DB 1; Length 18;
; Best Local Similarity 88.9%; Pred. No. 56;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1448 CACGACGACGACGCAA 1465
   |||||
Db 1 CACCACCAGCACGCAA 18
   |||||
;
RESULT 63
US-09-106-038A-24
; Sequence 24, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-106-038A-24
;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1406 CACACGACGACGACGAG 1423
   |||||
Db 1 CACCAGCGCAGCAGCAG 18
   |||||
;
RESULT 63
US-09-106-038A-25
; Sequence 25, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue

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;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,902D
; FILING DATE: 09-Dec-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Rysselberghe, Pierre C.
; REGISTRATION NUMBER: 33,557
; REFERENCE/DOCKET NUMBER: OHSU 306B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 224-6655
; TELEFAX: (503) 295-6679
; TELEX: 360619
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "primers directed to genomic
; intron DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-08-352-902D-60

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1223 CAAAAGCTTCAGATCTC 1240
Db      1 CAAAAGCTTCAGATCTC 18

RESULT 67
US-08-748-073-3
; Sequence 3, Application US/08748073
; Patent No. 6204008
; GENERAL INFORMATION:
; APPLICANT: Borneman, W. Scott
; APPLICANT: Goyal, Anil
; APPLICANT: Conder, Michael J.
; APPLICANT: Vinci, Victor A.
; TITLE OF INVENTION: BIOPROCESS FOR PRODUCTION OF DIPEPTIDE
; TITLE OF INVENTION: BASED COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,073
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: MK-19147F
```

```
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
US-08-748-073-3

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      983 CACCAGCAGCAGCACCAG 1000
Db      1 CACCAGCTCCAGCACCAG 18

RESULT 68
US-08-584-040-4471
; Sequence 4471, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4471
```

```
Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1094 ACATTGAGCCCGACAGAGC 1111
   |||: |||||: |||||: |||||:
Db 1 ACAUGCAGCCCGACUGAGC 18

RESULT 69
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0867
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-340

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
   |||||: |||||: |||||: |||||:
Db 1 GCAGCAGCAGCAGCAGCA 18

RESULT 70
US-09-280-030-28/c
; Sequence 28, Application US/09280030A
; Patent No. 6506595
; GENERAL INFORMATION:
; APPLICANT: Sato, Seiji
; APPLICANT: Higashikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAs ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; FILE REFERENCE: DNAs
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280,030A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a reverse primer for PCR amplification of
; OTHER INFORMATION: MWPp-MWPmp5 DNA
US-09-280-030-28

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
```

```
Db 18 GCAGCAGAGAGCAGCA 1
   |||||: |||||: |||||: |||||:

RESULT 71
US-09-265-503B-60
; Sequence 60, Application US/09265503B
; Patent No. 6538108
; GENERAL INFORMATION:
; APPLICANT: Liskay, Robert M.
; APPLICANT: Bronner, C. Eric
; APPLICANT: Baker, Sean M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Kolodner, Richard D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: RELATING TO DNA MISMATCH REPAIR GENES
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & Heuser
; STREET: 520 S.W. Yamhill Street, Suite 200
; CITY: Portland
; STATE: Oregon
; COUNTRY: U.S.A.
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,503B
; FILING DATE: March 10, 1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Rysselberghe, Pierre C.
; REGISTRATION NUMBER: 33,557
; REFERENCE/DOCKET NUMBER: OHSU 306D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 224-6655
; TELEFAX: (503) 295-6679
; TELEX: 360619
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "primers directed to genomic
; OTHER INFORMATION: intron DNA"
US-09-265-503B-60

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAAGCCTCAGATCTC 1240
   |||||: |||||: |||||: |||||:
Db 1 CAAAAGCCTCAGATCTC 18

RESULT 72
US-09-371-772B-2184
; Sequence 2184, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
```

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2184

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1094 ACATTCAGCCCAAGC 1111
      |||: ||||| |||||
Db      1 ACAUGCAGCCCAAGC 18

RESULT 73
US-09-685-664B-2184
; Sequence 2184, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-2184

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1094 ACATTCAGCCCAAGC 1111
      |||: ||||| |||||
Db      1 ACAUGCAGCCCAAGC 18

RESULT 74
US-10-272-865-14
; Sequence 14, Application US/10272865
; Patent No. 6828105
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
```

```
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for Treating sRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-272-865-14

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1271 GCCATGGAGCCCGTCAG 1288
      ||||| ||||| |||||
Db      1 GCCATGGAGCCCGTCAG 18

RESULT 75
US-10-272-865-34/C
; Sequence 34, Application US/10272865
; Patent No. 6828105
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for Treating sRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-272-865-34

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1271 GCCATGGAGCCCGTCAG 1288
      ||||| ||||| |||||
Db      18 GCCATGGAGCCCGTCAG 1

RESULT 76
US-08-292-620A-1659
; Sequence 1659, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF INTRACELLULAR ADHESION
```

```
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1659:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1659

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred.No.52;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2349 GGCACCTACCTTAGG 2364
Db 1 GGCCCCCUACCUAGG 16

RESULT 77
US-08-860-150-9/c
; Sequence 9, Application US/08860150B
; Patent No. 5981205
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Millward, Thomas A.
; TITLE OF INVENTION: NUCLEAR DBF2-RELATED (NDR) KINASES
; FILE REFERENCE: 4-20265/A/PCT
; CURRENT APPLICATION NUMBER: US/08/860,150B
; CURRENT FILING DATE: 1997-06-19
; EARLIER APPLICATION NUMBER: PCT/EP95/05052
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: 94810746.1
; EARLIER FILING DATE: 1994-12-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-08-860-150-9
```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-08-860-150-9

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred.No.52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3209 AAATGGAAAGCAGAAA 3224
Db 16 AAAAGGAAAGCAGAAA 1

RESULT 78
US-09-338-132-9/c
; Sequence 9, Application US/09338132
; Patent No. 6040164
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Millward, Thomas A.
; TITLE OF INVENTION: NUCLEAR DBF2-RELATED (NDR) KINASES
; FILE REFERENCE: 4-20265/A/PCT
; CURRENT APPLICATION NUMBER: US/09/338,132
; CURRENT FILING DATE: 1999-06-22
; EARLIER APPLICATION NUMBER: 08/860,150
; EARLIER FILING DATE: 1997-06-19
; EARLIER APPLICATION NUMBER: PCT/EP95/05052
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: 94810746.1
; EARLIER FILING DATE: 1994-12-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-338-132-9

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred.No.52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3209 AAATGGAAAGCAGAAA 3224
Db 16 AAAAGGAAAGCAGAAA 1

RESULT 79
US-09-071-845-1659
; Sequence 1659, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
```



```
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6407
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3494 AATTGCTCTAATAGA 3509
|||::||:|:|:|
Db 2 AAUUGCUCUAUUGA 17
```

```
RESULT 83
US-09-866-108A-7201
; Sequence 7201, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-866-108A-7202
```

```
US-09-866-108A-7201
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 322 GACCTTGCTATGAGC 337
|||||
Db 2 GACCTTGCGATGAGC 17
```

```
RESULT 84
US-09-866-108A-7202
; Sequence 7202, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7202
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 322 GACCTTGCTATGAGC 337
|||||
Db 1 GACCTTGCGATGAGC 16
```

```
RESULT 85
US-09-866-108A-8467
; Sequence 8467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
```

```

RESULT 86
US-09-866-108A-8468
; Sequence 8468, Application US/09866108A
; Patent No. 6586188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSION
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,451
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 242623.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,351
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006061
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006061

```

RESULT 88
US-09-212-771-18/c
; Sequence 18, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:

```
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-212-771-18

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAAGCAGCGGAGGAG 88
Db 18 GAAGCAGCGGAGGAG 3

RESULT 89
US-09-205-143-19
; Sequence 19, Application US/09205143
; Patent No. 6107091
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-16 EXPRESSION
; FILE REFERENCE: RTS-0032
; CURRENT APPLICATION NUMBER: US/09/205,143
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-143-19

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1532 GCCCAACGACGACG 1547
Db 3 GCCCAACGACGACG 18

RESULT 90
US-08-068-747-6/c
; Sequence 6, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Houseman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/068,747
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-6

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 91
US-08-068-747-11
; Sequence 11, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Houseman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
```



```
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-11

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30

RESULT 92
US-08-639A-30/c
; Sequence 30, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-639A-30

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 93
US-09-135-994-4/c
; Sequence 4, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Renum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
```

```
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-994-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 94
US-09-684-843A-4/c
; Sequence 4, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Renum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-684-843A-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 95
US-08-390-850-438/c
; Sequence 438, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
```

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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 438:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-390-850-438

```

```

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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Qy 560 AATGAAGTACCAACAT 576
Db 17 ACTGAGTGACCAACAT 1

```

```

RESULT 96
US-08-390-850-452/c
; Sequence 452, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994

```

```

; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-390-850-452

```

```

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1432 GCAGCAGCAACAGCAGC 1448
Db 17 GCAGCATCAACAGCATC 1

```

```

RESULT 97
US-08-373-124A-1513
; Sequence 1513, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1513:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1513

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 62;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 3008 GATTCTTTATTGAGAC 3024
Db 1 GAUUCUUUCUUGAACAC 17

RESULT 98

US-08-158-352-2/c
Sequence 2, Application US/08158352
Patent No. 5700922
GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
TITLE OF INVENTION: PNA-DNA-PNA Chimeric
TITLE OF INVENTION: Macromolecules
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESS: No. 5700922r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158.352
FILING DATE: herewith
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US92/11339
FILING DATE: December 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-1236
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-158-352-2

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 CGGAATTCAGCGAGAA 54
Db 17 CTGAATTCAGCGAGAA 1

RESULT 99

US-08-435-634-438/c
Sequence 438, Application US/08435634
Patent No. 5731295
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggan, James
APPLICANT: Gustofson, John
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
NUMBER OF SEQUENCES: 1151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435.634
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,850
FILING DATE: February 17, 1995
APPLICATION NUMBER: 08/354,920
FILING DATE: December 13, 1994
APPLICATION NUMBER: 08/152,487
FILING DATE: No. 5731295ember 12, 1993
APPLICATION NUMBER: 07/989,848
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 438:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-634-438

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 560 AATGAAGTACCAACAT 576
Db 17 ACTGAAGTACCAACAT 1

RESULT 100

US-08-435-634-452/c
Sequence 452, Application US/08435634
Patent No. 5731295
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
APPLICANT: Pavco, Pamela

```
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435.634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-452

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1432 GCAGCAGCAACAGCAGC 1448
Db 17 GCAGCATCAACAGCATC 1

RESULT 101
US-08-758-306-903/c
; Sequence 903, Application US/08/758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

```
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 903:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-903

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 252 TTGGGGGAGATCTCTCT 268
Db 17 TTGGGGGAGATCTCGCT 1

RESULT 102
US-08-435-628-1513
; Sequence 1513, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
```

; FILING DATE: 05-MAY-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/373,124
 ; FILING DATE: January 13, 1995
 ; APPLICATION NUMBER: 08/245,466
 ; FILING DATE: May 18, 1994
 ; APPLICATION NUMBER: 08/192,943
 ; FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: 07/987,132
 ; FILING DATE: December 7, 1992
 ; APPLICATION NUMBER: 07/936,422
 ; FILING DATE: August 26, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 209/035
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 1513:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-435-628-1513

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 47.1%; Pred. No. 62;
 Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 3008 GATCTTTATTGACAC 3024
 DB 1 GAUCUUCUUGAACAC 17

RESULT 103
 US-09-050-159-45
 ; Sequence 45, Application US/09050159A
 ; Patent No. 6197505
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6197505berg, Leif T
 ; APPLICANT: Andersson, Maria K
 ; APPLICANT: Linstrom, Per H
 ; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
 ; FILE REFERENCE: 1248/1D042
 ; CURRENT APPLICATION NUMBER: US/09/050,159A
 ; CURRENT FILING DATE: 1998-03-27
 ; EARLIER APPLICATION NUMBER: 60/042,930
 ; EARLIER FILING DATE: 1987-04-03
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 45
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
 ; US-09-050-159-45

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 62;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
 DB 1 CGGCGGCAGCAGCAACA 17

RESULT 104

US-09-050-159-51
 ; Sequence 51, Application US/09050159A
 ; Patent No. 6197505
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6197505berg, Leif T
 ; APPLICANT: Andersson, Maria K
 ; APPLICANT: Linstrom, Per H
 ; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
 ; FILE REFERENCE: 1248/1D042
 ; CURRENT APPLICATION NUMBER: US/09/050,159A
 ; CURRENT FILING DATE: 1998-03-27
 ; EARLIER APPLICATION NUMBER: 60/042,930
 ; EARLIER FILING DATE: 1987-04-03
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 51
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
 ; US-09-050-159-51

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 62;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
 DB 1 CGGCGGCAGCAGCAACA 17

RESULT 105
 US-09-108-911-2/c
 ; Sequence 2, Application US/09108911
 ; Patent No. 6277603
 ; GENERAL INFORMATION:
 ; APPLICANT: Cook, Phillip Dan
 ; TITLE OF INVENTION: PNA-DNA-PNA Chimeric Macromolecules
 ; FILE REFERENCE: ISIS3102
 ; CURRENT APPLICATION NUMBER: US/09/108,911
 ; CURRENT FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 08/877,317
 ; PRIOR FILING DATE: 1997-06-17
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Antisense Sequence
 ; US-09-108-911-2

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 62;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CGGAAATTCAGCGAGAA 54
 DB 17 CTGAAATGCGCGAGAA 1

RESULT 106
 US-08-584-040-1480
 ; Sequence 1480, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Stinchcomb, Dan T.


```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1869:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1869

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 430 GGAGCCAGGAGAGCTC 446
Db 17 GGAGCCAGGAGAGCTC 1

RESULT 109
US-08-584-040-1870/c
; Sequence 1870, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2571:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2571

Query Match
Best Local Similarity 47.1%; Score 13.8; DB 1; Length 17;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

; INFORMATION FOR SEQ ID NO: 1870:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1870

Query Match
Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 429 AGGAGCCAGGAGAGCT 445
Db 17 AGGAGCCAGGAGAGCT 1

RESULT 110
US-08-584-040-2571
; Sequence 2571, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2571:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2571

Query Match
Best Local Similarity 47.1%; Score 13.8; DB 1; Length 17;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
```

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QY      224 TCATTCTTGATCA 240
      :||: :||: :||: :||:
Db      1 UCAUGUCUUAUUCAA 17

RESULT 111
US-08-584-040-4365/c
; Sequence 4365, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4365

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1509 AACAGCAGCAGGTCA 1525
      ||||| ||||| |||||
Db      17 AACAGGAGGAGGTCA 1

RESULT 112
US-08-584-040-7233
; Sequence 7233, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James

```

```

; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7233

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2166 TGCTACTCTCAGGG 2182
      :||: :||: :||:
Db      1 UGUCUGUCUCACAGG 17

RESULT 113
US-08-584-040-7234
; Sequence 7234, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700

```



```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7234

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 62;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2167 GTCTACTTCTCAGCGGA 2183
|:|:|:|:|:|:|
Db 1 GUCUGUCUCACAGGA 17

RESULT 114
US-08-584-040-7450
; Sequence 7450, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040

```

```

; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7450:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7450

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 62;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2757 GTCTGAATCTCAGACCC 2773
|:|:|:|:|:|:|
Db 1 GCGUGACUCACAGACCC 17

RESULT 115
US-09-612-555-13/c
; Sequence 13, Application US/09612555
; Patent No. 6528257
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vishva M
; APPLICANT: Ganesan, Kallanman
; TITLE OF INVENTION: A Method for the Simultaneous Monitoring of Individual
; TITLE OF INVENTION: Mutants in Mixed Populations
; FILE REFERENCE: Method for Simultaneous Monitoring
; CURRENT APPLICATION NUMBER: US/09/612,555
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tag1 adapters
; US-09-612-555-13

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2753 AGGGCTCTGAATCTCAG 2769
|:|:|:|:|:|:|
Db 17 AGGGCTCTGAGGCTCAG 1

RESULT 116
US-09-371-772B-25
; Sequence 25, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

```


; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1095

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 62;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCTTGATATCAA 240
| : : : : : : : : : : : : : : : : : :
Db 1 UCAUGUCUUGAUUUCAA 17

RESULT 121
US-09-371-772B-2132/c
; Sequence 2132, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2132

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1509 AACAGCAGCAGAGCTCA 1525
| : : : : : : : : : : : : : : : : : :
Db 17 AACAGGAGGAGAGCTCA 1

RESULT 122
US-09-371-772B-3256
; Sequence 3256, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3256

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 62;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCGAATCTCAGACCC 2773
| : : : : : : : : : : : : : : : : : :
Db 1 GGCUGACUCUCAGACCC 17

RESULT 123
US-09-371-772B-4212
; Sequence 4212, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4212

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGCTACTTCTCTACGG 2181
| : : : : : : : : : : : : : : : : : :
Db 1 CUGUCUGUCUCACAG 17

RESULT 124
US-09-371-772B-6437
; Sequence 6437, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6437

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 62;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGAGC 1111
||: ||||| |||||
Db 1 CAUGCAGCCACUGAGC 17

RESULT 125
US-09-827-998-524
; Sequence 524, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMPRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 524
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-524

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAAATGACCCCAAGAGAA 489
||||| ||||| |||||
Db 1 CAAAGGAACCAAGAGAA 17

RESULT 126
US-09-866-108A-664
; Sequence 664, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 664
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-664

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAAGCCAGAGGA 680
||||| ||||| |||||
Db 1 TCAGCAAAGCCAGAGAA 17

RESULT 127
US-09-866-108A-665
; Sequence 665, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-665

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CAGCAAGCCAGAGAG 681
Db 1 CAGCAAGCCAGAGAG 17

RESULT 128

US-09-866-108A-1872
; Sequence 1872, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1873
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1873

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1022 CCCTCCTCTGCTGGACC 1038
Db 1 CCCTCCTGAGCTGGACC 17

RESULT 129

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1022 CCCTCCTCTGCTGGACC 1038
Db 1 CCCTCCTGAGCTGGACC 17

US-09-866-108A-1873
; Sequence 1873, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1873
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1873

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1023 CCTCCTCTGCTGGACCA 1039
Db 1 CCTCCTGAGCTGGACCA 17

RESULT 130

US-09-866-108A-2733
; Sequence 2733, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

```
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2733
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2733

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
DB 1 CTACGACGCTGAGGCC 17

RESULT 131
US-09-866-108A-7802
; Sequence 7802, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7803

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
DB 1 AGCAGCAGCAGCAGCAA 17
```

```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7802
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7802

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
DB 1 CAGCAGCAGCAGCAGCA 17

RESULT 132
US-09-866-108A-7803
; Sequence 7803, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7803

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
DB 1 AGCAGCAGCAGCAGCAA 17
```

```
RESULT 133
US-09-866-108A-10247
; Sequence 10247, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10247

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1187 TCAGCCAGGTGGGCA 1203
Db 1 TCAGCCAAAGTGGGCA 17

RESULT 134
US-09-866-108A-10747
; Sequence 10747, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10747
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10747

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RESULT 135
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; Sequence 25, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-25

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; Sequence 2132, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-2132

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
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; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
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; SOFTWARE: PatentIn version 3.0
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; TYPE: RNA
; ORGANISM: Mus musculus

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3.607 Million cell updates/sec

Title: US-10-698-070-1

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Listing first 496 summaries

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c 153	19	0.5	19	1	US-10-698-070-10	Sequence 10, Appl	c 226	17.4	0.5	21	1	US-10-012-137A-105	Sequence 105, App
c 154	19	0.5	19	1	US-10-922-544-26	Sequence 26, Appl	c 227	17.4	0.5	21	1	US-10-012-752A-105	Sequence 105, App
c 155	19	0.5	19	1	US-10-922-544-200	Sequence 200, App	c 228	17.4	0.5	21	1	US-10-012-754A-105	Sequence 105, App
c 156	19	0.5	20	1	US-10-289-762-6476	Sequence 6476, App	c 229	17.4	0.5	21	1	US-10-013-910A-105	Sequence 105, App
c 157	19	0.5	23	1	US-10-728-131-124	Sequence 124, App	c 230	17.4	0.5	21	1	US-10-013-911A-105	Sequence 105, App
c 158	18.8	0.5	22	1	US-09-888-615-120	Sequence 120, App	c 231	17.4	0.5	21	1	US-10-013-912A-105	Sequence 105, App
c 159	18.8	0.5	22	1	US-10-295-942-16	Sequence 16, Appl	c 232	17.4	0.5	21	1	US-10-015-653A-105	Sequence 105, App
c 160	18.8	0.5	23	1	US-10-177-308-24	Sequence 24, Appl	c 233	17.4	0.5	21	1	US-10-012-101B-105	Sequence 105, App
c 161	18.8	0.5	23	1	US-10-853-665-24	Sequence 24, Appl	c 234	17.4	0.5	21	1	US-10-012-101B-105	Sequence 105, App
c 162	18.4	0.5	20	1	US-09-861-893-15	Sequence 15, Appl	c 235	17.4	0.5	21	1	US-10-015-480A-105	Sequence 105, App
c 163	18.4	0.5	20	1	US-09-563-728A-6	Sequence 6, Appl	c 236	17.4	0.5	21	1	US-10-015-715A-105	Sequence 105, App
c 164	18.4	0.5	20	1	US-09-563-728A-15	Sequence 15, Appl	c 237	17.4	0.5	21	1	US-10-012-237A-105	Sequence 105, App
c 165	18.4	0.5	20	1	US-10-145-493B-51	Sequence 51, Appl	c 238	17.4	0.5	21	1	US-10-013-906A-105	Sequence 105, App
c 166	18.4	0.5	20	1	US-10-315-962-46	Sequence 46, Appl	c 239	17.4	0.5	21	1	US-10-015-388A-105	Sequence 105, App
c 167	18.4	0.5	20	1	US-10-296-263-15	Sequence 15, Appl	c 240	17.4	0.5	21	1	US-10-012-753A-105	Sequence 105, App
c 168	18.4	0.5	21	1	US-10-751-736-8810	Sequence 8810, App	c 241	17.4	0.5	21	1	US-10-015-385A-105	Sequence 105, App
c 169	18	0.5	18	1	US-10-054-387-48	Sequence 48, Appl	c 242	17.4	0.5	21	1	US-10-007-236A-105	Sequence 105, App
c 170	18	0.5	18	1	US-10-321-039-541	Sequence 541, App	c 243	17.4	0.5	21	1	US-10-015-519A-105	Sequence 105, App
c 171	18	0.5	18	1	US-10-360-854-11	Sequence 11, Appl	c 244	17.4	0.5	21	1	US-10-013-915A-105	Sequence 105, App
c 172	18	0.5	18	1	US-10-479-472A-11	Sequence 11, Appl	c 245	17.4	0.5	21	1	US-10-015-394A-105	Sequence 105, App
c 173	18	0.5	20	1	US-09-888-361-152	Sequence 152, App	c 246	17.4	0.5	21	1	US-10-015-390A-105	Sequence 105, App
c 174	18	0.5	20	1	US-10-705-715-152	Sequence 152, App	c 247	17.4	0.5	21	1	US-10-006-746A-105	Sequence 105, App
c 175	18	0.5	21	1	US-10-479-510-11	Sequence 11, Appl	c 248	17.4	0.5	21	1	US-10-226-254A-105	Sequence 105, App
c 176	17.8	0.5	21	1	US-10-380-195A-15	Sequence 15, Appl	c 249	17.4	0.5	21	1	US-10-011-795A-105	Sequence 105, App
c 177	17.8	0.5	21	1	US-10-751-736-11486	Sequence 11486, A	c 250	17.4	0.5	21	1	US-10-012-231A-105	Sequence 105, App
c 178	17.8	0.5	21	1	US-10-751-736-19232	Sequence 19232, A	c 251	17.4	0.5	21	1	US-10-015-395A-105	Sequence 105, App
c 179	17.8	0.5	21	1	US-10-764-730-11	Sequence 11, Appl	c 252	17.4	0.5	21	1	US-10-751-736-8809	Sequence 8809, App

253	17.4	0.5	21	1	US-10-751-736-39221	Sequence 39221, A	326	15	0.4	18	1	US-10-498-848-6	Sequence 6, Appli
254	17.4	0.5	21	1	US-10-012-149A-105	Sequence 105, App	c 337	14.8	0.4	18	1	US-09-280-030-28	Sequence 28, Appl
255	17.4	0.5	21	1	US-10-730-771-62	Sequence 62, Appl	328	14.8	0.4	18	1	US-09-426-548-43	Sequence 43, Appl
256	17	0.5	17	1	US-10-494-343-167	Sequence 167, App	329	14.8	0.4	18	1	US-09-861-893-11	Sequence 11, Appl
257	17	0.5	17	1	US-10-494-343-168	Sequence 168, App	330	14.8	0.4	18	1	US-10-272-865-14	Sequence 14, Appl
258	17	0.5	17	1	US-10-494-343-169	Sequence 169, App	c 331	14.8	0.4	18	1	US-10-272-865-34	Sequence 34, Appl
259	17	0.5	17	1	US-10-494-343-170	Sequence 170, App	332	14.8	0.4	18	1	US-10-422-671-14	Sequence 14, Appl
260	17	0.5	17	1	US-10-494-343-171	Sequence 171, App	c 333	14.8	0.4	18	1	US-10-422-671-34	Sequence 34, Appl
261	17	0.5	17	1	US-10-494-343-172	Sequence 172, App	334	14.8	0.4	18	1	US-10-349-607-60	Sequence 60, Appl
262	17	0.5	18	1	US-09-933-638A-9	Sequence 9, Appli	c 335	14.8	0.4	18	1	US-10-317-444-47	Sequence 47, App
263	17	0.5	18	1	US-09-933-638A-10	Sequence 10, Appl	336	14.8	0.4	18	1	US-10-317-444-48	Sequence 48, App
264	17	0.5	18	1	US-10-194-584-1	Sequence 1, Appli	c 337	14.8	0.4	18	1	US-10-317-444-49	Sequence 49, App
265	17	0.5	18	1	US-10-194-584-2	Sequence 2, Appli	338	14.8	0.4	18	1	US-10-317-444-50	Sequence 50, App
266	17	0.5	18	1	US-10-436-231-1	Sequence 1, Appli	339	14.8	0.4	18	1	US-10-138-674-2184	Sequence 2184, Ap
267	17	0.5	18	1	US-10-436-231-2	Sequence 2, Appli	340	14.8	0.4	18	1	US-10-287-949A-2184	Sequence 2184, Ap
268	16.8	0.4	20	1	US-09-948-002-35	Sequence 35, Appl	341	14.8	0.4	18	1	US-10-702-817-24	Sequence 24, Appl
269	16.8	0.4	20	1	US-09-920-032-22	Sequence 22, Appl	342	14.8	0.4	18	1	US-10-702-817-25	Sequence 25, Appl
270	16.8	0.4	20	1	US-10-060-301-43	Sequence 43, Appl	343	14.8	0.4	18	1	US-10-296-263-11	Sequence 11, Appl
271	16.8	0.4	20	1	US-10-147-196-22	Sequence 22, Appl	344	14.4	0.4	17	1	US-09-866-108-7201	Sequence 7201, Ap
272	16.8	0.4	20	1	US-10-388-263-554	Sequence 554, App	345	14.4	0.4	17	1	US-09-866-108-7202	Sequence 7202, Ap
273	16.8	0.4	20	1	US-10-210-479-79	Sequence 79, Appl	346	14.4	0.4	17	1	US-09-866-108-8467	Sequence 8467, Ap
274	16.8	0.4	20	1	US-10-633-163-35	Sequence 35, Appl	347	14.4	0.4	17	1	US-09-866-108-8468	Sequence 8468, Ap
275	16.8	0.4	20	1	US-10-712-795-22	Sequence 22, Appl	348	14.4	0.4	17	1	US-09-780-533A-234	Sequence 234, App
276	16.8	0.4	20	1	US-10-920-612-22	Sequence 22, Appl	349	14.4	0.4	17	1	US-09-780-533A-235	Sequence 235, App
277	16.8	0.4	20	1	US-10-831-901A-11559	Sequence 11559, A	350	14.4	0.4	17	1	US-09-848-754A-1158	Sequence 1158, Ap
278	16.8	0.4	20	1	US-09-906-419-91	Sequence 91, Appl	351	14.4	0.4	17	1	US-09-848-754A-3275	Sequence 3275, Ap
279	16.8	0.4	21	1	US-10-119-136-91	Sequence 91, Appl	c 352	14.4	0.4	17	1	US-09-827-395A-505	Sequence 505, App
280	16.8	0.4	21	1	US-10-119-136-91	Sequence 91, Appl	c 353	14.4	0.4	17	1	US-09-827-395A-765	Sequence 765, App
281	16.8	0.4	21	1	US-10-380-195A-2	Sequence 2, Appli	c 354	14.4	0.4	17	1	US-09-742-818-383	Sequence 383, App
282	16.8	0.4	21	1	US-10-380-195A-46	Sequence 46, Appl	355	14.4	0.4	17	1	US-09-792-818-524	Sequence 524, App
283	16.8	0.4	21	1	US-10-751-736-10540	Sequence 10540, A	356	14.4	0.4	17	1	US-09-817-879-2661	Sequence 2661, Ap
284	16.8	0.4	21	1	US-10-751-736-10541	Sequence 10541, A	c 357	14.4	0.4	17	1	US-10-061-201-574	Sequence 574, App
285	16.8	0.4	21	1	US-10-751-736-10541	Sequence 10541, A	358	14.4	0.4	17	1	US-10-061-201-575	Sequence 575, App
286	16.8	0.4	21	1	US-10-751-736-18508	Sequence 18508, A	359	14.4	0.4	17	1	US-10-430-882-505	Sequence 505, App
287	16.8	0.4	21	1	US-10-751-736-18509	Sequence 18509, A	c 360	14.4	0.4	17	1	US-10-430-882-765	Sequence 765, App
288	16.8	0.4	21	1	US-10-751-736-49304	Sequence 49304, A	c 361	14.4	0.4	17	1	US-10-138-674-1755	Sequence 1755, Ap
289	16.8	0.4	21	1	US-10-847-918-3217	Sequence 3217, Ap	362	14.4	0.4	17	1	US-10-138-674-6407	Sequence 6407, Ap
290	16.4	0.4	18	1	US-10-181-603-11	Sequence 11, Appl	363	14.4	0.4	17	1	US-10-138-674-8510	Sequence 8510, Ap
291	16.4	0.4	18	1	US-10-730-771-206	Sequence 206, App	364	14.4	0.4	17	1	US-10-287-949A-1755	Sequence 1755, Ap
292	16.4	0.4	20	1	US-09-865-866-61	Sequence 61, Appl	365	14.4	0.4	17	1	US-10-287-949A-6407	Sequence 6407, Ap
293	16.4	0.4	20	1	US-10-186-157-17	Sequence 17, Appl	366	14.4	0.4	17	1	US-10-287-949A-8510	Sequence 8510, Ap
294	16.4	0.4	20	1	US-10-380-126-39	Sequence 39, Appl	367	14.4	0.4	17	1	US-10-712-672-2609	Sequence 2609, Ap
295	16.4	0.4	20	1	US-10-831-901A-11557	Sequence 11557, A	c 368	14.4	0.4	17	1	US-10-669-841-5254	Sequence 5254, Ap
296	16.4	0.4	20	1	US-10-831-901A-11558	Sequence 11558, A	c 369	14.4	0.4	17	1	US-10-723-361-7201	Sequence 7201, Ap
297	16.4	0.4	20	1	US-10-643-038-61	Sequence 61, Appl	370	14.4	0.4	17	1	US-10-723-361-7202	Sequence 7202, Ap
298	16	0.4	17	1	US-09-792-818-608	Sequence 608, App	371	14.4	0.4	17	1	US-10-723-361-8467	Sequence 8467, Ap
299	16	0.4	17	1	US-10-494-343-166	Sequence 166, App	372	14.4	0.4	17	1	US-10-723-361-8468	Sequence 8468, Ap
300	16	0.4	17	1	US-10-494-343-173	Sequence 173, App	373	14.4	0.4	17	1	US-10-712-633-3573	Sequence 3573, Ap
301	16	0.4	18	1	US-10-436-231-5	Sequence 5, Appli	374	14.4	0.4	17	1	US-10-494-343-175	Sequence 175, App
302	16	0.4	18	1	US-10-436-231-6	Sequence 6, Appli	375	14.4	0.4	18	1	US-10-388-263-343	Sequence 343, App
303	16	0.4	20	1	US-10-148-835-86	Sequence 86, Appl	c 376	14.4	0.4	18	1	US-10-468-655-42	Sequence 42, Appl
304	16	0.4	20	1	US-10-704-263-201	Sequence 201, App	c 377	14.4	0.4	18	1	US-10-467-019-7	Sequence 7, Appli
305	15.8	0.4	19	1	US-10-923-329-8	Sequence 8, Appli	c 378	14.4	0.4	17	1	US-10-376-770-220	Sequence 220, App
306	15.8	0.4	19	1	US-10-923-329-204	Sequence 204, App	c 379	14	0.4	17	1	US-10-661-165-220	Sequence 220, App
307	15.6	0.4	30	1	US-10-215-432-43	Sequence 43, Appl	c 380	14	0.4	17	1	US-10-494-343-164	Sequence 164, App
308	15.4	0.4	17	1	US-09-848-754A-175	Sequence 175, App	381	14	0.4	17	1	US-10-011-993-35	Sequence 35, Appl
309	15.4	0.4	17	1	US-09-792-818-360	Sequence 360, App	c 382	14	0.4	30	1	US-10-357-322-4	Sequence 4, Appli
310	15.4	0.4	17	1	US-09-792-818-361	Sequence 361, App	c 383	14	0.4	30	1	US-09-179-5368-90	Sequence 90, Appl
311	15.4	0.4	17	1	US-09-792-818-362	Sequence 362, App	384	13.8	0.4	17	1	US-09-866-108-664	Sequence 664, App
312	15.4	0.4	17	1	US-09-792-818-363	Sequence 363, App	385	13.8	0.4	17	1	US-09-866-108-665	Sequence 665, App
313	15.4	0.4	17	1	US-09-792-818-609	Sequence 609, App	386	13.8	0.4	17	1	US-09-866-108-1872	Sequence 1872, Ap
314	15.4	0.4	17	1	US-10-138-674-2491	Sequence 2491, Ap	387	13.8	0.4	17	1	US-09-866-108-1873	Sequence 1873, Ap
315	15.4	0.4	17	1	US-10-287-949A-2491	Sequence 2491, Ap	388	13.8	0.4	17	1	US-09-866-108-2733	Sequence 2733, Ap
316	15.4	0.4	17	1	US-10-494-343-174	Sequence 174, App	389	13.8	0.4	17	1	US-09-866-108-7802	Sequence 7802, Ap
317	15.4	0.4	18	1	US-09-968-122-9	Sequence 9, Appli	390	13.8	0.4	17	1	US-09-866-108-7803	Sequence 7803, Ap
318	15.4	0.4	18	1	US-10-432-422-27	Sequence 27, Appl	391	13.8	0.4	17	1	US-09-866-108-10247	Sequence 10247, A
319	15.4	0.4	19	1	US-10-444-925-183	Sequence 183, App	392	13.8	0.4	17	1	US-09-866-108-10747	Sequence 10747, A
320	15.4	0.4	19	1	US-10-883-218-297	Sequence 297, App	393	13.8	0.4	17	1	US-09-827-998-524	Sequence 524, App
321	15.4	0.4	19	1	US-10-883-218-699	Sequence 699, App	394	13.8	0.4	17	1	US-09-872-462-243	Sequence 243, App
322	15.4	0.4	19	1	US-10-893-010-39	Sequence 39, Appl	395	13.8	0.4	17	1	US-09-872-462-244	Sequence 244, App
323	15.4	0.4	19	1	US-10-893-010-278	Sequence 278, App	396	13.8	0.4	17	1	US-09-872-462-245	Sequence 245, App
324	15	0.4	17	1	US-09-880-313A-228	Sequence 228, App	397	13.8	0.4	17	1	US-09-872-462-246	Sequence 246, App
325	15	0.4	17	1	US-10-494-343-165	Sequence 165, App	398	13.8	0.4	17	1		

; Sequence 4, Application US/10357322
; Publication No. US20030180768A1
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/10/357,322
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/684,843
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-322-4

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 3
US-09-801-274-1530
; Sequence 1530, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1530
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1530

Query Match 0.8%; Score 29; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 22;
Matches 29; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

Qy 1561 GCACGACGAGCAGCAACCAACGACGACAA 1591
Db 1 GCACGACGAGCAGCAGCAACCAACGACGACAA 31

RESULT 4
US-10-215-432-43
; Sequence 43, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; TITLE OF INVENTION: prevention and treatment of Huntington's disease

; FILE REFERENCE: NaPro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-43

Query Match 0.8%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 23;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCTGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 5
US-10-479-546-11/c
; Sequence 11, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-479-546-11

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 CTCCTGCCAACGACGACGCCCAATGG 210
Db 28 CTCCTGCCAACGACGACGCCCAATGG 1

RESULT 6
US-10-698-070-5/c
; Sequence 5, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyama, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 28
; TYPE: DNA

; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-5

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 AACAGGTAGTTAACTATCTCTGCGCAA 192
DB 28 AACAGGTAGTTAACTATCTCTGCGCAA 1

RESULT 7
US-10-698-070-6/c
; Sequence 6, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiya, Takafumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-6

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGCGAGAAGATCGCGTGCACAAT 70
DB 28 ATTGAGCGAGAAGATCGCGTGCACAAT 1

RESULT 8
US-10-418-182-174
; Sequence 174, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-174

Query Match 0.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1418 CAGCAGCAGCAGCAGCAGCAGCAACAG 1444
|||||

DB 1 CAGCAGCAGCAGCAGCAGCAGCAACAG 27

RESULT 9
US-10-698-070-7
; Sequence 7, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiya, Takafumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-7

Query Match 0.7%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGCGAGAAGATCGCGTGCACA 69
DB 1 ATTGAGCGAGAAGATCGCGTGCACA 27
|||||

RESULT 10
US-10-336-638-152
; Sequence 152, Application US/10336638
; Publication No. US20030170699A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/10/336,638
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/304,232
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/084,641
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-10-336-638-152

Query Match 0.7%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 49;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGCAGCAGCA 1428
DB 1 CAGCAGCAACAGCAGCAGCAGCAGCA 29
|||||

RESULT 11


```

US-10-956-157-111930
; Sequence 111930, Application US/10956157
; Publication NO. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 111930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111930

```

Query Match	0.7%	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%	Pred. No. 38;		
Matches 25;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 3347 AGAACTGTGGTGTCAATGTGTAATT 3371
|||
Db 1 AGAACTGTGGTGTCAATGTGTAATT 25

```

RESULT 12
US-10-956-157-111931
; Sequence 111931, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111931

```

Query Match	0.7;	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0;	Pred. No. 38;		
Matches 25;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

QY	3346	CAGAACTGTGGTGTCAATGTGTAAT	3370
Db	1	CAGAACTGTGGTGTCAATGTGTAAT	25

```

RESULT 13
US-10-956-157-111932
; Sequence 111932, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111932
; LENGTH: 25

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*
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111932

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels

Qy 3178 CAGGTGGACTACATGAAGATAACAT 3202
Db 1 CAGGTGGACTACATGAAGATAACAT 25

```

RESULT 14
US-10-956-157-111933
; Sequence 111933, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111933

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 3348 GAAC TGTGGTGTCAATGTGTAATTA 3372
|||||
Db 1 GAAC TGTGGTGTCAATGTGTAATTA 25

```

RESULT 15
US-10-956-157-111934
; Sequence 111934, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111934

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No.38;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 3349 AACTGTGGTGTCAATGTGTAATTAA 3373
|||||
Db 1 AACTGTGGTGTCAATGTGTAATTAA 25

RESULT 16
US-10-956-157-111935

```
; Sequence 111935, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111935
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111935

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3350 ACTGTGGTCAATGTAATAAT 3374
      |||||
Db 1 ACTGTGGTCAATGTAATAAT 25

RESULT 17
US-10-956-157-111936
; Sequence 111936, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111936
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111936

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3177 TCAGTGGACTACATGAAGATAACA 3201
      |||||
Db 1 TCAGTGGACTACATGAAGATAACA 25

RESULT 18
US-10-956-157-111937
; Sequence 111937, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111937
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Probe Sequence
US-10-956-157-111937

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3474 TTCCAAGCAACAACCTCCTTAATT 3498
      |||||
Db 1 TTCCAAGCAACAACCTCCTTAATT 25

RESULT 19
US-10-956-157-111938
; Sequence 111938, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111938
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111938

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3473 GTTCCAAGCAACAACCTCCTTAATT 3497
      |||||
Db 1 GTTCCAAGCAACAACCTCCTTAATT 25

RESULT 20
US-10-956-157-111939
; Sequence 111939, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111939

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3165 AACTGTTGATGTTTCAGTGGACTAC 3189
      |||||
Db 1 AACTGTTGATGTTTCAGTGGACTAC 25

RESULT 21
US-10-956-157-111940
; Sequence 111940, Application US/10956157
```

Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2.
; SEQ ID NO 111940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111940

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3724 GGGATGCTGCTAGTGAATTAAC 3748
Db 1 GGGATGCTGCTAGTGAATTAAC 25

RESULT 22

US-10-956-157-111941
; Sequence 111941, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111941

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3517 GGTTAATCTTCCATTGTGCTTT 3541
Db 1 GGTTAATCTTCCATTGTGCTTT 25

RESULT 23

US-10-956-157-111942
; Sequence 111942, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111942
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence

US-10-956-157-111942

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3325 ACAGTATCCAATTATCCAAACAGA 3349
Db 1 ACAGTATCCAATTATCCAAACAGA 25

RESULT 24

US-10-956-157-111943
; Sequence 111943, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111943

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3723 TGGGATGCTGCTAGTGAATTA 3747
Db 1 TGGGATGCTGCTAGTGAATTA 25

RESULT 25

US-10-956-157-111944
; Sequence 111944, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111944

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3726 GATGCTGCTAGTGAATTAACAA 3750
Db 1 GATGCTGCTAGTGAATTAACAA 25

RESULT 26

US-10-956-157-111945
; Sequence 111945, Application US/10956157
; Publication No. US20050118625A1

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111945

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3725 GGATGCTGTGCTAGTGATTAACA 3749
Db 1 GGATGCTGTGCTAGTGATTAACA 25

RESULT 27
US-10-956-157-111946
; Sequence 111946, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111946

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3725 GGATGCTGTGCTAGTGATTAACA 3749
Db 1 GGATGCTGTGCTAGTGATTAACA 25

RESULT 28
US-10-956-157-111947
; Sequence 111947, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111947
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111947

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3576 GAAATGTTATAGGTTTGTGGAGT 3600
Db 1 GAAATGTTATAGGTTTGTGGAGT 25

RESULT 29
US-10-956-157-111948
; Sequence 111948, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111948

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3727 ATGCTGTGCTAGTGATTAACAAA 3751
Db 1 ATGCTGTGCTAGTGATTAACAAA 25

RESULT 30
US-10-956-157-111949
; Sequence 111949, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111949

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3345 ACAGAACTGGTGTCATGTGTAA 3369
Db 1 ACAGAACTGGTGTCATGTGTAA 25

RESULT 31
US-10-956-157-111950
; Sequence 111950, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111945

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3575 TGAATGTTATAGGTTTGTGGAG 3599
Db 1 TGAATGTTATAGGTTTGTGGAG 25

RESULT 29
US-10-956-157-111948
; Sequence 111948, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111948

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3727 ATGCTGTGCTAGTGATTAACAAA 3751
Db 1 ATGCTGTGCTAGTGATTAACAAA 25

RESULT 30
US-10-956-157-111949
; Sequence 111949, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111949

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3345 ACAGAACTGGTGTCATGTGTAA 3369
Db 1 ACAGAACTGGTGTCATGTGTAA 25

RESULT 31
US-10-956-157-111950
; Sequence 111950, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111950

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3344 AACAGAACTGGTGTCAATGTGTA 3368
Db 1 AACAGAACTGGTGTCAATGTGTA 25

RESULT 32
US-10-956-157-111951
; Sequence 111951, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111951

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3344 AACAGAACTGGTGTCAATGTGTA 3368
Db 1 AACAGAACTGGTGTCAATGTGTA 25

RESULT 32
US-10-956-157-111951
; Sequence 111951, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111951

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3176 TTCAGGTGGACTACATGAAGATAAC 3200
Db 1 TTCAGGTGGACTACATGAAGATAAC 25

RESULT 33
US-10-956-157-111952
; Sequence 111952, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111952
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Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3175 GTTCAGGTGGACTACATGAAGATAA 3199
Db 1 GTTCAGGTGGACTACATGAAGATAA 25

RESULT 34
US-10-956-157-111953
; Sequence 111953, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111953

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 TGTTCAAGTGGACTACATGAAGATA 3198
Db 1 TGTTCAAGTGGACTACATGAAGATA 25

RESULT 35
US-10-956-157-122224
; Sequence 122224, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-122224

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3290 ATTGGGATCACTTTCCCTGCTCTAA 3314
Db 1 ATTGGGATCACTTTCCCTGCTCTAA 25

RESULT 36
US-10-956-157-136916
; Sequence 136916, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136916
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-136916

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3721 AGTGGGATGCTGTCTAGTGATTA 3745
Db 1 AGTGGGATGCTGTCTAGTGATTA 25

RESULT 37
US-10-956-157-137818
; Sequence 137818, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137818
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-137818

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3224 AGTAACTGCAGTGATGAACATTTTG 3248
Db 1 AGTAACTGCAGTGATGAACATTTTG 25

RESULT 38
US-10-956-157-141744
; Sequence 141744, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-141744

Query Match      0.7%; Score 25; DB 1; Length 25;
```

```
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3347 AGAAGCTGTGTGTCATGCTGAATT 3371
Db 1 AGAAGCTGTGTGTCATGCTGAATT 25

RESULT 39
US-10-956-157-148286
; Sequence 148286, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-148286

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3166 ACTGTTGATGTTTCAGGTGGACTACA 3190
Db 1 ACTGTTGATGTTTCAGGTGGACTACA 25

RESULT 40
US-10-956-157-148714
; Sequence 148714, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148714
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-148714

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3469 ACTAGTTCCCAAGCAACAACACTCCTT 3493
Db 1 ACTAGTTCCCAAGCAACAACACTCCTT 25

RESULT 41
US-10-956-157-149958
; Sequence 149958, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

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; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-149958

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3298 CACTTTTCCTGCTAAACTCCAGG 3322
      |||||||
DB 1 CACTTTTCCTGCTAAACTCCAGG 25

RESULT 42
US-10-956-157-151079
; Sequence 151079, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-151079

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3716 ACTTCAGTGGGATGCTGTCTAGT 3740
      |||||||
DB 1 ACTTCAGTGGGATGCTGTCTAGT 25

RESULT 43
US-10-956-157-152079
; Sequence 152079, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-152079

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3716 ACTTCAGTGGGATGCTGTCTAGT 3740
      |||||||
DB 1 ACTTCAGTGGGATGCTGTCTAGT 25

RESULT 44
US-10-956-157-156478
; Sequence 156478, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156478
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-156478

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3447 AAACCCCATGTCATGAGGAGTACT 3471
      |||||||
DB 1 AAACCCCATGTCATGAGGAGTACT 25

RESULT 45
US-10-956-157-160387
; Sequence 160387, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160387
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-160387

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3486 AACCTCCTTAATTTGCTCTAATAGAT 3510
      |||||||
DB 1 AACCTCCTTAATTTGCTCTAATAGAT 25

RESULT 46
US-10-956-157-164546
; Sequence 164546, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
```

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3646 ACATCCAGTGGATTACAGAAATTTCT 3670
      |||||||
DB 1 ACATCCAGTGGATTACAGAAATTTCT 25

RESULT 44
US-10-956-157-156478
; Sequence 156478, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156478
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-156478

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3447 AAACCCCATGTCATGAGGAGTACT 3471
      |||||||
DB 1 AAACCCCATGTCATGAGGAGTACT 25

RESULT 45
US-10-956-157-160387
; Sequence 160387, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160387
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-160387

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3486 AACCTCCTTAATTTGCTCTAATAGAT 3510
      |||||||
DB 1 AACCTCCTTAATTTGCTCTAATAGAT 25

RESULT 46
US-10-956-157-164546
; Sequence 164546, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
```

Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Caps 0;

APPLICANT: Mounts, William
TITLE OF INVENTION: ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217246
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-217246

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3480 GCAACAACTCTTAATTGCTCTA 3504
Db 1 GCAACAACTCTTAATTGCTCTA 25

RESULT 52

US-10-956-157-221650
; Sequence 221650, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-221650

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3557 GAAGCTTCAGGATAGTGAATG 3581
Db 1 GAAGCTTCAGGATAGTGAATG 25

RESULT 53

US-10-956-157-222074
; Sequence 222074, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 222074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-222074

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3635 GAACCTAGAAAACATCCAGTGGATT 3659
Db 1 GAACCTAGAAAACATCCAGTGGATT 25

RESULT 54

US-10-956-157-225637
; Sequence 225637, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225637

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3576 GAAATGTTATAGTTTCTTTGGAGT 3600
Db 1 GAAATGTTATAGTTTCTTTGGAGT 25

RESULT 55

US-10-956-157-235078
; Sequence 235078, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 235078
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-235078

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3464 GAGGTACTAGTTCACGCAACAAAC 3488
Db 1 GAGGTACTAGTTCACGCAACAAAC 25

RESULT 56

US-10-956-157-236490
; Sequence 236490, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 236490
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-236490

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3461 GAGGAGGTACTAGTTCNAGCAACA 3485
Db 1 GAGGAGGTACTAGTTCNAGCAACA 25

RESULT 57

US-10-956-157-238283
; Sequence 238283, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238283
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-238283

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3172 GATGTTTCAGGTGGACTACATGAAGA 3196
Db 1 GATGTTTCAGGTGGACTACATGAAGA 25

RESULT 58

US-10-956-157-238612
; Sequence 238612, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-238612

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3726 GATGCTGTCTAGTAGTAAACAA 3750

Db 1 GATGCTGTCTAGTAGTAAACAA 25

RESULT 59

US-10-956-157-239925
; Sequence 239925, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239925

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3508 GATAGGTATCGTTTAATCTTTCCAT 3532
Db 1 GATAGGTATCGTTTAATCTTTCCAT 25

RESULT 60

US-10-956-157-240345
; Sequence 240345, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-240345

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3322 GATACAGTATCCCAATTTATCCAAAC 3346
Db 1 GATACAGTATCCCAATTTATCCAAAC 25

RESULT 61

US-10-956-157-243640
; Sequence 243640, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157

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; FILE REFERENCE: 031896-043000 (AM 1010817)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04

```

; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-290105

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3710 TCCTCTACTTCAGTGGGATGCTGTG 3734
|||||
Db 1 TCCTCTACTTCAGTGGGATGCTGTG 25

RESULT 67

US-10-956-157-299227
; Sequence 299227, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299227
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-299227

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3371 TAAATGTGTAATAAGCTTCCCAA 3395
|||||
Db 1 TAAATGTGTAATAAGCTTCCCAA 25

RESULT 68

US-10-956-157-306169
; Sequence 306169, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 306169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-306169

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3514 TATGCTTTAATCTTTCCATTGTGC 3538
|||||
Db 1 TATGCTTTAATCTTTCCATTGTGC 25

RESULT 69

US-10-956-157-308532
; Sequence 308532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 308532
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-308532

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3302 TTTCCCTGTCTAACTCCAGGATAC 3326
|||||
Db 1 TTTCCCTGTCTAACTCCAGGATAC 25

RESULT 70

US-10-956-157-311335
; Sequence 311335, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 311335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-311335

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3546 TTAATTTTCTGAAGCTTGCAGGAT 3570
|||||
Db 1 TTAATTTTCTGAAGCTTGCAGGAT 25

RESULT 71

US-10-956-157-312666
; Sequence 312666, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 312666
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-312666

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3337 TTATCCAAACAGAACTGGTGTCAC 3361
Db 1 TTATCCAAACAGAACTGGTGTCAC 25

RESULT 72
US-10-956-157-317093
; Sequence 317093, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-317093

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3701 TTCCCAACATCCTCTACTTCAGTGG 3725
Db 1 TTCCCAACATCCTCTACTTCAGTGG 25

RESULT 73
US-10-956-157-319547
; Sequence 319547, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 319547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-319547

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3594 TTGGAGTAACCAACAGATGCAAA 3618
Db 1 TTGGAGTAACCAACAGATGCAAA 25
```

```
RESULT 74
US-09-885-441-42
; Sequence 42, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-885-441-42

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 AGCAGCAGCAGCAGCAACCAAC 1583
Db 1 AGCAGCAGCAGCAGCAACCAAC 24

RESULT 75
US-10-424-836-42
; Sequence 42, Application US/10424836
; Publication No. US20030224430A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-42

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 AGCAGCAGCAGCAGCAACCAAC 1583
Db 1 AGCAGCAGCAGCAGCAACCAAC 24
```

```
RESULT 76
US-10-719-900-175877
; Sequence 175877, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 175877
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-175877

Query Match          0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 58;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1299 AGCCTTTGTTTCATTTTAACTCAGA 1323
Db 1 AGCCTTTGTTTCATTTTAACTCAGA 25

RESULT 77
US-10-291-986-4/c
; Sequence 4, Application US/10291986
; Publication No. US20030215825A1
; GENERAL INFORMATION:
; APPLICANT: SUN-NING, TONG
; TITLE OF INVENTION: IMPROVED METHOD OF DETECTING MOLECULAR TARGET BY
; FILE REFERENCE: PARTICULATE BINDING
; CURRENT APPLICATION NUMBER: US/10/291,986
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: AU PS1597
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-291-986-4

Query Match          0.6%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 83;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAACAGCAGC 1448
Db 29 CAGCAGCAGCAGCAGCAACAGCAGC 5

RESULT 78
US-10-967-592-8/c
; Sequence 8, Application US/10967592
; Publication No. US20050053996A1
; GENERAL INFORMATION:
; APPLICANT: Tong, Sun-Wing
; TITLE OF INVENTION: MOLECULAR DETECTION AND ASSAY BY ELECTROBIOCHIP MICRO-ARRAY
; FILE REFERENCE: Dkt. #934-B-US
; CURRENT APPLICATION NUMBER: US/10/967,592
```

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; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 10/846,770
; PRIOR FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: 09/997,059
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic probe
; NAME/KEY: misc feature
; LOCATION: (1)..(29)
US-10-967-592-8

Query Match          0.6%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 83;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAACAGCAGC 1448
Db 29 CAGCAGCAGCAGCAGCAACAGCAGC 5

RESULT 79
US-09-848-754A-9122
; Sequence 9122, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9122
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9122

Query Match          0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAG 1432
Db 1 AGCAGCAGCAGCAGCAGCAGCAG 23

RESULT 80
US-10-479-546-10
; Sequence 10, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-479-546-10

Query Match          0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGAGAAGATGGCGACTTCGAACA 32
      |||||
Db 1 CGAGAAGATGGCGACTTCGAACA 23

RESULT 81
US-09-848-754A-9375/c
; Sequence 9375, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
; NAME/KEY: misc feature
; LOCATION: (2)..(8)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (18)..(24)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (9)..(17)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
US-09-848-754A-9375

Query Match          0.6%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAG 1432
      |||||
Db 24 AGCAGCAGCAGCAGCAGCAG 2

RESULT 82
US-10-719-900-7258
; Sequence 7258, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-7258

Query Match          0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1331 AACGACGAGATGCTTCTGTTTG 1354
      |||||
Db 2 AACGACGAGATGCTTCTTCTTTG 25

RESULT 83
US-10-719-956-496780
; Sequence 496780, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 496780
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-496780

Query Match          0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2126 GTTCAACACACACACCATTTAACT 2149
      |||||
Db 1 GTTCAACACACACACCATTTAACT 24

RESULT 84
US-10-418-182-156/c
; Sequence 156, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-156

Query Match          0.6%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1450 GCAGCAGCAACAGCAACAGCAACAGCA 1476
||||| ||||| ||||| ||||| |||||
Db 27 GCAGCAACAAACAACAGCAACAGCA 1

RESULT 85

US-10-738-642-25
; Sequence 25, Application US/10738642
; Publication No. US20040241854A1
; GENERAL INFORMATION:
; APPLICANT: Paulson, Henry
; APPLICANT: Miller, Victor
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: siRNA-Mediated Gene Silencing
; FILE REFERENCE: 875.101US1
; CURRENT APPLICATION NUMBER: US/10738,642
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/212,322
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/322,086
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/430,351
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/US03/16887
; PRIOR FILING DATE: 2003-05-26
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-738-642-25

Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGC 1430
||||| ||||| ||||| ||||| |||||
Db 1 CAGCAGCAGCAGCAGCAGCAGC 22

RESULT 86

US-10-738-642-26/c
; Sequence 26, Application US/10738642
; Publication No. US20040241854A1
; GENERAL INFORMATION:
; APPLICANT: Paulson, Henry
; APPLICANT: Miller, Victor
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: siRNA-Mediated Gene Silencing
; FILE REFERENCE: 875.101US1
; CURRENT APPLICATION NUMBER: US/10738,642
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/212,322
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/322,086
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/430,351
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/US03/16887
; PRIOR FILING DATE: 2003-05-26
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-738-642-26

Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1411 GCAGCAGCAGCAGCAGCAGCAG 1432
||||| ||||| ||||| ||||| |||||
Db 22 GCAGCAGCAGCAGCAGCAGCAG 1

RESULT 87

US-10-494-343-535
; Sequence 535, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 535
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-535

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAACAGCAGCAGCAG 1450
||||| ||||| ||||| ||||| |||||
Db 4 GCAGCAGCAACAGCAGCAGCAG 25

RESULT 88

US-10-494-343-536
; Sequence 536, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 536
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-536

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAACAGCAGCAGCAG 1450
||||| ||||| ||||| ||||| |||||
Db 3 GCAGCAGCAACAGCAGCAGCAG 24


```
RESULT 89
US-10-494-343-537
; Sequence 537, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-537

Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 2 GCAGCAGCAGCAACAGCAGCAG 23

RESULT 90
US-10-494-343-538
; Sequence 538, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-538

Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 1 GCAGCAGCAGCAACAGCAGCAG 22

RESULT 91
US-10-719-900-175878
; Sequence 175878, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 175878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-175878

Query Match      0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1299 AGCCTTTGTTTCATTTTAACTCAGA 1323
Db 1 AGCCTTTGTTTCCTTTTAACTCAGA 25

RESULT 92
US-10-719-900-917073
; Sequence 917073, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-917073

Query Match      0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1314 TTAAGTCAGATCAAGCAACAGCA 1338
Db 1 TTAAGTCAGATCAAGCAACAGCA 25

RESULT 93
US-10-956-157-73632
; Sequence 73632, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-73632
```

```
US-10-956-157-73632
Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1574 CAACAACACAGCAGCAACACAGCAGC 1598
|||||
Db 1 CAACAACACACACACATACACAGCAGC 25

RESULT 94
US-10-956-157-73633
; Sequence 73633, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73633

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1575 AACAAACACAGCAACACAGCAGCA 1599
|||||
Db 1 AACAAACACACAAATAACAGCAGCA 25

RESULT 95
US-10-956-157-73638
; Sequence 73638, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73638

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1576 ACAACAACAGCAACACAGCAGCAG 1600
|||||
Db 1 ACAACAACACAAATAACAGCAGCAGC 25

RESULT 96
US-10-956-157-73638
; Sequence 73638, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73638

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1577 ACAACAACAGCAACACAGCAGCAG 1600
|||||
Db 1 ACAACAACACAAATAACAGCAGCAGC 25

RESULT 97
US-10-956-422355/c
; Sequence 422355, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-422355

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2219 ATGGGGATGTGGAATCTGCCTT 2243
|||||
Db 1 ATAGGGATGTATGGAACCTGCCTT 25

RESULT 98
US-10-719-956-576464
; Sequence 576464, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576464
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-576464
```

```
Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2326 TCAGAAACAACCTATGATGCCACGG 2350
 ||| ||||| ||||| |||||
Db 1 TCAGAAACAACCTCTGATGCCACGG 25

```

RESULT 99
US/10-719-956-682692/c
; Sequence 682692, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator
; SEQ ID NO 682692

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-682692

```

Query Match 0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. NO. 89;
Matches 23; Conservative 0; Mismatches 2; Indels

QY 2751 TCAGGGGTCTGAATCTCAGACCCAA 2775
|||||
Db 25 TCAGGGGTCTGAACCTCAGACCCAA 1

RESULT 100
US-10-032-585-4161/c
; Sequence 4161, Application US/10032585
; Publication No. US20030180953A

```

; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4161
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4161

```

Query Match 0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels

[illegible]

RESULT 101
US-10-467-019-7/c
; Sequence 7, Application US/10467019
; Publication No. US20040048314A1

```

; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. US20040048314A1e1 Physiological Active Peptide and Its Use
; FILE REFERENCE: P01-0295PCT
; CURRENT APPLICATION NUMBER: US/10/467,019
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: JP2001-026820
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer, hbv8-F1 primer
; US-10-467-019-7

```

Query Match 0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels

Qy 1407 AACAGCAGCAGCAGCAGCAGCAG 1432
|||
Db 26 AACAGCAGCGGCAGCAGCAGAGTAG 1

```

RESULT 102
US-09-888-326-240/c
; Sequence 240, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing
; FILE OF INVENTION: Cell Lysis and Treat
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 21

```

```

; REF: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: phosphorothiate backbone
US-09-888-326-240

```

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
|||
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 103
US-09-776-479-780/c
; Sequence 780, Application US/09776479

[illegible]

; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 104

US-09-776-479-780/c
; Sequence 780, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 105

US-10-112-653-753/c
; Sequence 753, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Beig, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 753
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-753

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 106

US-10-017-995-780/c
; Sequence 780, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 107

US-10-314-578-780/c
; Sequence 780, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 108

US-10-831-778-780/c
; Sequence 780, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 109

US-10-494-343-534
; Sequence 534, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-534

Query Match 0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAACAGCAGCA 1449
Db 5 GCAGCAGCAACAGCAGCA 25

RESULT 110

US-10-494-343-539
; Sequence 539, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-539

Query Match 0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1430 CAGCAGCAACAGCAGCAG 1450
Db 1 CAGCAGCAACAGCAGCAG 21

RESULT 111

US-10-433-561-46
; Sequence 46, Application US/10433561
; Publication No. US2004029178A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. US20040029178A1el G Protein-Coupled Receptor Proteins and DNAs
; FILE REFERENCE: P01-0255PCT
; CURRENT APPLICATION NUMBER: US/10/433,561
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: JP 2000-364801
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: JP 2001-087482
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-145434
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: JP 2001-270838
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 191
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-433-561-46

Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1418 CAGCAGCAGCAGCAGCAGCA 1441

```

; Sequence 46, Application US/10477726
; Publication No. US20040110231A1
; GENERAL INFORMATION:
; APPLICANT: TAKEDA Chemical Industries, Ltd.
; TITLE OF INVENTION: Screening method
; FILE REFERENCE: P02-0058PCT
; CURRENT APPLICATION NUMBER: US/10/477,726
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 2001-145411
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-477-726-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGCAGCAGCAGCAGCAGTAA 24

RESULT 113
US-10-500-175A-46
; Sequence 46, Application US/10500175A
; Publication No. US20050124539A1
; GENERAL INFORMATION:
; APPLICANT: Hirokazu Matsumoto
; APPLICANT: Jiro Noguchi
; APPLICANT: Mioko Harada
; APPLICANT: Masaaki Mori
; TITLE OF INVENTION: Body weight gain inhibitor
; FILE REFERENCE: 61536 (46342)
; CURRENT APPLICATION NUMBER: US/10/500,175A
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: PCT/JP01/13781
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JP2001-403260
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP2002-93096
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 150
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-500-175A-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGCAGCAGCAGCAGCAGTAA 24

RESULT 114
US-10-311-019B-46
; Sequence 46, Application US/10311019B
; Publication No. US20050153391A1
; GENERAL INFORMATION:
; APPLICANT: MORI, Masaaki
; APPLICANT: SHIMOMURA, Yukio
; APPLICANT: HARADA, Mioko
; APPLICANT: ASAMI, Taiji
; APPLICANT: MATSUMOTO, Yoshio
; APPLICANT: ADACHI, Yuka
; APPLICANT: SUGO, Tsukasa
; APPLICANT: ABE, Michiko
; APPLICANT: GOTO, Mika nee KURIHARA
; APPLICANT: KITADA, Chioko
; APPLICANT: WATANABE, Takuya
; TITLE OF INVENTION: Ligand for GPR8 and its DNA
; FILE REFERENCE: 2739 USOP
; CURRENT APPLICATION NUMBER: US/10/311,019B
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: PCT/JP01/05257
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191089
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: JP 2000-275013
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: JP 2001-116000
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-311-019B-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGCAGCAGCAGCAGCAGTAA 24

RESULT 115
US-10-719-900-7257
; Sequence 7257, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-7257

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1331 AACCGACAGATGCTTCTCTGTTTG 1354
      |||||
Db 2 AACCGACAGATCCCTTCTCTTTTG 25
```

```
RESULT 116
US-10-719-900-13951
; Sequence 13951, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13951

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1225 AAAGCCTCAGGATCTCAGTGAAG 1248
      ||||| ||||| ||||| |||||
Db 1 AAAGCCTCAGGACCTCAATCGAAG 24

RESULT 117
US-10-719-900-13952
; Sequence 13952, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13952

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1225 AAAGCCTCAGGATCTCAGTGAAG 1248
      ||||| ||||| ||||| |||||
Db 1 AAAGCCTCAGGACCTCAATCGAAG 24

RESULT 118
US-10-719-900-132626/c
; Sequence 132626, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132626
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-132626

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1571 CAGCAACAACAACAGCAACAGCAG 1594
      ||||| ||||| ||||| |||||
Db 25 CAGCAACAACGACGACGACGACAG 2

RESULT 119
US-10-719-900-883394
; Sequence 883394, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 883394
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-883394

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1289 GGCAACACCAAGCCTTGTTTCAT 1312
      ||||| ||||| ||||| |||||
Db 2 GGCAATACCAAGCCTTGTTTCAT 25

RESULT 120
US-10-956-157-73631
; Sequence 73631, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-73631

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAACAGCAG 1597
      ||||| ||||| ||||| |||||
Db 2 CAACAACAACAACATTAACAGCAG 25

RESULT 121
```

```
US-10-719-956-496781
; Sequence 496781, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 496781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-496781

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2126 GTTCAACACACACACATTTTAACT 2149
Db 1 GTCTCAACACACTCCATTTTAACT 24

RESULT 122
US-10-028-415-27/c
; Sequence 27, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
; TITLE OF INVENTION: Death
; FILE REFERENCE: 11000.1004c3
; CURRENT APPLICATION NUMBER: US/10/028,415
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/NZ01/00286
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,809
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/036,004
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 08/713,557
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Human
US-10-028-415-27

Query Match          0.5%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1397 CAACAGCAGCAACAGCAGCAGC 1418
Db 22 CACCAGCAGCAACAGCAGCAGC 1

RESULT 123
US-10-719-900-833923/c
; Sequence 833923, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 833923
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-833923

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3198 AACATGCTTAAATGGAAGCAG 3222
Db 25 AACATGCATTAATAATGACACGAGA 1

RESULT 124
US-10-719-900-907760
; Sequence 907760, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 907760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-907760

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1210 TGTCTTCATCGCAGCAAAAGCCTCAG 1234
Db 1 TGTGCTTCTCGCAGCAAAAGCCTCAG 25

RESULT 125
US-10-719-900-917074
; Sequence 917074, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-917074

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```



```
Qy 1314 TTAACCTCAGATCAAGCGAACCAGCA 1338
      ||||| ||||| ||||| ||||| |||||
Db 1 TTAACCTCAGACTAGCAAAACCAGCA 25

RESULT 126
US-10-809-189-74107
; Sequence 74107, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittlemann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-74107

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1597 GCAGCAGCAGCAGCAACCACTCT 1621
      ||||| ||||| ||||| ||||| |||||
Db 1 GCAGCAGCAGCAGCAGCAACCACTCT 25

RESULT 127
US-10-719-956-24229
; Sequence 24229, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-24229

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2105 AACCCAGGCTTGGCAAAACCCAGTTT 2129
      ||||| ||||| ||||| ||||| |||||
Db 1 AACCCAGGCTTGACAAACCCAGTCT 25

RESULT 128
US-10-719-956-24230
; Sequence 24230, Application US/10719956
; Publication No. US20040146910A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24230
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-24230

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2105 AACCCAGGCTTGGCAAAACCCAGTTT 2129
      ||||| ||||| ||||| ||||| |||||
Db 1 AACCCAGGCTTGTCAAACCCAGTCT 25

RESULT 129
US-10-719-956-149049
; Sequence 149049, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-149049

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2654 AGGCAGTGGCTCTCTCAACCACT 2678
      ||||| ||||| ||||| ||||| |||||
Db 1 AGGCAGTGGCTCTCTCTGACCACT 25

RESULT 130
US-10-719-956-174099
; Sequence 174099, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 174099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-174099
```

```
Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2219 ATGGGGATGTATGGAATCTGCCTT 2243
||| ||||| ||||| ||||| |||||
Db 1 ATAGGGATGTATCGAAACCTGCCTT 25

RESULT 131
US-10-719-956-222455
; Sequence 222455, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 222455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-222455

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2133 CACACACATTTTAACCTCCCAATTC 2157
||| ||||| ||||| ||||| |||||
Db 1 CACACACATTTTAACCTCGAATTC 25

RESULT 132
US-10-719-956-422354/c
; Sequence 422354, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422354
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-422354

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2724 CACTAAATGGCAACCAACCTGGTCC 2748
||| ||||| ||||| ||||| |||||
Db 25 CATTAAATGGGCTAACTTGGGTCC 1

RESULT 133
US-10-719-956-471981/c
; Sequence 471981, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 471981
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-471981

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2696 ATGAGACCCCATGAACCAATGAGCC 2720
||| ||||| ||||| ||||| |||||
Db 25 ATGAGACCTGTGGAACCAATGAACC 1

RESULT 134
US-10-719-956-553657/c
; Sequence 553657, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-553657

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1398 AACAGCAGCAACAGCAGCAGCAGCA 1422
||| ||||| ||||| ||||| |||||
Db 25 AACAGCATTAACAGCAGCAGCAGTA 1

RESULT 135
US-10-719-956-576463
; Sequence 576463, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-576463
```

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2326 TCAAAACACCTATGATGCCACGG 2350
Db 1 TCAGAACCAACCTGATGCCACGG 25

RESULT 136

US-10-719-956-585024/c
; Sequence 585024, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 585024

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-585024

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3011 TCATTATTGACACAGACCCCTGGTA 3035
Db 25 TCATTATTGAAACACAGACCGGGA 1

RESULT 137

US-10-719-956-627844
; Sequence 627844, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 627844

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-627844

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2230 TGGAAATCTGCTTGAATCAACCT 2254
Db 1 TGGAAACCTGCTTGTGAACCAACCT 25

RESULT 138

US-10-719-956-643296/c
; Sequence 643296, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 643296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-643296

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2566 AGGAGTCGCTTCCCAACAGGTACA 2590
Db 25 AGGAGTCGCTTCCCAACAGGTACA 1

RESULT 139

US-10-719-956-682691/c
; Sequence 682691, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 682691

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-682691

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2751 TCAGGGTCTGAATCTCAGACCCAA 2775
Db 25 TCAGGGTCTGATCTCAGACCCAA 1

RESULT 140

US-10-371-474-63
; Sequence 63, Application US/10371474
; Publication No. US20030144242A1

; GENERAL INFORMATION:

; APPLICANT: Donna T. Ward

; APPLICANT: William Gaarde

; APPLICANT: Brett P. Monia

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK4 EXPRESSION

; FILE REFERENCE: RTS-0169

; CURRENT APPLICATION NUMBER: US/10/371,474

; CURRENT FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: US/09/676,436

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 63

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-63

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GCAGCAGCAGCAGCAGCAGC 20

RESULT 141
US-10-322-585-4667/c
; Sequence 4667, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4667
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4667

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 CAACAACAGCAGCAGCAGCA 1572
Db 20 CAACAACAGCAGCAGCAGCA 1

RESULT 142
US-10-032-585-5708/c
; Sequence 5708, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5708
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5708

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1555 AACACAGCAGCAGCAGCAGC 1574
Db 20 AACACAGCAGCAGCAGCAGC 1

RESULT 143
```

```
US-10-494-343-533
; Sequence 533, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 533
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-533

Query Match          0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGC 1448
Db 6 GCAGCAGCAGCAACAGCAGC 25

RESULT 144
US-10-494-343-540
; Sequence 540, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-540

Query Match          0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1431 AGCAGCAGCAACAGCAGCAG 1450
Db 1 AGCAGCAGCAACAGCAGCAG 20

RESULT 145
US-10-215-432-37
; Sequence 37, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kniec
```

```
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: Napro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated clone of gene-alteration directed by a
; OTHER INFORMATION: chimera
US-10-215-432-37

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db      1 CAGCAGCAGTAGCAGCAGCAG 21

RESULT 146
US-10-215-432-44
; Sequence 44, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: Napro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-44

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db      1 CAGCAGCAGTAGCAGCAGCAG 21

RESULT 147
US-10-418-182-96/c
; Sequence 96, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-132
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-96

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db      21 AGCAGCAGCGCAGCAGCAGCAGC 1

RESULT 148
US-10-418-182-114/c
; Sequence 114, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-114

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1576 ACAACACAGCAACACACAGCA 1596
Db      21 ACAACACAGCAACACACACACA 1

RESULT 149
US-10-418-182-132
; Sequence 132, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-132

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1538 CAGCAGCAGCAGCAGCAACAA 1558
Db      21 CAGCAGCAGCAGCAGCAACAA 1558
```



```
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Naseem
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; PENDING FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
US-10-922-544-26

Query Match          0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 1 CAGCAGCAGCAGCAGCAGC 19

RESULT 155
US-10-922-544-200/c
; Sequence 200, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Naseem
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; PENDING FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
```

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; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-922-544-200

Query Match          0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 19 CAGCAGCAGCAGCAGCAGC 1

RESULT 156
US-10-289-762-6476/c
; Sequence 6476, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6476
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6476

Query Match          0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAGCAGCAGCAGCAGC 1472
Db 19 CAGCAGCAGCAGCAGCAGC 1

RESULT 157
US-10-728-131-124/c
; Sequence 124, Application US/10728131
; Publication No. US20050075303A1
; GENERAL INFORMATION:
; APPLICANT: Neepser, Michael P.
; APPLICANT: McClements, William L.
; APPLICANT: Jansen, Kathrin U.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Chen, Ling
; APPLICANT: Wang, Xin-Min
; TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
; FILE REFERENCE: 20413YCA
; CURRENT APPLICATION NUMBER: US/10/728,131
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 09/642,405
; PRIOR FILING DATE: 2000-08-21
```

; PRIOR APPLICATION NUMBER: PCY/US00/22932
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/210,143
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/150,728
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-124

Query Match 0.5%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 CAACAACAGCAGCAGCAGC 1517
| | | | | | | | | | | | | | | | | | | | | |
Db 22 CAACAACAGCAGCAGCAGC 4

RESULT 158
US-09-888-615-120/c
; Sequence 120, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAN, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-888-615-120

Query Match 0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 980 CAGCACCAGCAGCAGCAGCAGC 1001
| | | | | | | | | | | | | | | | | | | | | |
Db 22 CTGCACCAGCAGCAGCAGCAGC 1

RESULT 159
US-10-295-942-16/c
; Sequence 16, Application US/10295942
; Publication No. US20030109480A1
; GENERAL INFORMATION:
; APPLICANT: Corder, Roger
; APPLICANT: Smith, Adrian
; APPLICANT: Higenbottam, Tim
; APPLICANT: Rothblatt, Martine
; APPLICANT: Vane, John
; APPLICANT: Jones, Delphine
; TITLE OF INVENTION: INHIBITORS OF ENDOTHELIN-1 SYNTHESIS
; FILE REFERENCE: 080618/0123
; CURRENT APPLICATION NUMBER: US/10/295,942

; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/527,240
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ASON
US-10-295-942-16

Query Match 0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 807 TGGCCAACTCTGCCCTCTCCAC 828
| | | | | | | | | | | | | | | | | | | | | |
Db 22 TGGCCGACTCTGCACCTCTCCAC 1

RESULT 160
US-10-177-308-24/c
; Sequence 24, Application US/10177308
; Publication No. US20030175262A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/177,308
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21,076
US-10-177-308-24

Query Match 0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAGC 1442
| | | | | | | | | | | | | | | | | | | | | |
Db 23 CAGTAGTAGCAGCAGCAGCAGC 2

RESULT 161
US-10-853-665-24/c
; Sequence 24, Application US/10853665
; Publication No. US20040259163A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/853,665
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: US/10/177,308
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0

[illegible][illegible][illegible]

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Dy 1 CAGCAGCAGCAGCAGCAG 18

Sequence 132, Application CS/07060300
; Publication No. US2003006494A1
; GENERAL INFORMATION:
; APPLICANT: Susan Murray

Query Match	0.5%;	Score 18;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.4e+02;		
Matches 18;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

US-10-705715-1527C
; Sequence 152, Application US/10705715
; Publication No. US20040147472A1
; GENERAL INFORMATION:

```

, TITLE OF INVENTION: ANTISENSE MODULATION C
, REFERENCE TO PUBLISHED DOCUMENTS:
, FILE NUMBER: 08-0679
, FILING DATE: 03-11-03
, CURRENT APPLICATION NUMBER: US/10/705,715
, PRIOR APPLICATION NUMBER: US/09/888,361

```

```
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-705-715-152

Query Match          0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1602 AGCAGCAGCAACACCAT 1619
Db 20 AGCAGCAGCAACACCAT 3

RESULT 175
US-10-479-510-11/c
; Sequence 11, Application US/10479510
; Publication No. US20040157230A1
; GENERAL INFORMATION:
; APPLICANT: Cavid Tech AB
; TITLE OF INVENTION: A method for measuring DNA polymerization and
; TITLE OF INVENTION: applications of the method.
; FILE REFERENCE: 110063501
; CURRENT APPLICATION NUMBER: US/10/479,510
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/297,773
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: template
US-10-479-510-11

Query Match          0.5%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 176
US-10-380-195A-15
; Sequence 15, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; TITLE OF INVENTION: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy
; FILE REFERENCE: UBC.P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 21

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
US-10-380-195A-15

Query Match          0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 1 CAGTAGCAGCAGCAGCAGCGG 21

RESULT 177
US-10-751-736-11486/c
; Sequence 11486, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-11486

Query Match          0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGCAGC 1427
Db 21 AACATCAGCAGCGCAGCAGC 1

RESULT 178
US-10-751-736-19232/c
; Sequence 19232, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19232
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-19232

Query Match          0.5%; Score 17.8; DB 1; Length 21;
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Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2146 AACTCCCAATTCAGCCTCT 2166
Db 21 AATCTCAATTCAGCCTCT 1

RESULT 179
US-10-764-730-11
; Sequence 11, Application US/10764730
; Publication No. US20050032134A1
; GENERAL INFORMATION:
; APPLICANT: Mueller-Hermelink, Hans Konrad
; APPLICANT: Vollmers, Heinz Peter
; APPLICANT: Hensel, Frank
; TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 50308/009002
; CURRENT APPLICATION NUMBER: US/10/764,730
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: PCT/DE02/02699
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: DE 10210425.5
; PRIOR FILING DATE: 2002-03-09
; PRIOR APPLICATION NUMBER: DE 10136009.6
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-764-730-11

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1426 GCAGCAGCAGCAGCAACAGCA 1446
Db 1 GCAGCTTCAGCAGCAACAGCA 21

RESULT 180
US-09-263-959-793/c
; Sequence 793, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/POCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 793:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-793

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCA 1428
Db 19 AGCAGCAGCAGCAGCAGCA 1

RESULT 181
US-10-922-544-29
; Sequence 29, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sitna Therapeutics, Inc.
; APPLICANT: Uman, Nassim
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/204 (MBHB03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-922-544-29

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 980 CAGCACCAGCAGCAGCACC 998
Db 1 CAGCACCAGCAGCAGCACC 1
```

Db 1 CAGCAGCAGCAGCAGCACC 19

RESULT 182

US-10-922-544-203/c
; Sequence 203, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Naasim
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT FILING DATE: 2004-08-19
; PRIOR FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-922-544-203

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 980 CAGCAGCAGCAGCAGCACC 998

Db 19 CAGCAGCAGCAGCAGCACC 1

RESULT 183

US-09-563-728A-7/c
; Sequence 7, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-7

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429

Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 184

US-09-563-728A-16/c
; Sequence 16, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-16

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429

Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 185

US-10-145-493B-52/c
; Sequence 52, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-52

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 186
US-10-315-962-67
; Sequence 67, Application US/10315962
; Publication No. US20040109848A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF AP-2 ALPHA EXPRESSION
; FILE REFERENCE: PTS-0046
; CURRENT APPLICATION NUMBER: US/10/315,962
; CURRENT FILING DATE: 2000-12-09
; NUMBER OF SEQ ID NOS: 126
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-315-962-67

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCGGCAGCAGCAGCAGCAG 19

RESULT 187
US-09-946-374-105/c
; Sequence 105, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
```

```
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
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; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
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; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
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; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401

; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 188
US-10-006-856A-105/c
; Sequence 102, Application US/10006856A
; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Poni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006.856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 189

US-10-006-818A-105/c
; Sequence 105, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 190

US-10-006-485A-105/c
; Sequence 105, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099741
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-15
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919

; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
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; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR APPLICATION NUMBER: 60/102330
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418

Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 191

US-10-013-907A-105/c
; Sequence 105, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105

; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-907A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 192

US-10-015-499A-105/c
; Sequence 105, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-499A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 193

US-10-015-393A-105/c
; Sequence 105, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 194

US-10-015-869A-105/c
; Sequence 105, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-869A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 195

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US-10-012-121A-105/c
; Sequence 105, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred.No. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 196
US-10-006-116A-105/c
; Sequence 105, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; Prior Application NUMBER: 60/098716
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098723
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098749
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098750
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
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; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
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; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
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; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
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; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257

; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
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; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 197

US-10-006-117A-105/c
; Sequence 105, Application US/10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PLC13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-117A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 198
US-10-017-527A-105/c
; Sequence 105, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1CG3
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098741
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098792
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-30
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30

1	PRIOR FILING DATE: 1998-09-01	60/101477
2	PRIOR APPLICATION NUMBER: 60/098803	60/101477
3	PRIOR FILING DATE: 1998-09-02	60/101477
4	PRIOR FILING DATE: 1998-09-02	60/101477
5	PRIOR APPLICATION NUMBER: 60/098821	60/101477
6	PRIOR FILING DATE: 1998-09-02	60/101477
7	PRIOR APPLICATION NUMBER: 60/098843	60/101477
8	PRIOR FILING DATE: 1998-09-02	60/101477
9	PRIOR APPLICATION NUMBER: 60/099536	60/101477
10	PRIOR FILING DATE: 1998-09-09	60/101477
11	PRIOR APPLICATION NUMBER: 60/099596	60/101477
12	PRIOR FILING DATE: 1998-09-09	60/101477
13	PRIOR APPLICATION NUMBER: 60/099598	60/101477
14	PRIOR FILING DATE: 1998-09-09	60/101477
15	PRIOR APPLICATION NUMBER: 60/099602	60/101477
16	PRIOR FILING DATE: 1998-09-09	60/101477
17	PRIOR APPLICATION NUMBER: 60/099642	60/101477
18	PRIOR FILING DATE: 1998-09-09	60/101477
19	PRIOR APPLICATION NUMBER: 60/099741	60/101477
20	PRIOR FILING DATE: 1998-09-10	60/101477
21	PRIOR APPLICATION NUMBER: 60/099754	60/101477
22	PRIOR FILING DATE: 1998-09-10	60/101477
23	PRIOR APPLICATION NUMBER: 60/099763	60/101477
24	PRIOR FILING DATE: 1998-09-10	60/101477
25	PRIOR APPLICATION NUMBER: 60/099792	60/101477
26	PRIOR FILING DATE: 1998-09-10	60/101477
27	PRIOR APPLICATION NUMBER: 60/099808	60/101477
28	PRIOR FILING DATE: 1998-09-10	60/101477
29	PRIOR APPLICATION NUMBER: 60/099812	60/101477
30	PRIOR FILING DATE: 1998-09-10	60/101477
31	PRIOR APPLICATION NUMBER: 60/099815	60/101477
32	PRIOR FILING DATE: 1998-09-10	60/101477
33	PRIOR APPLICATION NUMBER: 60/099816	60/101477
34	PRIOR FILING DATE: 1998-09-10	60/101477
35	PRIOR APPLICATION NUMBER: 60/100385	60/101477
36	PRIOR FILING DATE: 1998-09-15	60/101477
37	PRIOR APPLICATION NUMBER: 60/100388	60/101477
38	PRIOR FILING DATE: 1998-09-15	60/101477
39	PRIOR APPLICATION NUMBER: 60/100390	60/101477
40	PRIOR FILING DATE: 1998-09-15	60/101477
41	PRIOR APPLICATION NUMBER: 60/100584	60/101477
42	PRIOR FILING DATE: 1998-09-16	60/101477
43	PRIOR APPLICATION NUMBER: 60/100627	60/101477
44	PRIOR FILING DATE: 1998-09-16	60/101477
45	PRIOR APPLICATION NUMBER: 60/100661	60/101477
46	PRIOR FILING DATE: 1998-09-16	60/101477
47	PRIOR APPLICATION NUMBER: 60/100662	60/101477
48	PRIOR FILING DATE: 1998-09-16	60/101477
49	PRIOR APPLICATION NUMBER: 60/100664	60/101477
50	PRIOR FILING DATE: 1998-09-16	60/101477
51	PRIOR APPLICATION NUMBER: 60/100683	60/101477
52	PRIOR FILING DATE: 1998-09-17	60/101477
53	PRIOR APPLICATION NUMBER: 60/100684	60/101477
54	PRIOR FILING DATE: 1998-09-17	60/101477
55	PRIOR APPLICATION NUMBER: 60/100710	60/101477
56	PRIOR FILING DATE: 1998-09-17	60/101477
57	PRIOR APPLICATION NUMBER: 60/100711	60/101477
58	PRIOR FILING DATE: 1998-09-17	60/101477
59	PRIOR APPLICATION NUMBER: 60/100848	60/101477
60	PRIOR FILING DATE: 1998-09-18	60/101477
61	PRIOR APPLICATION NUMBER: 60/100849	60/101477
62	PRIOR FILING DATE: 1998-09-18	60/101477
63	PRIOR APPLICATION NUMBER: 60/100919	60/101477
64	PRIOR FILING DATE: 1998-09-17	60/101477
65	PRIOR APPLICATION NUMBER: 60/100930	60/101477
66	PRIOR FILING DATE: 1998-09-17	60/101477
67	PRIOR APPLICATION NUMBER: 60/101014	60/101477
68	PRIOR FILING DATE: 1998-09-18	60/101477
69	PRIOR APPLICATION NUMBER: 60/101068	60/101477
70	PRIOR FILING DATE: 1998-09-18	60/101477
71	PRIOR APPLICATION NUMBER: 60/101071	60/101477
72	PRIOR FILING DATE: 1998-09-18	60/101477
73	PRIOR APPLICATION NUMBER: 60/101279	60/101477
74	PRIOR FILING DATE: 1998-09-22	60/101477

; PRIOR FILING DATE: 1998-10-14
 ; PRIOR APPLICATION NUMBER: 60/104987
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105000
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105002
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: 60/105104
 ; PRIOR FILING DATE: 1998-10-21
 ; PRIOR APPLICATION NUMBER: 60/105169
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: 60/105266
 ; PRIOR FILING DATE: 1998-10-22
 ; PRIOR APPLICATION NUMBER: 60/105693
 ; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105694
 ; PRIOR FILING DATE: 1998-10-26
 ; PRIOR APPLICATION NUMBER: 60/105807
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 ; PRIOR APPLICATION NUMBER: 60/105881
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 ; PRIOR APPLICATION NUMBER: 60/105882
 ; PRIOR FILING DATE: 1998-10-27
 ; PRIOR APPLICATION NUMBER: 60/106023
 ; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 201
 US-10-013-430A-105/c
 ; Sequence 105, Application US/10013430A
 ; Publication No. US20030092883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2830P1C31
 ; CURRENT APPLICATION NUMBER: US/10/013,430A
 ; CURRENT FILING DATE: 2002-06-25
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 105
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-013-430A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2
 RESULT 202
 US-10-011-671A-105/c
 ; Sequence 105, Application US/10011671A
 ; Publication No. US20030096954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2830P1C27
 ; CURRENT APPLICATION NUMBER: US/10/011,671A
 ; CURRENT FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
 ; PRIOR FILING DATE: 1998-09-01
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 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098803
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098821
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098843
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/099536
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 ; PRIOR FILING DATE: 1998-09-10
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 ; PRIOR APPLICATION NUMBER: 60/099816
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 ; PRIOR APPLICATION NUMBER: 60/100385
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100388
 ; PRIOR FILING DATE: 1998-09-15

;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100584
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
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;; PRIOR FILING DATE: 1998-09-18
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;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101014
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;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/102207
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;; PRIOR APPLICATION NUMBER: 60/102240
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102307
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102330
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102331
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102484
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102487

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 203
US-10-012-755A-105/c

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; Sequence 105, Application US/10012755A
; Publication No. US20030096955A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C28
; CURRENT APPLICATION NUMBER: US/10/012,755A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-755A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 204
US-10-015-386A-105/c
; Sequence 105, Application US/10015386A
; Publication No. US20030099625A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C55
; CURRENT APPLICATION NUMBER: US/10/015,386A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
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US-10-015-386A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 205
US-10-011-692A-105/c
; Sequence 105, Application US/10011692A
; Publication No. US20030109672A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C30
; CURRENT APPLICATION NUMBER: US/10/011,692A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-692A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 206
US-10-006-768A-105/c
; Sequence 105, Application US/10006768A
; Publication No. US20030113793A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
```

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-768A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1400 CAGCAGCAACAGCAGCAGC 1418
Db       ||| ||||| ||||| ||||| |||||
          20 CAGGAGCAACAGCAGCAGC 2

RESULT 207
US-10-017-610A-105/c
; Sequence 105, Application US/10017610A
; Publication No. US20030113795A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C64
; CURRENT APPLICATION NUMBER: US/10/017,610A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/099754
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; PRIOR APPLICATION NUMBER: 60/099763
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; PRIOR FILING DATE: 1998-09-24
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;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/102207
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102240
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102307
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102330
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102331
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102484
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102487
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102570
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103396
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match
Best Local Similarity 0.5%; Score 17.4; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 208
US-10-006-063A-105/c
; Sequence 105, Application US/10006063A
; Publication No. US20030114652A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C3
; CURRENT APPLICATION NUMBER: US/10/006,063A
; CURRENT FILING DATE: 2002-03-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-063A-105

Query Match
Best Local Similarity 0.5%; Score 17.4; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 209
US-10-020-063A-105/c
; Sequence 105, Application US/10020063A
; Publication No. US20030119097A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C65
; CURRENT APPLICATION NUMBER: US/10/020,063A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-020-063A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 210
US-10-015-391A-105/c
; Sequence 105, Application US/10015391A
; Publication No. US20030120053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C59
; CURRENT APPLICATION NUMBER: US/10/015,391A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 211
US-10-017-407A-105/c
; Sequence 105, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C61
; CURRENT APPLICATION NUMBER: US/10/017,407A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 212
US-10-011-833A-105/c
; Sequence 105, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C65
; CURRENT APPLICATION NUMBER: US/10/020,063A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-020-063A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 210
US-10-015-391A-105/c
; Sequence 105, Application US/10015391A
; Publication No. US20030120053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C59
; CURRENT APPLICATION NUMBER: US/10/015,391A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 211
US-10-017-407A-105/c
; Sequence 105, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C61
; CURRENT APPLICATION NUMBER: US/10/017,407A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 212
US-10-011-833A-105/c
; Sequence 105, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; Prior Filing DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-833A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 213
US-10-006-041A-105/c
; Sequence 105, Application US/10006041A
; Publication No. US20030130490A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-041A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 214
US-10-015-822A-105/c
; Sequence 105, Application US/10015822A
; Publication No. US20030130491A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C38
; CURRENT APPLICATION NUMBER: US/10/015,822A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-822A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 215
US-10-015-387A-105/c
; Sequence 105, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
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; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-387A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 216
US-10-006-130A-105/c
; Sequence 105, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Pan, James
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-130A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 217
US-10-006-172A-105/c
; Sequence 105, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Pan, James
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; Prior Application NUMBER: 60/098716
; Prior FILING DATE: 1998-09-01
; Prior APPLICATION NUMBER: 60/098723
; Prior FILING DATE: 1998-09-01
; Prior APPLICATION NUMBER: 60/098749
; Prior FILING DATE: 1998-09-01
; Prior APPLICATION NUMBER: 60/098750
; Prior FILING DATE: 1998-09-01
; Prior APPLICATION NUMBER: 60/098803
; Prior FILING DATE: 1998-09-02
; Prior APPLICATION NUMBER: 60/098821
; Prior FILING DATE: 1998-09-02
; Prior APPLICATION NUMBER: 60/098843
; Prior FILING DATE: 1998-09-02
; Prior APPLICATION NUMBER: 60/099536
; Prior FILING DATE: 1998-09-09
; Prior APPLICATION NUMBER: 60/099596
; Prior FILING DATE: 1998-09-09
; Prior APPLICATION NUMBER: 60/099598
; Prior FILING DATE: 1998-09-09
; Prior APPLICATION NUMBER: 60/099602
; Prior FILING DATE: 1998-09-09
; Prior APPLICATION NUMBER: 60/099642
; Prior FILING DATE: 1998-09-09
; Prior APPLICATION NUMBER: 60/099741
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099754
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099763
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099792
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099808
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099812
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099815
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/099816
; Prior FILING DATE: 1998-09-10
; Prior APPLICATION NUMBER: 60/100385
; Prior FILING DATE: 1998-09-15
; Prior APPLICATION NUMBER: 60/100388
; Prior FILING DATE: 1998-09-15
; Prior APPLICATION NUMBER: 60/100390
; Prior FILING DATE: 1998-09-15
; Prior APPLICATION NUMBER: 60/100584
; Prior FILING DATE: 1998-09-16
; Prior APPLICATION NUMBER: 60/100627
; Prior FILING DATE: 1998-09-16
; Prior APPLICATION NUMBER: 60/100661
; Prior FILING DATE: 1998-09-16
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; Prior FILING DATE: 1998-09-16
; Prior APPLICATION NUMBER: 60/100664
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; Prior FILING DATE: 1998-09-17
; Prior APPLICATION NUMBER: 60/100684
; Prior FILING DATE: 1998-09-17
; Prior APPLICATION NUMBER: 60/100710
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; Prior APPLICATION NUMBER: 60/100711
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
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; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
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; PRIOR FILING DATE: 1998-10-07

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; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
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; PRIOR APPLICATION NUMBER: 60/103633
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; PRIOR FILING DATE: 1998-10-22
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; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
;

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 218

US-10-017-253A-105/c
; Sequence 105, Application US/10017253A
; Publication No. US20030166055A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

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; FILE REFERENCE: P2830P1C62
; CURRENT APPLICATION NUMBER: US/10/017,253A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-253A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 219
US-10-015-392A-105/c
; Sequence 105, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-392A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 220
US-10-017-306A-105/c
; Sequence 105, Application US/10017306A
; Publication No. US20030170718A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C66
; CURRENT APPLICATION NUMBER: US/10/017,306A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-306A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2
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RESULT 221
US-10-017-867A-105/c
; Sequence 105, Application US/10017867A
; Publication No. US20030180792A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830FIC60
; CURRENT APPLICATION NUMBER: US/10/017.867A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
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; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
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; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30

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; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
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; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
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; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
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; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
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Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
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RESULT 222

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US-10-012-064A-105/c
; Sequence 105, Application US/10012064A
; Publication No. US20030180836A1
; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830F1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-012-064A-105
```

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Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 223

```
US-10-013-909A-105/c
; Sequence 105, Application US/10013909A
; Publication No. US20030186318A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C35
; CURRENT APPLICATION NUMBER: US/10/013,909A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-909A-105

```

```

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

```

RESULT 224

```

US-10-015-671A-105/c
; Sequence 105, Application US/10015671A
; Publication No. US20030186319A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-671A-105

```

```

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

```

RESULT 225

```

US-10-015-610A-105/c

```

```

; Sequence 105, Application US/10015610A
; Publication No. US2003018631A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C52
; CURRENT APPLICATION NUMBER: US/10/015,610A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-610A-105

```

```

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

```

RESULT 226

```

US-10-012-137A-105/c
; Sequence 105, Application US/10012137A
; Publication No. US20030187189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

```

```
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C29
; CURRENT APPLICATION NUMBER: US/10/012,137A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-137A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 227
US-10-012-752A-105/c
; Sequence 105, Application US/10012752A
; Publication No. US20030187190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-752A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 228
US-10-012-754A-105/c
; Sequence 105, Application US/10012754A
; Publication No. US20030187191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C18
; CURRENT APPLICATION NUMBER: US/10/012,754A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-754A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 229
US-10-013-910A-105/c
; Sequence 105, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-910A-105
Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. NO. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 230
US-10-013-911A-105/c
; Sequence 105, Application US/10013911A
; Publication No. US2003018193A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC39
; CURRENT APPLICATION NUMBER: US/10/013.911A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
```


Publication No. US20030187195A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C43
 CURRENT APPLICATION NUMBER: US/10/015,653A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-015-653A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 233

US-10-012-101B-105/c
 Sequence 105, Application US/10012101B
 Publication No. US20030187239A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C6
 CURRENT APPLICATION NUMBER: US/10/012,101B
 CURRENT FILING DATE: 2001-12-06
 Prior application removed - See file Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-012-101B-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 234

US-10-015-480A-105/c
 Sequence 105, Application US/10015480A
 Publication No. US20030190667A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C50
 CURRENT APPLICATION NUMBER: US/10/015,480A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-015-480A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 235

US-10-015-715A-105/c
 Sequence 105, Application US/10015715A
 Publication No. US20030190668A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC56
; CURRENT APPLICATION NUMBER: US/10/015,715A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-715A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 236

```
US-10-012-237A-105/c
; Sequence 105, Application US/10012237A
; Publication No. US20030191281A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC21
; CURRENT APPLICATION NUMBER: US/10/012,237A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-237A-105
```

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Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2
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RESULT 237

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US-10-013-906A-105/c
; Sequence 105, Application US/10013906A
; Publication No. US20030191282A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC36
; CURRENT APPLICATION NUMBER: US/10/013,906A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
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; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
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; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
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; PRIOR APPLICATION NUMBER: 60/102207
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; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258

; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 238
US-10-015-388A-105/c
; Sequence 105, Application US/10015388A
; Publication No. US20030191299A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

US-10-015-385A-105/c

Sequence 105, Application US/10015385A
Publication No. US20030195347A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2830P1C51

CURRENT APPLICATION NUMBER: US/10/015,385A

CURRENT FILING DATE: 2002-07-25

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 477

SEQ ID NO 105

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-015-385A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||

Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 241

US-10-007-236A-105/c

Sequence 105, Application US/10007236A
Publication No. US20030198993A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2830P1C12

CURRENT APPLICATION NUMBER: US/10/007,236A

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 477

SEQ ID NO 105

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

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; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-007-236A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 242
US-10-015-389A-105/c
; Sequence 105, Application US/10015389A
; Publication No. US20030199675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-015-389A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 243
US-10-015-519A-105/c
; Sequence 105, Application US/10015519A
; Publication No. US20030203401A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C37
; CURRENT APPLICATION NUMBER: US/10/013,915A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-013-915A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 244
US-10-013-915A-105/c
; Sequence 105, Application US/10013915A
; Publication No. US20030204053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C37
; CURRENT APPLICATION NUMBER: US/10/013,915A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-013-915A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 245
US-10-015-394A-105/c
; Sequence 105, Application US/10015394A
; Publication No. US20030204054A1
; GENERAL INFORMATION:
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```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C41
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-394A-105
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 246
US-10-015-390A-105/c
; Sequence 105, Application US/10015390A
; Publication No. US20030216562A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C5
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C53
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/10/015,390A
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-390A-105
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 247
US-10-006-746A-105/c
; Sequence 105, Application US/10006746A
; Publication No. US20030220471A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C5
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
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;	PRIOR APPLICATION NUMBER:	60/101730
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101741
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101743
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101915
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/101916
;	PRIOR FILING DATE:	1998-09-24
;	PRIOR APPLICATION NUMBER:	60/102207
;	PRIOR FILING DATE:	1998-09-29
;	PRIOR APPLICATION NUMBER:	60/102240
;	PRIOR FILING DATE:	1998-09-29
;	PRIOR APPLICATION NUMBER:	60/102307
;	PRIOR FILING DATE:	1998-09-29
;	PRIOR APPLICATION NUMBER:	60/102330
;	PRIOR FILING DATE:	1998-09-29
;	PRIOR APPLICATION NUMBER:	60/102331
;	PRIOR FILING DATE:	1998-09-29
;	PRIOR APPLICATION NUMBER:	60/102484
;	PRIOR FILING DATE:	1998-09-30
;	PRIOR APPLICATION NUMBER:	60/102487
;	PRIOR FILING DATE:	1998-09-30
;	PRIOR APPLICATION NUMBER:	60/102570
;	PRIOR FILING DATE:	1998-09-30
;	PRIOR APPLICATION NUMBER:	60/102571
;	PRIOR FILING DATE:	1998-09-30
;	PRIOR APPLICATION NUMBER:	60/102684
;	PRIOR FILING DATE:	1998-10-01
;	PRIOR APPLICATION NUMBER:	60/102687
;	PRIOR FILING DATE:	1998-10-01
;	PRIOR APPLICATION NUMBER:	60/102965
;	PRIOR FILING DATE:	1998-10-02
;	PRIOR APPLICATION NUMBER:	60/103258
;	PRIOR FILING DATE:	1998-10-06
;	PRIOR APPLICATION NUMBER:	60/103314
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103315
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103328
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103395
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103396
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103401
;	PRIOR FILING DATE:	1998-10-07
;	PRIOR APPLICATION NUMBER:	60/103449
;	PRIOR FILING DATE:	1998-10-06
;	PRIOR APPLICATION NUMBER:	60/103633
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103678
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103679
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103711
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/104257
;	PRIOR FILING DATE:	1998-10-14
;	PRIOR APPLICATION NUMBER:	60/104987
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105000
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105002
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105104
;	PRIOR FILING DATE:	1998-10-21
;	PRIOR APPLICATION NUMBER:	60/105169
;	PRIOR FILING DATE:	1998-10-22
;	PRIOR APPLICATION NUMBER:	60/105266
;	PRIOR FILING DATE:	1998-10-22
;	PRIOR APPLICATION NUMBER:	60/105693

Tue Aug 16 13:15:19 2005

; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 248
US-10-226-254A-105/c
; Sequence 105, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/226,254A
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-226-254A-105/c
; Sequence 105, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/226,254A
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-226-254A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 249
US-10-011-795A-105/c
; Sequence 105, Application US/10011795A
; Publication No. US20040005626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/011,795A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-011-795A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 250
US-10-012-231A-105/c
; Sequence 105, Application US/10012231A
; Publication No. US20040014130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.


```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-231A-105

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```

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

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RESULT 251

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US-10-015-395A-105/c
; Sequence 105, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-395A-105

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```

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

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RESULT 252

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US-10-751-736-8809/c
; Sequence 8809, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

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```

; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; Prior Application Number: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8809
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-8809

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Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1555 ACAACAGCAGCAGCAGCAG 1573
      ||| ||||| ||||| |||||
Db 21 AGAACAGCAGCAGCAGCAG 3

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RESULT 253

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US-10-751-736-39221
; Sequence 39221, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; Prior Application Number: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39221
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-39221

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Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 1429 GCAGCAGCAACAGCAGCAG 1447
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Db 1 GCAGCAGCAACAGCAGCAG 19

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RESULT 254

```

US-10-012-149A-105/c
; Sequence 105, Application US/10012149A
; Publication No. US20050043520A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey

```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC26
; CURRENT APPLICATION NUMBER: US/10/012.149A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-149A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 255
US-10-730-771-62
; Sequence 62, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul S.
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-62

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AGCAACAGCAGCAGCAGCAGC 1424
      ||| ||||| ||||| |||||
Db 1 AGGAACAGCAACAGCAGCAGC 21

RESULT 256
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US-10-494-343-167
; Sequence 167, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuomy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 167
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-167

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGC 1445
      ||| ||||| ||||| |||||
Db 1 GCAGCAGCAGCAACAGC 17

RESULT 257
US-10-494-343-168
; Sequence 168, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuomy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 168
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-168

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1430 CAGCAGCAGCAACAGCA 1446
      ||| ||||| ||||| |||||
Db 1 CAGCAGCAGCAACAGCA 17

RESULT 258
US-10-494-343-169
; Sequence 169, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
```

```
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-169

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1431 AGCAGCAGCAACAGCAG 1447
Db 1 AGCAGCAGCAACAGCAG 17
|||||
RESULT 259
US-10-494-343-170
; Sequence 170, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-170

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1432 GCAGCAGCAACAGCAGC 1448
Db 1 GCAGCAGCAACAGCAGC 17
|||||
RESULT 260
US-10-494-343-171
; Sequence 171, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
```

```
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-171

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCA 1416
Db 1 CAGCAGCAACAGCAGCA 17
|||||
RESULT 261
US-10-494-343-172
; Sequence 172, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-172

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1401 AGCAGCAACAGCAGCAG 1417
Db 1 AGCAGCAACAGCAGCAG 17
|||||
RESULT 262
US-09-933-638A-9
; Sequence 9, Application US/09933638A
; Patent No. US20020160952A1
; GENERAL INFORMATION:
; APPLICANT: Kazantsev, Aleksey G.
; APPLICANT: Thompson, Leslie M.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: INHIBITION OF PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 01997-289001
; CURRENT APPLICATION NUMBER: US/09/933,638A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/226,502
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Fast-SEQ for Windows Version 4.0
```

```
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-9

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 CAACAGCAGCAACAGCA 1413
Db 1 CAACAGCAGCAACAGCA 17

RESULT 263
US-10-194-584-2/c
; Sequence 2, Application US/10194584
; Publication No. US20030027288A1
; GENERAL INFORMATION:
; APPLICANT: Housman, David E.
; APPLICANT: Preisinger, Elizabeth A.
; APPLICANT: Kazantsev, Aleksey G.
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGENTS WHICH INHIBIT AGGREGATION
; TITLE OF INVENTION: OF POLYPEPTIDES
; FILE REFERENCE: 01997-261002
; CURRENT APPLICATION NUMBER: US/10/194,584
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/405,048
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-10-194-584-2

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 CAGCAGCAACAGCAACA 1467
Db 18 CAGCAGCAACAGCAACA 2

RESULT 266
US-10-436-231-1
; Sequence 1, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Sorge, Joseph A
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT APPLICATION NUMBER: US/10/436,231
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/452,481
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-1

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-10

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 CAGCAGCAACAGCAACA 1467
Db 18 CAGCAGCAACAGCAACA 2

RESULT 264
US-10-194-584-1
; Sequence 1, Application US/10194584
; Publication No. US20030027288A1
; GENERAL INFORMATION:
; APPLICANT: Housman, David E.
; APPLICANT: Preisinger, Elizabeth A.
; APPLICANT: Kazantsev, Aleksey G.
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGENTS WHICH INHIBIT AGGREGATION
; TITLE OF INVENTION: OF POLYPEPTIDES
; FILE REFERENCE: 01997-261002
; CURRENT APPLICATION NUMBER: US/10/194,584
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/405,048
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-10
```



```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 272
US-10-388-263-554
; Sequence 554, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 554
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-554

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 273
US-10-210-479-79/c
; Sequence 79, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-79

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1645 AGCCAGCCTTTGCTAAGGT 1664
Db 20 AGCCAGCCTTTGCTAAGGT 1

RESULT 274
US-10-633-163-35
; Sequence 35, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-35

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GTAGCAGCAGCGCAGCAGCAGC 20

RESULT 275
US-10-712-795-22
; Sequence 22, Application US/10712795
; Publication No. US20040214325A1
; GENERAL INFORMATION:
; APPLICANT: Crooke et al.
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: 30566/39662
; CURRENT APPLICATION NUMBER: US/10/712,795
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,234
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US03/15493
; PRIOR FILING DATE: 2003-05-13
; NUMBER OF SEQ ID NOS: 892
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-712-795-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
```

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACGACGACGACGCA 1551
|||||
Db 1 GCCCGCCGACGACGACGCA 20

RESULT 276

US-10-920-612-22
; Sequence 22, Application US/10920612
; Publication No. US2005009088A1
; GENERAL INFORMATION:
; APPLICANT: Crooke et al.
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION

; FILE REFERENCE: 30566/39634A
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: PCT/US03/15493
; PRIOR FILING DATE: 2003-11-15
; PRIOR APPLICATION NUMBER: US 10/712,795
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,234
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 892

; SEQ ID NO 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-920-612-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACGACGACGACGCA 1551
|||||
Db 1 GCCCGCCGACGACGACGCA 20

RESULT 277

US-10-831-901A-11559
; Sequence 11559, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27

; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11559

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1543 GCAGCAGCAGCAACAACAGC 1562
|||||
Db 1 GTAGCAGCAGCAACAATAGC 20

RESULT 278

US-10-831-901A-11560
; Sequence 11560, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426

; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27

; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11560

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1542 AGCAGCAGCAGCAACAACAG 1561
|||||
Db 1 AGTAGCAGCAGCAACAATAG 20

RESULT 279

US-09-906-419-91
; Sequence 91, Application US/09906419

```
; Publication No. US20030037357A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOM-04679
; CURRENT APPLICATION NUMBER: US/09/906,419
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/220,474
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-906-419-91

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGGCTTTTCAAGGAACGTG 2921
Db 2 CAGGGCTTCTCAAGGAATG 21

RESULT 280
US-10-119-136-91
; Sequence 91, Application US/10119136
; Publication No. US20030097676A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOM-04695
; CURRENT APPLICATION NUMBER: US/10/119,136
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/906,419
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/220,474
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-119-136-91

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGGCTTTTCAAGGAACGTG 2921
Db 2 CAGGGCTTCTCAAGGAATG 21

RESULT 281
US-10-410-031-91
; Sequence 91, Application US/10410031
; Publication No. US20040010817A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay M.
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John A.
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 283
US-10-380-195A-46
; Sequence 46, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 283
US-10-380-195A-2
; Sequence 2, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
; US-10-380-195A-2

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 283
US-10-380-195A-46
; Sequence 46, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A
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; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
US-10-380-195A-46

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1532 GCCCAACAGCAGCAGCAGCA 1551
    ||||| ||||| ||||| |||||
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 284
US-10-751-736-10540/c
; Sequence 10540, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10540
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-10540

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
    ||||| ||||| ||||| |||||
Db 20 GCAGCAGCAGCAGCAGCATC 1

RESULT 285
US-10-751-736-10541/c
; Sequence 10541, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
```

```
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10541
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-10541

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 974 ATGCAGCAGCAGCAGCAGCA 993
    ||||| ||||| ||||| |||||
Db 20 ATGCAGCAGCAGCAGCAGCA 1

RESULT 286
US-10-751-736-18508/c
; Sequence 18508, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18508
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-18508

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2147 ACTCCCAATTCAGCCTCCT 2166
    ||||| ||||| ||||| |||||
Db 21 AATCTCAATTCAGCCTCCT 2

RESULT 287
US-10-751-736-18509/c
; Sequence 18509, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18509
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-18509
```

```
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2146 AACTCCCAATTCAGCCTCC 2165
      ||||| ||||| ||||| |||||
Db 20 AAATCTCAATTCAGCCTCC 1

RESULT 288
US-10-751-736-49304/c
; Sequence 49304, Application US/10751736
; Publication No. US2004026230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49304
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-49304

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1967 AAAATTGCTCCACAGATCA 1986
      ||||| ||||| ||||| |||||
Db 21 AAAATTGCAGCACAGATCA 2

RESULT 289
US-10-847-918-3217
; Sequence 3217, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3217
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-3217

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACGACGACGCA 1419
      ||||| ||||| ||||| |||||
```

```
Db 1 CAGCATCAACGCGCAGCAGCA 20

RESULT 290
US-10-181-603-11
; Sequence 11, Application US/10181603
; Publication No. US20030049662A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION
; FILE REFERENCE: RTSP-0342
; CURRENT APPLICATION NUMBER: US/10/181,603
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01165
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/487,444
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-603-11

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1406 CAACAGCAGCAGCAGCAG 1423
      ||||| ||||| ||||| |||||
Db 1 CGACAGCAGCAGCAGCAG 18

RESULT 291
US-10-730-771-206
; Sequence 206, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-206

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```
RESULT 296
US-10-831-901A-11558
; Sequence 11558, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11558

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1545 AGCAGCAGCAACACAGC 1562
Db 2 AGCAGCAGCAACATAGC 19
|||||

RESULT 297
US-10-643-038-61
; Sequence 61, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-61
```

```
Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2556 TGACGTCTGCAGGAGTCC 2573
Db 3 TGACTTCTGCAGGAGTCC 20
|||||

RESULT 298
US-09-792-818-608
; Sequence 608, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; TITLE OF INVENTION: (Grid) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 608
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-608

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCACACGCA 990
Db 2 UGCAGCAGCACACGCA 17
|||||

RESULT 299
US-10-494-343-166
; Sequence 166, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 166
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-166

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCACCAACAG 1444
|||||
```

```
Db      2 GCAGCAGCAGCAACAG 17

RESULT 300
US-10-494-343-173
; Sequence 173, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuyvy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aescima Sequence Listing Engine
; SEQ ID NO 173
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-173

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1402 GCAGCAGCAGCAGCAG 1417
      |||||
Db      1 GCAGCAACAGCAGCAG 16

RESULT 301
US-10-436-231-5
; Sequence 5, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Sorge, Joseph A
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT APPLICATION NUMBER: US/10/436,231
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/452,481
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-5

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGC 1424
      |||||
Db      1 CAGCAGCAGCAGCAGC 16

RESULT 302
US-10-436-231-6/c
; Sequence 6, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Sorge, Joseph A
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT APPLICATION NUMBER: US/10/436,231
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/452,481
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-6

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGC 1424
      |||||
Db      18 CAGCAGCAGCAGCAGC 3

RESULT 303
US-10-148-835-86/c
; Sequence 86, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Designed
; OTHER INFORMATION: oligonucleotide primer for PCR
US-10-148-835-86

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      986 CAGCAGCAGCAGCAGCAGC 1001
      |||||
Db      18 CAGCAGCAGCAGCAGCAGC 3

RESULT 304
US-10-704-263-201/c
; Sequence 201, Application US/10704263
; Publication No. US20050101013A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: James Karras
; TITLE OF INVENTION: MODULATION OF STATS EXPRESSION
; FILE REFERENCE: RFS-0569
; CURRENT APPLICATION NUMBER: US/10/704,263
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 213
; SEQ ID NO 201
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-704-263-201
    Query Match          0.4%; Score 16; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 CAACAACAGCAGCAGC 1568
    |||||
Db 20 CAACAACAGCAGCAGC 5

RESULT 305
US-10-923-329-8/c
; Sequence 8, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
; FILE REFERENCE: 400/225 (MBH04-672)
; CURRENT APPLICATION NUMBER: US/10/923,329
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-329-204

    Query Match          0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGC 1427
    |||||
Db 1 CAGCAGTAGTAGCAGCAGC 19

RESULT 307
US-10-215-432-43/c
; Sequence 43, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: NApPro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-43

    Query Match          0.4%; Score 15.6; DB 1; Length 30;
    Best Local Similarity 70.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-704-263-201
    Query Match          0.4%; Score 16; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 CAACAACAGCAGCAGC 1568
    |||||
Db 20 CAACAACAGCAGCAGC 5

RESULT 306
US-10-923-329-204
; Sequence 204, Application US/10923329
; Publication No. US20050164968A1
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Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
DB 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
RESULT 308
US-09-848-754A-175
; Sequence 175, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 175
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-175
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3633 GAGAACCTAGAAAACAT 3649
DB 1 GAGAACCUAGAAAUCAU 17
RESULT 309
US-09-792-818-360
; Sequence 360, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 360
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-360
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 985 CCAGCAGCAGCAGCAGCAGC 1001
DB 1 CCUGCAGCAGCAGCAGCAGC 17
RESULT 310
US-09-792-818-361
; Sequence 361, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-361
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 976 GCAGCAGCAGCAGCAGC 992
DB 1 GCAGCAGCAGCAGCAGC 17
```

```
RESULT 311
US-09-792-818-362
; Sequence 362, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 362
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-362
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 978 AGCAGCAGCAGCAGCAGC 994
DB 1 AGCAGCAGCAGCAGCAGC 17
```

```
RESULT 312
US-09-792-818-363
; Sequence 363, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
```

;
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 363
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-363

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 979 GCAGCACCAGCAGCAGC 995
Db 1 GCAGCACCAGCACCAGC 17

RESULT 313
US-09-792-818-609
; Sequence 609, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 609
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-609

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 CAGCAGCAGCAGCAGCC 1002
Db 1 CAGCACCAGCACCAGCC 17

RESULT 314
US-10-138-674-2491/c
; Sequence 2491, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17

;
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2491
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1

RESULT 315
US-10-287-949A-2491/c
; Sequence 2491, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-2491

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1

RESULT 316
US-10-494-343-174
; Sequence 174, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-174

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1505 CAGCAACAGCAGCAGAG 1521
 |||||
 Db 1 CAGCAACAGCAGCAGGG 17

RESULT 317
 US-09-968-122-9
 ; Sequence 9, Application US/09968122
 ; Publication No. US20030158397A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramos, Juan Luis
 ; APPLICANT: Ben-Bassat, Arie
 ; APPLICANT: Godoy, Patricia
 ; APPLICANT: Ramos-Gonzalez, Maria Isabel
 ; APPLICANT: Duque, Estrella
 ; TITLE OF INVENTION: Methods for Production of p-Hydroxybenzoate in Bacteria
 ; FILE REFERENCE: BC1030 US NA
 ; CURRENT APPLICATION NUMBER: US/09/968,122
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/236,879
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 9
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: artificial sequence, primer
 ; FEATURE:
 ; OTHER INFORMATION: :
 US-09-968-122-9

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 977 CAGCAGCACCAGCAGCA 993
 |||||
 Db 1 CAGCAGCACCAGCATCA 17

RESULT 318
 US-10-432-422-27/c
 ; Sequence 27, Application US/10432422
 ; Publication No. US20040076981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta Participations AG
 ; APPLICANT: Cornell Research Foundation, Inc.
 ; APPLICANT: Yoder, Olen
 ; APPLICANT: Turgeon, Barbara G.
 ; APPLICANT: Lu, Shen-wen
 ; TITLE OF INVENTION: Fungal Iron Reductase Gene
 ; FILE REFERENCE: 1360.017W01
 ; CURRENT APPLICATION NUMBER: US/10/432,422
 ; CURRENT FILING DATE: 2003-05-21
 ; PRIOR APPLICATION NUMBER: US 60/252,732
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 60/252,649
 ; PRIOR FILING DATE: 2000-11-22
 ; NUMBER OF SEQ ID NOS: 210
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-10-432-422-27

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 978 AGCAGCACCAGCAGCAG 994
 |||||
 Db 18 AGAAGCACCAGCAGCAG 2

RESULT 319
 US-10-444-925-183
 ; Sequence 183, Application US/10444925
 ; Publication No. US20040009946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Stephen Patrick
 ; APPLICANT: Klinghoffer, Richard
 ; APPLICANT: Wilson, Linda K.
 ; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
 ; TITLE OF INVENTION: BY RNA INTERFERENCE
 ; FILE REFERENCE: 200125.441
 ; CURRENT APPLICATION NUMBER: US/10/444,925
 ; CURRENT FILING DATE: 2003-05-23
 ; NUMBER OF SEQ ID NOS: 599
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 183
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Small interfering RNA
 US-10-444-925-183

Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 70.6%; Pred. No. 2.4e+02;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3674 CCATATTCACTCTCTCAC 3690
 |||||
 Db 2 CCAUUAUCACACCCUCAC 18

RESULT 320
 US-10-883-218-297
 ; Sequence 297, Application US/10883218
 ; Publication No. US20050124567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haeberli, Peter
 ; APPLICANT: McSwigen, James
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
 ; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
 ; FILE REFERENCE: 400/195 (MBHB04-535)
 ; CURRENT APPLICATION NUMBER: US/10/883,218
 ; CURRENT FILING DATE: 2004-07-01
 ; PRIOR APPLICATION NUMBER: PCT/US04/16390
 ; PRIOR FILING DATE: 2003-05-24
 ; PRIOR APPLICATION NUMBER: US 10/826,966
 ; PRIOR FILING DATE: 2004-04-16
 ; PRIOR APPLICATION NUMBER: US 10/757,803
 ; PRIOR FILING DATE: 2004-01-14
 ; PRIOR APPLICATION NUMBER: US 10/720,448
 ; PRIOR FILING DATE: 2003-11-24
 ; PRIOR APPLICATION NUMBER: US 10/693,059
 ; PRIOR FILING DATE: 2003-10-23
 ; PRIOR APPLICATION NUMBER: US 10/444,853
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: US 10/427,160
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: PCT/US03/05346
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: PCT/US03/05028
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 930
 ; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 297
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-883-218-297

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 143 CTCACGGGTTCTTGAA 159
      ||||| ||||| |||||
Db 1 CUCCAGGUGUUCUGAA 17

RESULT 321
US-10-883-218-699/c
; Sequence 699, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Haeblerli, Peter
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
; FILE REFERENCE: 400/195 (MBH04-535)
; CURRENT APPLICATION NUMBER: US/10/883,218
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 699
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-883-218-699

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 143 CTCACGGGTTCTTGAA 159
      ||||| ||||| |||||
Db 19 CTCACAGGTTCTTGAA 3

RESULT 322
US-10-893-010-39/c
; Sequence 39, Application US/10893010
```

```
; Publication No. US20050164224A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 400/170 (MBH02-1005-C)
; CURRENT APPLICATION NUMBER: US/10/893,010
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/US 03/03662
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-893-010-39

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 549 AGGAACGTGTTCAATGAA 565
      ||||| ||||| |||||
Db 17 AGGAAGTGTTCATGAA 1

RESULT 323
US-10-893-010-278
; Sequence 278, Application US/10893010
; Publication No. US20050164224A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 400/170 (MBH02-1005-C)
; CURRENT APPLICATION NUMBER: US/10/893,010
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/US 03/03662
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
```

```
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region
US-10-893-010-278

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 549 AGGAAGUGUCAAUGAA 565
Db 3 AGGAAGUGUCAAUGAA 19

RESULT 324
US-09-880-313A-228
; Sequence 228, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 228
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-228

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2586 GTACACCTGCAGCCT 2600
Db 1 GTACACCTGCAGCCT 15

RESULT 325
US-10-494-343-165
; Sequence 165, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shanon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
```

```
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 165
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-494-343-165

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACA 1443
Db 3 GCAGCAGCAGCAACA 17

RESULT 326
US-10-498-848-6
; Sequence 6, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-498-848-6

Query Match          0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3447 AAACCCCATGTCATG 3461
Db 4 AAACCCCATGTCATG 18

RESULT 327
US-09-280-030-28/c
; Sequence 28, Application US/09280030A
; Patent No. US20010021515A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Seiji
; APPLICANT: Higashikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAs ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; TITLE OF INVENTION: DNAs
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280,030A
; CURRENT FILING DATE: 1999-03-26
```

```
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a reverse primer for PCR amplification of
; OTHER INFORMATION: MWPsp-MWPmp5 DNA
US-09-280-030-28

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGAGAGCAGCA 1

RESULT 328
US-09-426-548-43
; Sequence 43, Application US/09426548
; Patent No. US20010044936A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, David
; APPLICANT: Lin-Goerke, Julli L.
; APPLICANT: Ling, Jessica
; TITLE OF INVENTION: No. US20010044936A1el Mutations in Human MLH1 and MSH2 Genes Used
; TITLE OF INVENTION: Diagnosing Colorectal Cancer
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-43

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCCTCAGATCTC 1240
Db 1 CAAAAGCTTCAGATCTC 18

RESULT 329
US-09-861-893-11
; Sequence 11, Application US/09861893
; Patent No. US20020045257A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CpG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/09/861,893
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-893-11

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1024 CTCCTCTGCTGGACCATC 1041
Db 1 CTCCTCTGCGGGCCATC 18

RESULT 330
US-10-272-865-14
; Sequence 14, Application US/10272865
; Publication No. US20030171335A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TITLE OF INVENTION: Treating ssRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-272-865-14

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGCTCAG 1288
Db 1 GCCATGGAGGCCCATCAG 18

RESULT 331
US-10-272-865-34/c
; Sequence 34, Application US/10272865
; Publication No. US20030171335A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TITLE OF INVENTION: Treating ssRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-272-865-34
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Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 18 GCCATGGAGGCCCATCAG 1

RESULT 332

US-10-422-671-14
; Sequence 14, Application US/10422671
; Publication No. US20030224353A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TREATING HEPATITIS C VIRUS
; FILE REFERENCE: 50450-8046.US01
; CURRENT APPLICATION NUMBER: US/10/422,671
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/272,865
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-422-671-14

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 1 GCCATGGAGGCCCATCAG 18

RESULT 333

US-10-422-671-34/c
; Sequence 34, Application US/10422671
; Publication No. US20030224353A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TREATING HEPATITIS C VIRUS
; FILE REFERENCE: 50450-8046.US01
; CURRENT APPLICATION NUMBER: US/10/422,671
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/272,865
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-422-671-34

Query Match 0.4%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 18 GCCATGGAGGCCCATCAG 1

RESULT 334

US-10-349-607-60
; Sequence 60, Application US/10349607
; Publication No. US20030224463A1
; GENERAL INFORMATION:
; APPLICANT: Liskay, Robert M.
; APPLICANT: Bronner, Eric C.
; APPLICANT: Baker, Sean M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Kolodner, Richard D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA MISMATCH REPAIR GENES
; FILE REFERENCE: OHSU 3066
; CURRENT APPLICATION NUMBER: US/10/349,607
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 09/265,503
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 08/352,902
; PRIOR FILING DATE: 1994-12-04
; PRIOR APPLICATION NUMBER: 08/209,521
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: 08/168,877
; PRIOR FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-607-60

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCCTCAGATCTC 1240
|||||
Db 1 CAAAAGCCTCAGATCTC 18

RESULT 335

US-10-317-444-447/c
; Sequence 447, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; APPLICANT: Keys, Christine
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7 Sakai
US-10-317-444-447

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCACACACAGCA 1596


```
; ORGANISM: Homo sapiens
US-10-287-949A-2184

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTGAGCCGACGAGC 1111
    |||: ||||| |||||
Db 1 ACAUGCAGCCGACGAGC 18

RESULT 341
US-10-702-817-24
; Sequence 24, Application US/10702817
; Publication No. US20040147471A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10/702,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106,038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-24

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 CAACGAGCAGCAGCAGCAG 1423
    ||| ||||| |||||
Db 1 CACGAGCGGACGAGCAG 18

RESULT 342
US-10-702-817-25
; Sequence 25, Application US/10702817
; Publication No. US20040147471A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10/702,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106,038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-25
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Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 977 CAGCAGCAGCAGCAGCAG 994
    ||| ||||| |||||
Db 1 CAGGAGCAGCAGCGGCGAG 18

RESULT 343
US-10-296-263-11
; Sequence 11, Application US/10296263
; Publication No. US20050153440A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CPG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/10/296,263
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-263-11

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1024 CTCCTCTGCTGGACCATC 1041
    ||||| ||||| |||||
Db 1 CTCCTCTGCGGGGCATC 18

RESULT 344
US-09-866-108-7201
; Sequence 7201, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7201

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCTATGAGC 337
|||||
Db 2 GACCTTGCCTATGAGC 17

RESULT 345

US-09-866-108-7202
; Sequence 7202, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8467
; LENGTH: 17

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7202

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCTATGAGC 337
|||||
Db 1 GACCTTGCCTATGAGC 16

RESULT 346

US-09-866-108-8467
; Sequence 8467, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8467
; LENGTH: 17


```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1158
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1158

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3633 GAGAACCTAGAAACA 3648
DB      |||||:|||||
        2 GAGAACCUAGAAUCA 17

RESULT 351
US-09-848-754A-3275
; Sequence 3275, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3275
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3275

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3634 AGAACCTAGAAACAAT 3649
DB      |||||:|||||
        1 AGAACCUAGAAUCAU 16

RESULT 352
US-09-827-395A-505/c
; Sequence 505, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-505/c

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2649 CCAGAGCGGCGAGTGGC 2664
DB      |||||:|||||
        16 CCAGAGCGGCGAGTGGC 1

RESULT 353
US-09-827-395A-765/c
; Sequence 765, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-765

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2650 CCAGAGCGGCGAGTGGCT 2665
DB      |||||:|||||
        17 CCAGAGCGGCGAGTGGCT 2

RESULT 354
US-09-740-332-2661/c
; Sequence 2661, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2661

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1660 AAGGTCACCTTTGCCA 1675
| | | | | | | | | | | | | | | | | |
Db 16 AAGGTCACCTTTGACA 1

RESULT 355
US-09-792-818-383
; Sequence 383, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 383
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-383

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCUGCAGCAGC 1424
| | | | | | | | | | | | | | | | | |
Db 2 CAGCAGCUGCAGCAGC 17

RESULT 356
US-09-792-818-524
; Sequence 524, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-524

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCUGCAGCAGC 1424
| | | | | | | | | | | | | | | | | |
Db 1 CAGCAGCUGCAGCAGC 16

RESULT 357

US-09-817-879-2661/c
; Sequence 2661, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2661

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1660 AAGGTCACCTTTGCCA 1675
| | | | | | | | | | | | | | | | | |
Db 16 AAGGTCACCTTTGACA 1

RESULT 358
US-10-061-201-574
; Sequence 574, Application US/10061201
; Publication No. US2003016229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 574
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-574

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2553 CCCTGACGCTGCGAGG 2568
||| ||||| ||||| |||||
Db 2 CCACAGCGCTGCGAGG 17

RESULT 359
US-10-061-201-575
; Sequence 575, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006653
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 575
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-575

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2553 CCCTGACGCTGCGAGG 2568
||| ||||| ||||| |||||
Db 1 CCACAGCGCTGCGAGG 16

RESULT 360
US-10-430-882-505/c
; Sequence 505, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 575
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-505

; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-505

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2649 CCACAGGGCGAGTGGC 2664
||||| ||||| ||||| |||||
Db 16 CCACAGCGCGAGTGGC 1

RESULT 361
US-10-430-882-765/c
; Sequence 765, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-765

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2650 CCACAGGGCGAGTGGCT 2665
||||| ||||| ||||| |||||
Db 17 CCACAGCGCGAGTGGCT 2

RESULT 362
US-10-138-674-1755
; Sequence 1755, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1755

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 1 AAUUGCUCUAAUUGA 16

RESULT 363

US-10-138-674-6407
; Sequence 6407, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6407

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 2 AAUUGCUCUAAUUGA 17

RESULT 364

US-10-138-674-8510
; Sequence 8510, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8510
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-138-674-8510

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3343 AAACAGAACTGTGCTG 3358
|||||:|:|:|:|:|:|
Db 2 AAACAAAACUGUGGUG 17

RESULT 365

US-10-287-949A-1755
; Sequence 1755, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1755

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 1 AAUUGCUCUAAUUGA 16

RESULT 366

US-10-287-949A-6407
; Sequence 6407, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6407

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:~|:|:|:|:|:|
Db 2 AAUUGCUCUAAUUGA 17

```
RESULT 367
US-10-287-949A-8510
; Sequence 8510, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8510
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8510

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3343 AAACAGAACTGTGGTG 3358
||||| ||||| ||||| |||||
Db 2 AAACAAACUGUGGUG 17

RESULT 368
US-10-712-672-2609/c
; Sequence 2609, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MEH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2609
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2609

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2851 CCAGCCACCATCCCTG 2866
||||| ||||| ||||| |||||
Db 17 CCAGCGACCATCCCTG 2

RESULT 369
US-10-669-841-5254/c
; Sequence 5254, Application US/10669841
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
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; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5254
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5254

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675
||||| ||||| ||||| |||||
Db 16 AAGGTCACCTTTGACA 1

RESULT 370
US-10-723-361-7201
; Sequence 7201, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: Ji, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
```

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; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7201
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 322 GACCTTGCCCTATGAGC 337
Db 2 GACCTTGCCGATGAGC 17
|||||
```

```
RESULT 371
US-10-723-361-7202
; Sequence 7202, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7202
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 322 GACCTTGCCCTATGAGC 337
Db 1 GACCTTGCCGATGAGC 16
|||||
```

```
RESULT 372
US-10-723-361-8467
; Sequence 8467, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
```

```
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8467
```

```
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 602 GAACTGGAGAACATGA 617
|||
```

```
Db      2 GAGCTGGAGAACATGA 17

RESULT 373
; Sequence 8468, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723.361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8468
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8468

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      602 GAACTGGAGAACATGA 617
      ||| ||||| ||||| |||||
Db      1 GAGCTGGAGAACATGA 16

RESULT 374
; Sequence 3573, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: MHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712.633
; CURRENT FILING DATE: 2003-11-13
```

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; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3573
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-3573

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      3343 AAACAGNACTGTGTG 3358
      ||||| ||||| ||||| |||||
Db      2 AAACAAAACUGUGUG 17

RESULT 375
US-10-494-343-175
; Sequence 175, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 175
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-175

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1506 AGCAACAGCAGCAGAG 1521
      ||||| ||||| ||||| |||||
Db      1 AGCAACAGCAGCAGGG 16

RESULT 376
US-10-388-263-343/c
; Sequence 343, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
```



```
; APPLICANT: Freier, Susan M.
; APPLICANT: Samori, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-343

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAAGCGGCGGAGGAG 88
Db 18 GAAGCGGAGGAGGAG 3

RESULT 377
US-10-468-655-42/c
; Sequence 42, Application US/10468655
; Publication No. US20040197784A1
; GENERAL INFORMATION:
; APPLICANT: Miano, Joseph W.
; APPLICANT: Streb, Jeffrey W.
; APPLICANT: Chen, Jiyan
; TITLE OF INVENTION: RETINOID INDUCIBLE PROTEINS OF VASCULAR SMOOTH MUSCLE
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 176/61022
; CURRENT APPLICATION NUMBER: US/10/468,655
; CURRENT FILING DATE: 2003-08-20
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/271,183
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-468-655-42

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCGCAACAG 1444
Db 17 GCAGCATCAGCAACAG 2

RESULT 378
US-10-467-019-7
; Sequence 7, Application US/10467019
; Publication No. US20040048314A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. US20040048314A1e1 Physioloical Active Peptide and Its Use
; FILE REFERENCE: P01-0295PCT
; CURRENT APPLICATION NUMBER: US/10/467,019
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: JP2001-026820
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer, hBv8-F1 primer
US-10-467-019-7

Query Match          0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1931 CTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCCGCTGCTG 24

RESULT 379
US-10-376-770-220/c
; Sequence 220, Application US/10376770
; Publication No. US20040106102A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: RAPID ANALYSIS OF VARIATIONS IN A GENOME
; FILE REFERENCE: 543312000320
; CURRENT APPLICATION NUMBER: US/10/376,770
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 262
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6, 7
; OTHER INFORMATION: These nucleotides may be absent
US-10-376-770-220

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 TGTTCAGGTGGACT 3187
Db 14 TGTTCAGGTGGACT 1

RESULT 380
US-10-661-165-220/c
; Sequence 220, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 543312000420
; CURRENT APPLICATION NUMBER: US/10/661,165
; CURRENT FILING DATE: 2003-09-11
```

```
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (6)...(7)
; OTHER INFORMATION: These nucleotides may be absent
US-10-661-165-220

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3174 TGTTCAGGTGGACT 3187
Db 14 TGTTCAGGTGGACT 1

RESULT 381
US-10-494-343-164
; Sequence 164, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PR0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 164
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-164

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAAC 1442
Db 4 GCAGCAGCAGCAAC 17

RESULT 382
US-10-011-993-35/c
; Sequence 35, Application US/10011993
; Publication No. US20030119004A1
; GENERAL INFORMATION:
; APPLICANT: WENZ, H. MICHAEL
; APPLICANT: SCHROTH, GARY P.
; APPLICANT: CHEN, CAIFU
; TITLE OF INVENTION: METHODS FOR QUANTITATING NUCLEIC ACIDS USING COUPLED
; FILE REFERENCE: 07414.0030-00000
; CURRENT APPLICATION NUMBER: US/10/011,993
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: PCT/US01/17329
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 09/724,755
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/584,905
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: This sequence may encompass 1-10 cag repeats
US-10-011-993-35

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 383
US-10-357-322-4/c
; Sequence 4, Application US/10357322
; Publication No. US20030180768A1
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/10/357,322
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/684,843
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-322-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 384
US-09-179-536B-90
; Sequence 90, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
```

APPLICANT: Hubert K ster
David M. Lough
Guobing Xiang
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20444
FILING DATE: 06-NOV-1997
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-SEP-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/746,055
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/746,036
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,590
FILING DATE: 06-NO. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-NO. US20020042112A1-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 858-597-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-179-536B-90

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1399 ACAGCAGCAACAGCAGC 1415
Db 1 ACAGCAGCAACAGCATC 17

RESULT 385
US-09-866-108-664

Sequence 664, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aemica Sequence Listing Engine
SEQ ID NO 664
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-664
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 664 TCAGCAAGCCAGAGGA 680
Db 1 TCAGCAAGCCAGAGAA 17
RESULT 386
US-09-866-108-665
Sequence 665, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark


```
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10747
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10747

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1771 TGTGTTAGGCCAGAAC 1787
Db 1 TGTGTTGGCCTGAACA 17

RESULT 394
US-09-827-998-524
; Sequence 524, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 524
; LENGTH: 17

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10747
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10747

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1771 TGTGTTAGGCCAGAAC 1787
Db 1 TGTGTTGGCCTGAACA 17

RESULT 394
US-09-827-998-524
; Sequence 524, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 524
; LENGTH: 17
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-524

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 473 CAAATGACCCCAAGAGAA 489
Db 1 CAAAGGAACCAAGAGAA 17

RESULT 395
US-09-872-462-243
; Sequence 243, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AECOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 243
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-243

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2673 ACCAGTTAACCAACGCA 2689
Db 1 ACCAGTTAAGACCATCA 17

RESULT 396
US-09-872-462-244
; Sequence 244, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AECOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
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; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 244
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-244

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2674 CCAGTTAACACCCAGCAG 2690
||||| |||||
Db 1 CCAGTTAAGACCATCAG 17

RESULT 397
US-09-872-462-245
; Sequence 245, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-245

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2675 CAGTTAACACCCAGCAGT 2691
||||| |||||
Db 1 CAGTTAAGACCATCAGT 17

RESULT 398
US-09-872-462-246
; Sequence 246, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 246
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-246

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2676 AGTTAACACCCAGCAGTG 2692
||||| |||||
Db 1 AGTTAAGACCATCAGTG 17

RESULT 399
US-09-872-462-247
; Sequence 247, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong

APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-247

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2677 GTTAACACCCAGCAGTGC 2693
Db 1 GTTAAGACCATCAGTGC 17

RESULT 400
US-09-864-785-140
; Sequence 140, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-140

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1176 AGGCGGCGCCCTCAGCC 1192

Db 1 AGGCGGCGCCCTCAGCC 17

RESULT 401
US-09-864-785-366
; Sequence 366, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-366

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1792 CCCGAGTCCAGTCCTA 1808
Db 1 CCCCGUCCAGGCCUA 17

RESULT 402
US-09-864-785-375
; Sequence 375, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 375
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-375

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.9e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 756 CCTCAGGCTCTCCTCAG 772
Db 1 CCCCGGCGCCCTCAG 17

RESULT 403
US-09-864-785-1591/c
; Sequence 1591, Application US/09864785

```
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1591
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1591

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1407 AACGACGACGACGACG 1423
DB 17 AACTGCAGCTGCAGCAG 1

RESULT 404
US-09-780-533A-766
; Sequence 766, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-766

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCACGACGACGACGACG 1427
DB 1 GCGGACGACGACGACGACG 17

RESULT 405
US-09-780-533A-767
; Sequence 767, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
```

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; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 767
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-767

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCACGACGACGACGACG 1427
DB 1 GCACGACGACGACGACG 17

RESULT 406
US-09-780-533A-1103
; Sequence 1103, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1103
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1103

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1687 GCTCCTACTTCAGCAAA 1703
DB 1 GAUCCUACUUCAGAAAA 17

RESULT 407
US-09-780-533A-1549
; Sequence 1549, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1549
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1549

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCA 1425
Db 1 CAGCAGCAGCAGCAUCA 17

RESULT 408
US-09-780-533A-1792
; Sequence 1792, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1792
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1792

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCA 1425
Db 1 CGGCAGCAGCUGCAGCA 17

RESULT 409
US-09-780-533A-2456
; Sequence 2456, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2456
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2456

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1700 CAAATGCAGATCAGCC 1716
Db 1 CAAAAGCAGAAUCUGCC 17

RESULT 410
US-09-927-046-332
; Sequence 332, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-332

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1648 CCAGCCTTTGCTAAGGT 1664
Db 1 CCAGGCAUUGCUAAGGU 17

RESULT 411
US-09-927-046-811/c
; Sequence 811, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 811
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-811

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 269 GCAGGCAAGGTGCCT 285

Db 17 GCAGGAAAAGCTGCCT 1

RESULT 412

US-09-877-478-618/c
; Sequence 618, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-618

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1154 GTAATGGCTAACTACAT 1170
Db 17 GTAATGATTAATACTACAT 1

RESULT 413

US-09-877-478-2137/c
; Sequence 2137, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-2137

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1153 AGTAATGGCTAACTACA 1169
Db 17 AGTAATGATTAATACTACA 1

RESULT 414

US-09-776-474-125/c
; Sequence 125, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK-1)
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-125

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 666 AGCAAGCCAGAGGAGC 682
Db 17 AGCAGAGCTAGAGGAGC 1

RESULT 415

US-09-776-474-478/c
; Sequence 478, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim

```
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-478

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      667  GCAAAGCCAGGAGGAGCA 683
Db      17  GCAGAGCTAGAGGAGCA 1

RESULT 416
US-09-776-474-833/c
; Sequence 833, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 833
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-833

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      665  GAGCAAGCCAGGAGGAG 681
Db      17  CAGCAGAGCTAGAGGAG 1

RESULT 417
US-09-780-164-191/c
; Sequence 191, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-780-164-191/c

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3416  TAAAAAGGTAATAGAA 3432
Db      17  TAAAAAGGAAACAGAA 1

RESULT 418
US-09-780-164-194/c
; Sequence 194, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-780-164-194

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3201  ATGCTTAAAAATCGAAA 3217
Db      17  ATGTTTAAAAAAGGAAA 1

RESULT 419
US-09-827-395A-504/c
; Sequence 504, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 504
; LENGTH: 17
```

```

; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; US-09-297-576A-90

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1399 ACAGCAGCACAGCAGC 1415
DB 1 ACAGCAGGACAGCATC 17
||||| |||||||
||||| |||||||

RESULT 422
US-09-792-818-458
; Sequence 458, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 458
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-792-818-458

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```
Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2508 CACCAACTGGCCCTCT 2524
Db 1 CAACAAGCGGGCCCU 17

RESULT 423
US-09-792-818-607
; Sequence 607, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-607

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCACCA 999
Db 1 CCCCUGCAGCAGCACCA 17

RESULT 424
US-09-817-879-2156/c
; Sequence 2156, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2156
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2156

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 693 CCTCCTTACCCATGAG 709
Db 17 CATCCTTACCCATGAG 1
```

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RESULT 425
US-10-060-830-706
; Sequence 706, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 706
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-706

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 CGGCCCTCAGCCAGG 1196
Db 1 CTGCTCCTCAGCCAGG 17

RESULT 426
US-10-060-830-709
; Sequence 709, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
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; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 709
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-709

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTCAGGCC 781
|||||
Db 1 CTCCTCAGCCAGGCC 17

RESULT 427

US-10-156-306-1337/c
; Sequence 1337, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MH001-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1337
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1337

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 672 GCCAGAGGACACACT 688
|||||
Db 17 GCCAGAGGACCAACT 1

RESULT 428

US-10-156-306-7003/c
; Sequence 7003, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MH001-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7003
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7003

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 TGGAAATCGCTTGTGA 2246
|||||
Db 17 TGGAAATCGCTTGTGA 1

RESULT 429

US-10-238-700-3082/c
; Sequence 3082, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: 400/057 (MH001-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238.700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3082
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3082

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 237 TCAAAAGAAATTCGTGT 253
|||||
Db 17 TCAAAAGACTTGGTGT 1

RESULT 430

US-10-061-201-572
; Sequence 572, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061.201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 572
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-572

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;


```
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2550 AAGCCTGACGCTGCAG 2566
    |||||
Db 1 AACCCAGACGCTGCAG 17

RESULT 431
US-10-061-201-573
; Sequence 573, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 573
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-573

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2551 AGCCCTGACGCTGCAG 2567
    |||||
Db 1 ACCCCAGACGCTGCAG 17

RESULT 432
US-10-061-201-981/c
; Sequence 981, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 573
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-573

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2551 AGCCCTGACGCTGCAG 2567
    |||||
Db 1 ACCCCAGACGCTGCAG 17

RESULT 433
US-10-061-201-1567/c
; Sequence 1567, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1567

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2211 TTCAGAAATATGGGATG 2227
    |||||
Db 17 TTCTGAAATATGGGATG 1
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 981
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-981

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3090 AAACAAGAAAGGGAAGA 3106
    |||||
Db 17 AAACAAGATAGGGAAGA 1

RESULT 433
US-10-061-201-1567/c
; Sequence 1567, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1567
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1567

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2211 TTCAGAAATATGGGATG 2227
    |||||
Db 17 TTCTGAAATATGGGATG 1
```

```

; Publication No. US20030191077A1
; GENERAL INFORMATION: Fosnaugh, Kathy
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1406
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-1406

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      977  CAGCAGCACCAGCAGCA 993
Db      17  CATCAGCGCCAGCAGCA 1

RESULT 437
US-10-230-006-2208/c
; Sequence 2208, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION: Fosnaugh, Kathy
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2208
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2208

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      978  AGCAGCACCAGCAGCAG 994
Db      17  ATCAGCGCCAGCAGCAG 1

RESULT 438
US-10-357-488-9
; Sequence 9, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
; APPLICANT: Centre For DNA Fingerprinting and Diagnostics
; TITLE OF INVENTION: No. US20030194730A1el FISSR-PCR primers and markers and a method c
; TITLE OF INVENTION: primers and markers for identifying genetic constitution and bre
; TITLE OF INVENTION: varieties.
; FILE REFERENCE: 782-Indian
; CURRENT APPLICATION NUMBER: US/10/357,488
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 280/MAS/2002
; PRIOR FILING DATE: 2002-04-08
;

; Publication No. US10148687
; Sequence 56, Application US/10148687
; Publication No. US20030185836A1
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU PQ4400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-56

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      2394  TTGGAGCTGGATCTGTT 2410
Db      1  TTGGTGGCGGATCTGTT 17

RESULT 436
US-10-230-006-1406/c
; Sequence 1406, Application US/10230006
```

```

; Publication No. US20030191077A1
; GENERAL INFORMATION: Fosnaugh, Kathy
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1406
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-1406

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      977  CAGCAGCACCAGCAGCA 993
Db      17  CATCAGCGCCAGCAGCA 1

RESULT 437
US-10-230-006-2208/c
; Sequence 2208, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION: Fosnaugh, Kathy
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2208
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2208

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      978  AGCAGCACCAGCAGCAG 994
Db      17  ATCAGCGCCAGCAGCAG 1

RESULT 438
US-10-357-488-9
; Sequence 9, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
; APPLICANT: Centre For DNA Fingerprinting and Diagnostics
; TITLE OF INVENTION: No. US20030194730A1el FISSR-PCR primers and markers and a method c
; TITLE OF INVENTION: primers and markers for identifying genetic constitution and bre
; TITLE OF INVENTION: varieties.
; FILE REFERENCE: 782-Indian
; CURRENT APPLICATION NUMBER: US/10/357,488
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 280/MAS/2002
; PRIOR FILING DATE: 2002-04-08
;

; Publication No. US10148687
; Sequence 56, Application US/10148687
; Publication No. US20030185836A1
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU PQ4400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-56

Query Match      0.4%;   Score 13.8;   DB 1;   Length 17;
Best Local Similarity 88.2%;   Pred. No. 2.9e+02;
Matches 15;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      2394  TTGGAGCTGGATCTGTT 2410
Db      1  TTGGTGGCGGATCTGTT 17

RESULT 436
US-10-230-006-1406/c
; Sequence 1406, Application US/10230006
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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-9

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1554 AACACAGCAGCAGCAG 1570
    |||||||
Db 1 AAATACAGCAGCAGCAG 17

RESULT 439
US-10-430-882-504/c
; Sequence 504, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 504
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-504

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2651 CAGAGGGCAGTGGCTCC 2667
    |||||
Db 17 CAGAGGGCAGTGGCTGC 17

RESULT 440
US-10-307-005-1147/c
; Sequence 1147, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
```

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; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1147
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucumis sativus
US-10-307-005-1147

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 CCAGCAGCTCAACACAGA 944
    |||||
Db 17 CCAGCTGCTCAACACGA 17

RESULT 441
US-10-307-005-1148
; Sequence 1148, Application US/10307005.
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gampier
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1148
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucumis sativus
US-10-307-005-1148

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 CCAGCAGCTCAACACAGA 944
    |||||
Db 1 CCAGCTGCTCAACACGA 17

RESULT 442
US-10-307-005-1167/c
; Sequence 1167, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
```

```
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1167
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucurbita sp.
US-10-307-005-1167

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 928 CCAGCAGCTCAAAACAGA 944
Db 17 CCAGCTGCTCAAAACCGA 1

RESULT 443
US-10-307-005-1168
; Sequence 1168, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1168
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucurbita sp.
US-10-307-005-1168

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 928 CCAGCAGCTCAAAACAGA 944
Db 1 CCAGCTGCTCAAAACCGA 17

RESULT 444
US-10-307-005-2559/c
; Sequence 2559, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-307-005-2559

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAAAACAGATA 946
Db 17 AGCAGCTCAAGCAGCTA 1

RESULT 445
US-10-307-005-2560
; Sequence 2560, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-307-005-2560

Query Match          0.4%; Score 13.8; DB 1; Length 17;
```

```
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 AGCAGCTCAACAGATA 946
DB 1 AGCAGCTCAACAGCTA 17

RESULT 446
US-10-342-902-618/c
; Sequence 618, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-618

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 GTAATGGCTAACTACAT 1170
DB 17 GTAATGATTAACTACAT 1

RESULT 447
US-10-342-902-2137/c
; Sequence 2137, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
```

```
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-2137

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1153 AGTAATGGCTAACTACA 1169
DB 17 AGTAATGATTAACTACA 1

RESULT 448
US-10-675-685-524
; Sequence 524, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 524
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-524

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAATGACCAAGAGAA 489
DB 1 CAATGACCAAGAGAA 17

RESULT 449
US-10-138-674-25
; Sequence 25, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-25

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TGCTACTTCTCAGCGG 2182
|||:|:|:|:|:|:|
Db 1 UGUCGUCUUCACAGG 17

RESULT 450
US-10-138-674-26
; Sequence 26, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-26

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2167 GCTACTTCTCAGCGG 2183
|||:|:|:|:|:|:|
Db 1 GUCUGUCUUCACAGG 17

RESULT 451
US-10-138-674-414/c
; Sequence 414, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 414
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-414

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 430 GGAGCCAGGAGAGACTC 446
|||||:|:|:|:|:|:|
Db 17 GGAGCCAGGAGAGACTC 1

RESULT 452
US-10-138-674-415/c
; Sequence 415, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 415
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-415

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 AGGAGCCAGGAGAGACT 445
|||||:|:|:|:|:|:|
Db 17 AGGAGCCAGGAGAGACT 1

RESULT 453
US-10-138-674-1095
; Sequence 1095, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1095

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.9e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 224 TCATTCTTGATATCAA 240
:|:|:|:|:|:|:|:|:|
Db 1 UCAUGUCUUGAUUCAA 17

RESULT 454
US-10-138-674-2132/c

```
; Sequence 2132, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-2132

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGGAGCAGAGCTCA 1

RESULT 455
US-10-138-674-3256
; Sequence 3256, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3256

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCGTGAATCTCAGACCC 2773
Db 1 GGCUGACUCUCACAGCCC 17

RESULT 456
US-10-138-674-4212
; Sequence 4212, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
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; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4212

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGTCTACTTCTCACGG 2181
Db 1 CUGUCUGCUCUCACAG 17

RESULT 457
US-10-138-674-6437
; Sequence 6437, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6437

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGAGC 1111
Db 1 CAUGCAGCCACAGAGC 17

RESULT 458
US-10-138-674-7508/c
; Sequence 7508, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7508
; LENGTH: 17
; TYPE: RNA
```



```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 415
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-415

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 AGGAGCCAGAGAGACT 445
Db 17 AGGAGCCAGAGAGAGT 1

RESULT 464
US-10-287-949A-1095
; Sequence 1095, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1095

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 224 TCATTCTTGATATCAA 240
Db 1 UCAUGUCUUGAUUCAA 17

RESULT 465
US-10-287-949A-2132/c
; Sequence 2132, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-2132

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGAGGAGAGAGCTCA 1

RESULT 466
US-10-287-949A-3256
; Sequence 3256, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3256

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2757 GTCTGANTCTCAGACCC 2773
Db 1 GCGUGACUCUCAGACCC 17

RESULT 467
US-10-287-949A-4212
; Sequence 4212, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4212

Query Match
0.4%; Score 13.8; DB 1; Length 17;
```

```

US-10-287-949A-8718
; Sequence 8718, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8718
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8718

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. NO. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1093 GACATTGAGCCACAGA 1109
|||: |||||: ||
Db 1 GACAUGCAGCCACUGA 17

RESULT 471
US-10-712-672-765
; Sequence 765, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-765

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GCGCGCCTTCGAGGAGG 107
|||||: |||||: ||
Db 1 GCGCGCCCCCGAGGAGG 17

RESULT 472
US-10-712-672-1142
; Sequence 1142, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

```

; APPLICANT: Chowrira, Bharat
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1142
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-1142

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.9e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 853 TCAGAGCCAGGCTCAGC 869
 :|||||||:|
 Db 1 UCAGAGCCAGUCUACC 17

RESULT 473
 US-10-712-672-1409
 ; Sequence 1409, Application US/10712672
 ; Publication No. US20040102413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1409
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-1409

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 2.9e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1016 GCCTTGCCCTCCTCTGC 1032
 |||:|||||:|
 Db 1 GCCCGCCCUCCUUGC 17

RESULT 474
 US-10-712-672-2180
 ; Sequence 2180, Application US/10712672
 ; Publication No. US20040102413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Chowrira, Bharat

; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2180
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-2180

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1390 CCAACAGCAACAGCAGC 1406
 |||||||||
 Db 1 CGCCAGCAACAGCAGC 17

RESULT 475
 US-10-380-236A-18
 ; Sequence 18, Application US/10380236A
 ; Publication No. US20040126860A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 ; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 ; APPLICANT: HUMAN SERVICES
 ; APPLICANT: Epstein, Neal
 ; APPLICANT: Hasanzadeh, Shahin
 ; APPLICANT: Davis, Julien S.
 ; APPLICANT: Whitsky, Steven S.
 ; TITLE OF INVENTION: Optimize Cardiac Contraction Through Differential Phosphorylation
 ; FILE REFERENCE: 4239-64779
 ; CURRENT APPLICATION NUMBER: US/10/380,236A
 ; CURRENT FILING DATE: 2003-09-25
 ; PRIOR APPLICATION NUMBER: US 60/232,246
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,456
 ; PRIOR FILING DATE: 2000-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/28639
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-380-236A-18

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 845 TCAGTCCCTCAGAGCCA 861
 |||||
 Db 1 TCAGAGCCCGCAGAGCCA 17

RESULT 476
 US-10-669-841-618/c
 ; Sequence 618, Application US/10669841
 ; Publication No. US20040127446A1

```
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-618

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1154 GTAATGGCTAACTACAT 1170
      ||||| ||||| ||||| |||||
DB      17 GTAATGATTAACTACAT 1

RESULT 477
US-10-669-841-1973/c
; Sequence 1973, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-07-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-618

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1153 AGTAATGGCTAACTACA 1169
      ||||| ||||| ||||| |||||
DB      17 AGTAATGATTAACTACA 1

RESULT 478
US-10-669-841-4749/c
; Sequence 4749, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
```

;; PRIOR FILING DATE: 2000-07-07
;; PRIOR APPLICATION NUMBER: US 09/504,321
;; PRIOR FILING DATE: 2000-02-15
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 16207
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4749
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION:
;; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4749

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 693 CCTCCTTACCCATGAG 709
Db 17 CATCCTTACCCATAG 1

RESULT 479

US-10-723-361-664
; Sequence 664, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 664
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-664

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 664 TCAGCAAGCCAGAGG 680
Db 1 TCAGCAAGCCAGAGG 17

RESULT 480

US-10-723-361-665
; Sequence 665, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-665

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CAGCAAGCCAGAGG 681
Db 1 CAGCAAGCCAGAGG 17

RESULT 481

US-10-723-361-1872
; Sequence 1872, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng

US-10-723-361-1872

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666

Length 17;
Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
Db 1 CTACGACGCTGAGGCC 17

RESULT 484

US-10-723-361-7802
; Sequence 7802, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7802
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7802

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCTGAGCA 1425
Db 1 CAGCAGCAGCTGAGCA 17

RESULT 485

US-10-723-361-7803
; Sequence 7803, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7803

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCA 1441
Db 1 AGCAGCAGCAGCA 17

RESULT 486

US-10-723-361-10247
; Sequence 10247, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 10247
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-361-10247

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1187 TCAGCCAGGCTGGCA 1203
|||||
Db 1 TCAGCCAAAGTGGCA 17

RESULT 487

US-10-723-361-10747
; Sequence 10747, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

;; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

;; FILE REFERENCE: PB0105
;; CURRENT APPLICATION NUMBER: US/10/723.361
;; CURRENT FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: US 09/866,108
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 10747
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-723-361-10747

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1771 TGTGTCAGCCAGACA 1787
|||||
Db 1 TGTGTTGCTGACACA 17

RESULT 488

US-10-712-633-505/c
; Sequence 505, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan

;; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
;; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND (

;; FILE REFERENCE: MBHB02-325PCT (400/047)
;; CURRENT APPLICATION NUMBER: US/10/712.633

;; CURRENT FILING DATE: 2003-11-13
;; PRIOR APPLICATION NUMBER: US 60/005,974
;; PRIOR FILING DATE: 1995-10-26
;; PRIOR APPLICATION NUMBER: US 08/584,040
;; PRIOR FILING DATE: 1996-01-08
;; PRIOR APPLICATION NUMBER: US 09/371,772
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 09/708,690
;; PRIOR FILING DATE: 2000-11-07
;; PRIOR APPLICATION NUMBER: US 09/870,161
;; PRIOR FILING DATE: 2001-05-29
;; PRIOR APPLICATION NUMBER: US 60/334,461
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: US 10/138,674
;; PRIOR FILING DATE: 2002-05-03
;; NUMBER OF SEQ ID NOS: 5989
;; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 505
;; LENGTH: 17
;; TYPE: RNA

;; ORGANISM: Homo Sapiens

US-10-712-633-505

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3552 TTCTGTAAGCTTCAGG 3568
|||||
Db 17 TGCTGAATCTTCAGG 1

RESULT 489

US-10-712-633-3854
; Sequence 3854, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan

;; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
;; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND (

;; FILE REFERENCE: MBHB02-325PCT (400/047)
;; CURRENT APPLICATION NUMBER: US/10/712.633

;; CURRENT FILING DATE: 2003-11-13
;; PRIOR APPLICATION NUMBER: US 60/005,974
;; PRIOR FILING DATE: 1995-10-26
;; PRIOR APPLICATION NUMBER: US 08/584,040
;; PRIOR FILING DATE: 1996-01-08
;; PRIOR APPLICATION NUMBER: US 09/371,772
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 09/708,690
;; PRIOR FILING DATE: 2000-11-07


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; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3854
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-3854

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1093 GACATTTCAGCCACAGA 1109
Db 1 GACAUGCAGCCACUGA 17

RESULT 490
US-10-494-343-809
; Sequence 809, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 809
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-809

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 150 GTTCTTGAAGAGAAA 166
Db 1 GTTCTTGAAGAGAAA 17

RESULT 491
US-10-498-462-1977/c
; Sequence 1977, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 1977
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-1977

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1772 GTGCTAGCCAGACAC 1788
Db 17 GTGCTGGCCAGAGAC 1

RESULT 492
US-10-730-771-197
; Sequence 197, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-197

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 815 TCTGCCCTCTCCACTTC 831
Db 1 TCTGCCCTCTGCACCTC 17

RESULT 493
US-10-497-091-296/c
; Sequence 296, Application US/10497091
; Publication No. US20050074863A1
; GENERAL INFORMATION:
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: WILLIAMS, Steven
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
; FILE REFERENCE: MER-130
; CURRENT APPLICATION NUMBER: US/10/497,091
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/BP02/13351
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP02020634.8
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RESULT 495
US-10-724-270-1761/c
; Sequence 1761, Application US/10724270
; Publication No. US2005008031A1
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: MCSwiggan, James
; TITLE OF INVENTION: Nucleic Acid Treat
; TITLE OF INVENTION: RAS, HER2 and HI

QY 1286 CAGGGCAACACCAAGCC 1302
|||
Db 17 CAGGGCAACACACGCC 1

Search completed: August 16, 2005, 13:15:12
Job time : 24 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 12:53:56 ; Search time 23 Seconds
(without alignments)
3.347 Million cell updates

Title: US-10-698-070-1

Perfect score:

Sequence: 1 aggtggcggcgagaagatgg.....taaacaaaaatatagagctg 3763

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 544 seqs, 10230 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 17

Maximum DB seq length:	17
Maximum DB seq length:	35

Post-processing: Minimum Match 0%

FORC-PROCESSING: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 553 summaries

Database : fetch1rnq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.4	0.8	33	1	ABX79926
2	30	0.8	30	1	AA244310
3	30	0.8	30	1	AAS13781
4	30	0.8	30	1	ADN97254
5	30	0.8	31	1	AAQ98457
6	30	0.8	31	1	AA224936
7	29.4	0.8	31	1	AA131042
8	28.4	0.8	30	1	AB281777
9	28	0.7	28	1	ABA00946
10	25.4	0.7	29	1	AAQ3392
11	25	0.7	25	1	AB281787
12	25	0.7	25	1	AB281768
13	24	0.6	24	1	ABN87602
14	24	0.6	24	1	ADN97255
15	24	0.6	24	1	ADN97164
16	24	0.6	24	1	ADP68635
17	23.4	0.6	29	1	ADMA48412
18	23	0.6	23	1	ABA00945
19	23	0.6	23	1	ADC59319
20	22.4	0.6	27	1	ADQ43735
21	22	0.6	22	1	ADC59320
22	22	0.6	25	1	ADC38187
23	22	0.6	25	1	ADC38189
24	22	0.6	25	1	ADC38186
25	22	0.6	25	1	ADC38188
26	21.2	0.6	26	1	ABST1093
27	21.2	0.6	26	1	AB230010
28	21.2	0.6	26	1	ADG69029
29	21	0.6	21	1	AAF59580
30	21	0.6	21	1	ABST78286
31	21	0.6	21	1	ABL38849
32	21	0.6	21	1	ABK10202
33	21	0.6	21	1	ACH03118

C	34	21	0.6	21	1	ADB37082
	35	21	0.6	25	1	ADC38190
	36	21	0.6	25	1	ADC38185
	37	20.8	0.6	24	1	ABL61611
	38	20.8	0.6	24	1	ABK94601
	39	20.8	0.6	24	1	ABX92931
	40	20.8	0.6	24	1	ABZ58841
	41	20.8	0.6	24	1	ADC51835
C	42	20.4	0.5	22	1	ABK88725
	43	20	0.5	20	1	AAD37201
C	44	20	0.5	20	1	ABZ30516
	45	20	0.5	20	1	ABZ31489
	46	20	0.5	21	1	AAQ31496
	47	20	0.5	25	1	ADC38191
	48	20	0.5	25	1	ADC38184
	49	19.8	0.5	24	1	ADN97247
	50	19.4	0.5	21	1	ABZ81769
	51	19.4	0.5	22	1	AAZ76808
C	52	19.4	0.5	24	1	ABX03797
	53	19.2	0.5	24	1	ADN06499
	54	19.2	0.5	24	1	ADS94518
C	55	19	0.5	20	1	AAZ97150
	56	19	0.5	23	1	AAZ76807
C	57	18.8	0.5	22	1	AAZ54149
	58	18.8	0.5	23	1	AAZ85525
C	59	18.8	0.5	23	1	ABV72153
	60	18.8	0.5	23	1	ADH62525
C	61	18.4	0.5	20	1	AAZ57248
	62	18.4	0.5	20	1	AAZ55806
C	63	18.4	0.5	20	1	AAH43116
	64	18.4	0.5	20	1	AAZ89545
C	65	18.4	0.5	20	1	AAZ89536
	66	18.4	0.5	20	1	AAZ20967
C	67	18.4	0.5	20	1	ABZ86076
	68	18.4	0.5	20	1	ABD22306
C	69	18.4	0.5	20	1	ADP20499
	70	18	0.5	18	1	AAZ63144
C	71	18	0.5	18	1	AAZ13717
	72	18	0.5	18	1	ADN97239
C	73	18	0.5	18	1	ADQ26674
	74	18	0.5	18	1	ADQ26644
C	75	18	0.5	18	1	ADQ26638
	76	18	0.5	18	1	ADQ26610
	77	18	0.5	18	1	ADQ26696
C	78	18	0.5	18	1	ADQ26614
	79	18	0.5	18	1	ADQ63261
C	80	18	0.5	20	1	AAZ69372
	81	18	0.5	20	1	AAZ69373
C	82	18	0.5	20	1	ADC65856
	83	18	0.5	20	1	ADD69519
C	84	18	0.5	21	1	ABZ75647
	85	17.8	0.5	21	1	ABK70327
	86	17.8	0.5	22	1	ABX94818
	87	17.4	0.5	19	1	AAZ39475
C	88	17.4	0.5	19	1	ADH70599
	89	17.4	0.5	20	1	AAZ86505
C	90	17.4	0.5	20	1	AAZ55807
	91	17.4	0.5	20	1	AAZ35086
C	92	17.4	0.5	20	1	AAH43117
	93	17.4	0.5	20	1	AAH56611
C	94	17.4	0.5	20	1	AAZ89537
	95	17.4	0.5	20	1	AAZ89546
C	96	17.4	0.5	20	1	ABZ86068
	97	17.4	0.5	20	1	ABZ85596
C	98	17.4	0.5	20	1	ABZ86071
	99	17.4	0.5	20	1	ABZ86075
C	100	17.4	0.5	20	1	ABD22298
	101	17.4	0.5	20	1	ABD22301
C	102	17.4	0.5	20	1	ABD22305
	103	17.4	0.5	20	1	ABD21826
C	104	17.4	0.5	20	1	ADP20520
	105	17.4	0.5	21	1	AAZ37188
C	106	17.4	0.5	21	1	AAZ73260

C 107	17.4	0.5	21	1	AAF54275	Primer #26 used in	C 180	16.8	0.4	20	1	ADH66495	Human glucocorticoid
C 108	17.4	0.5	21	1	ACD68312	Novel human secret	C 181	16.8	0.4	20	1	ADH66562	Human glucocorticoid
C 109	17.4	0.5	21	1	ACH04414	Human secreted/tra	C 182	16.8	0.4	20	1	ADH64132	Human glucocorticoid
C 110	17.4	0.5	21	1	ACD67958	Novel human secret	C 183	16.8	0.4	20	1	ADJ60872	Oligonucleotide as
C 111	17.4	0.5	21	1	ADC17974	Human PRO PCR prim	C 184	16.8	0.4	20	1	ADJ60872	Human G protein-co
C 112	17.4	0.5	21	1	ADD70620	Human secreted/tra	C 185	16.8	0.4	20	1	ADO46361	Human oligonucleot
C 113	17.4	0.5	21	1	ADD39697	Human secreted/tra	C 186	16.8	0.4	20	1	ADO32574	Antisense 2'-MOE g
C 114	17.4	0.5	21	1	ADD70143	Human secreted/tra	C 187	16.8	0.4	20	1	ADO32574	HOXB1 RT-PCR prime
C 115	17.4	0.5	21	1	ADD38264	Human secreted/tra	C 188	16.8	0.4	20	1	ADQ26559	Primer HOX11:857L2
C 116	17.4	0.5	21	1	ADD38264	Human secreted/tra	C 189	16.8	0.4	21	1	AAV40968	Human gene single
C 117	17.4	0.5	21	1	ADD38743	Human secreted/tra	C 190	16.8	0.4	21	1	AAV40968	Human polymorphic
C 118	17.4	0.5	21	1	ADD40174	Human secreted/tra	C 191	16.8	0.4	21	1	AAH89072	Synthetic antisense
C 119	17.4	0.5	21	1	ADE03095	Human secreted/tra	C 192	16.8	0.4	21	1	ABK70314	Synthetic antisense
C 120	17.4	0.5	21	1	ADE20007	Human secreted/tra	C 193	16.8	0.4	21	1	ABK70358	Plant AMP-binding
C 121	17.4	0.5	21	1	ADE49918	Human secreted/tra	C 194	16.8	0.4	21	1	ADL23446	Arabidopsis thalia
C 122	17.4	0.5	21	1	ADE21476	Human secreted/tra	C 195	16.8	0.4	21	1	ADL23446	Human ADAM19 gene
C 123	17.4	0.5	21	1	ADP29901	Human secreted/tra	C 196	16.8	0.4	21	1	ADP75370	PCR primer 2 used
C 124	17.4	0.5	21	1	ADP55794	Human secreted/tra	C 197	16.8	0.4	21	1	ADP45615	Forward primer #48
C 125	17.4	0.5	21	1	ADH99298	Human secreted/tra	C 198	16.8	0.4	21	1	AAAF26668	Human Smad7 phosph
C 126	17.4	0.5	21	1	ADP25789	Human secreted/tra	C 199	16.8	0.4	21	1	AAAF26668	Simple sequence re
C 127	17.4	0.5	21	1	ADP24688	Human secreted/tra	C 200	16.8	0.4	21	1	AAAF26668	GAGA-B receptor la
C 128	17.4	0.5	21	1	ADP29424	Human secreted/tra	C 201	16.8	0.4	21	1	ABA93493	Huntington's disea
C 129	17.4	0.5	21	1	ADH02993	Human secreted/tra	C 202	16.8	0.4	21	1	ABA93493	Huntington's disea
C 130	17.4	0.5	21	1	ADH02993	Human secreted/tra	C 203	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 131	17.4	0.5	21	1	ADH03947	Human secreted/tra	C 204	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 132	17.4	0.5	21	1	ADH03470	Human secreted/tra	C 205	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 133	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 206	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 134	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 207	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 135	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 208	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 136	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 209	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 137	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 210	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 138	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 211	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 139	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 212	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 140	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 213	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 141	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 214	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 142	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 215	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 143	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 216	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 144	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 217	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 145	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 218	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 146	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 219	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 147	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 220	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 148	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 221	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 149	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 222	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 150	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 223	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 151	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 224	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 152	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 225	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 153	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 226	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 154	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 227	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 155	17.4	0.5	21	1	ADH04424	Human secreted/tra	C 228	16.8	0.4	21	1	ABZ81757	Huntington's disea
C 156	16.8	0.4	20	1	AAV30272	SCA2 gene CAG repe	C 229	16.8	0.4	20	1	AAH57033	Human oestrogen re
C 157	16.8	0.4	20	1	ADD68486	SNP typing-related	C 230	16.8	0.4	20	1	AAH57033	Chimeric phosphoro
C 158	16.8	0.4	20	1	ABZ86069	Human oligonucleot	C 231	15.8	0.4	19	1	AAH57779	Cell-cycle depende
C 159	16.8	0.4	20	1	ABZ85597	Human oligonucleot	C 232	15.8	0.4	19	1	ADQ62508	Huntington's disea
C 160	16.8	0.4	20	1	ABZ85597	Human oligonucleot	C 233	15.8	0.4	30	1	ABZ81777	EST polymorphic DN
C 161	16.8	0.4	20	1	ABZ86062	Human oligonucleot	C 234	15.6	0.4	33	1	ABX79926	Mouse flk-1 VEGF r
C 162	16.8	0.4	20	1	ABZ86062	Human oligonucleot	C 235	15.6	0.4	33	1	ABX79926	Human EGF-R target
C 163	16.8	0.4	20	1	ABZ86061	Human oligonucleot	C 236	15.4	0.4	17	1	AAV97395	Human GRD zingyme
C 164	16.8	0.4	20	1	ABZ86070	Human oligonucleot	C 237	15.4	0.4	17	1	AAV97395	Human GRD zingyme
C 165	16.8	0.4	20	1	ABZ86070	Human oligonucleot	C 238	15.4	0.4	17	1	ABL46976	Human GRD NCH rib
C 166	16.8	0.4	20	1	ACC62133	Human oligonucleot	C 239	15.4	0.4	17	1	ABL46976	Human GRD NCH rib
C 167	16.8	0.4	20	1	ABD284008	Toxicologically re	C 240	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 168	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 241	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 169	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 242	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 170	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 243	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 171	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 244	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 172	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 245	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 173	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 246	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 174	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 247	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 175	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 248	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 176	16.8	0.4	20	1	ABD22299	Human stannioalcali	C 249	15.4	0.4	17	1	ABL46729	Human GRD NCH rib
C 177	16.8	0.4	20	1	ADH18033	Human glucocorticoid	C 250	15.4	0.4	17	1	ADH54086	Human GRD mRNA su
C 178	16.8	0.4	20	1	ADH65922	Human glucocorticoid	C 251	15.4	0.4	17	1	ADH54086	Human GRD mRNA su
C 179	16.8	0.4	20	1	ADH64974	Human glucocorticoid	C 252	15.4	0.4	18	1	AAQ91051	HHV-6 associated M

253	15.4	0.4	18	1	AAV94830	Human IL-2 recepto	326	14.4	0.4	17	1	ACN04426	WNV Zinzyne subatr
c 254	15.4	0.4	18	1	AAA10553	Smad2 antisense ol	c 327	14.4	0.4	17	1	ABT34779	Tumour suppressi
c 255	15.4	0.4	18	1	AAS07309	CPS1/TESI genomic	c 328	14.4	0.4	17	1	ADB05069	Human MD212 scann
c 256	15.4	0.4	18	1	ABL40838	P. putida exbB and	c 329	14.4	0.4	17	1	ADB05010	Human MD212 scann
c 257	15.4	0.4	18	1	ABS68433	Sequencing primer	c 330	14.4	0.4	17	1	ACD62073	HCV minus strand D
c 258	15.4	0.4	18	1	ADG88997	Pseudomonas putida	c 331	14.4	0.4	17	1	ACC54185	Murine oligonucleo
c 259	15.4	0.4	19	1	AAH82737	cdk3 ribozyme bind	c 332	14.4	0.4	17	1	ADC37826	Human AMLPla scann
c 260	15.4	0.4	19	1	AAA82738	cdk3 ribozyme bind	c 333	14.4	0.4	17	1	ADB45768	Tumour suppressi
c 261	15.4	0.4	19	1	AAH57900	Cell-cycle depende	c 334	14.4	0.4	17	1	ADI50387	Human tumour suppr
c 262	15.4	0.4	19	1	AAH57899	Cell-cycle depende	c 335	14.4	0.4	17	1	ADI49572	Human tumour suppr
c 263	15.4	0.4	19	1	AAH54283	Mouse Cbfal PCR pr	c 336	14.4	0.4	17	1	ADI51822	Human tumour suppr
c 264	15.4	0.4	19	1	ADN34019	Upper strand of cy	c 337	14.4	0.4	17	1	ACC53755	Human tumour suppr
c 265	15.4	0.4	19	1	ADN34258	Lower strand of cy	c 338	14.4	0.4	17	1	ACC52683	Human tumour suppr
c 266	15.4	0.4	19	1	ADH01571	Protein tyrosine p	c 339	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 267	15.4	0.4	19	1	ADR80899	Human glucose-6-ph	c 340	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 268	15.4	0.4	19	1	ADR80898	Human glucose-6-ph	c 341	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 269	15	0.4	17	1	ACD82527	Nucleic acid cloni	c 342	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 270	15	0.4	17	1	ADC37816	Human AMLPla scann	c 343	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 271	15	0.4	17	1	ADL50157	Human tumour suppr	c 344	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 272	15	0.4	18	1	ADC40522	Human G-protein co	c 345	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 273	15	0.4	18	1	ADN08161	Human S9-RNA RT-PC	c 346	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 274	15	0.4	31	1	AAQ98457	Sense probe CAG-30	c 347	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 275	15	0.4	31	1	AAZ24996	Oligonucleotide CA	c 348	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 276	14.8	0.4	18	1	AAQ90869	hMLH1 gene exon 9	c 349	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 277	14.8	0.4	18	1	AAQ71721	Human KDR VEGF rec	c 350	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 278	14.8	0.4	18	1	AAZ59187	Reverse primer for	c 351	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 279	14.8	0.4	18	1	AAZ48499	Human TNFR1 mRNA i	c 352	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 280	14.8	0.4	18	1	AAZ48498	Human TNFR1 mRNA i	c 353	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 281	14.8	0.4	18	1	AAZ86831	Human Smad1 antise	c 354	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 282	14.8	0.4	18	1	AAZ89196	Human riboprotein	c 355	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 283	14.8	0.4	18	1	AAF88307	C. officinalis cal	c 356	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 284	14.8	0.4	18	1	AAS20963	PCR primer Igf2r-I	c 357	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 285	14.8	0.4	18	1	ABT04994	TNFR1 expression m	c 358	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 286	14.8	0.4	18	1	ABT04995	TNFR1 expression m	c 359	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 287	14.8	0.4	18	1	ABL01690	Human MLH1 (hMLH1)	c 360	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 288	14.8	0.4	18	1	ABX80015	EST polymorphic DN	c 361	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 289	14.8	0.4	18	1	AAZ56267	Hepatitis E virus	c 362	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 290	14.8	0.4	18	1	AAZ56287	Hepatitis E virus	c 363	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 291	14.8	0.4	18	1	ADC69962	Primer oligo used	c 364	14.4	0.4	17	1	ACA99718	G-protein coupled
c 292	14.8	0.4	18	1	ADD28828	Escherichia coli 0	c 365	14.4	0.4	17	1	ACA99718	G-protein coupled
c 293	14.8	0.4	18	1	ADD28830	Escherichia coli 0	c 366	14.4	0.4	17	1	ACA99718	G-protein coupled
c 294	14.8	0.4	18	1	ADD28831	Escherichia coli 0	c 367	14.4	0.4	17	1	ACA99718	G-protein coupled
c 295	14.8	0.4	18	1	ADD28829	Escherichia coli 0	c 368	14.4	0.4	17	1	ACA99718	G-protein coupled
c 296	14.8	0.4	18	1	ABZ97839	Human etaxin olig	c 369	14.4	0.4	17	1	ADH53228	Human APC (adenoma
c 297	14.8	0.4	18	1	ADM95720	SNP-containing car	c 370	14.4	0.4	17	1	ADH53228	Human APC (adenoma
c 298	14.8	0.4	18	1	ADM95724	SNP-containing car	c 371	14.4	0.4	17	1	ADH53228	Human APC (adenoma
c 299	14.8	0.4	18	1	ADM77392	Human fibrocytein	c 372	14.4	0.4	17	1	ADH53228	Human APC (adenoma
c 300	14.8	0.4	18	1	ABD30870	Human etaxin-deri	c 373	14.4	0.4	17	1	ADH53228	Human APC (adenoma
c 301	14.8	0.4	18	1	ADJ59713	Concatemer of Bota	c 374	14.4	0.4	30	1	AAZ44310	Human SCA7 primer
c 302	14.8	0.4	18	1	ADJ59712	Oligonucleotide as	c 375	14.4	0.4	30	1	AAZ44310	Human SCA7 primer
c 303	14.8	0.4	18	1	ADO45203	Human oligonucleot	c 376	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 304	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 377	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 305	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 378	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 306	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 379	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 307	14.6	0.4	30	1	ADN97224	AGC1 locus. Undie	c 380	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 308	14.4	0.4	17	1	AAT53479	Rat ICAM hammerhea	c 381	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 309	14.4	0.4	17	1	AAT33778	Primer/probe (CTA)	c 382	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 310	14.4	0.4	17	1	AAV71238	Human KDR VEGF rec	c 383	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 311	14.4	0.4	17	1	AAV20589	Integrin alpha 6 s	c 384	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 312	14.4	0.4	17	1	AAA25734	Oestrogen receptor	c 385	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 313	14.4	0.4	17	1	AAA25735	Oestrogen receptor	c 386	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 314	14.4	0.4	17	1	ABK00234	Human NOGO Hamme	c 387	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 315	14.4	0.4	17	1	ABK00235	Human NOGO Hamme	c 388	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 316	14.4	0.4	17	1	ABL46891	Human GRID G-cleav	c 389	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 317	14.4	0.4	17	1	ABL46891	Human GRID G-cleav	c 390	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 318	14.4	0.4	17	1	AAV84750	Lactococcus lactis	c 391	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 319	14.4	0.4	17	1	ABN08476	Human GDMPLP-1 17-m	c 392	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 320	14.4	0.4	17	1	ABN07209	Human GDMPLP-1 17-m	c 393	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 321	14.4	0.4	17	1	ABN07210	Human GDMPLP-1 17-m	c 394	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 322	14.4	0.4	17	1	ABN07210	Human GDMPLP-1 17-m	c 395	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 323	14.4	0.4	17	1	ABV89862	Human POSHL1 scann	c 396	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 324	14.4	0.4	17	1	ABV89861	Human POSHL1 scann	c 397	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 325	14.4	0.4	17	1	ACN12567	WNV minus strand 2	c 398	13.8	0.4	17	1	AAV81598	Oligonucleotide us

399	13.8	0.4	17	1	AAC61245	Human ACE, AGT and Hammerhead ribozym	c 472	13.8	0.4	17	1	ABT37737	Tumour suppression
c 400	13.8	0.4	17	1	AAF07477	Hammerhead ribozym	473	13.8	0.4	17	1	ACA06321	NFKB sub-unit modu
401	13.8	0.4	17	1	AAF05460	Hammerhead ribozym	474	13.8	0.4	17	1	ACA06547	NFKB sub-unit modu
c 402	13.8	0.4	17	1	AAF04887	Hammerhead ribozym	475	13.8	0.4	17	1	ACA06556	NFKB sub-unit modu
c 403	13.8	0.4	17	1	AAF04439	Hammerhead ribozym	c 476	13.8	0.4	17	1	ACA07772	Human MDZ12b scann
404	13.8	0.4	17	1	AACT73225	Forward primer #39	477	13.8	0.4	17	1	ADB05972	Human MDZ2 scannin
c 405	13.8	0.4	17	1	AAAD09710	Cryptosporidium pa	c 478	13.8	0.4	17	1	ADB00149	Human MDZ4 scannin
c 406	13.8	0.4	17	1	AAH94700	Human Chk1 ribozym	c 479	13.8	0.4	17	1	ADB02404	Human MDZ3 scannin
c 407	13.8	0.4	17	1	AAH95053	Human Chk1 ribozym	c 480	13.8	0.4	17	1	ADA99981	Human MDZ3 scannin
c 408	13.8	0.4	17	1	AAH95442	Human Chk1 ribozym	c 481	13.8	0.4	17	1	ADA99394	Human MDZ3 scannin
c 409	13.8	0.4	17	1	ABK01103	Human NOGO Inozyme	c 482	13.8	0.4	17	1	ADB00150	Human MDZ3 scannin
c 410	13.8	0.4	17	1	ABK00766	Human NOGO Inozyme	c 483	13.8	0.4	17	1	ADA99390	Human MDZ4 scannin
c 411	13.8	0.4	17	1	ABK02892	Human CD20 Hammerh	c 484	13.8	0.4	17	1	ADB02405	Human MDZ3 scannin
c 412	13.8	0.4	17	1	ABK02895	Human CD20 Hammerh	c 485	13.8	0.4	17	1	ADA99395	Human MDZ3 scannin
413	13.8	0.4	17	1	ABK00767	Human NOGO Inozyme	c 486	13.8	0.4	17	1	ADZ61649	Human H-Ras DNazym
414	13.8	0.4	17	1	ABK01792	Human NOGO Inozyme	c 487	13.8	0.4	17	1	ACD51476	HBV Hammerhead rib
415	13.8	0.4	17	1	ABK01549	Human NOGO G-Cleav	c 488	13.8	0.4	17	1	ACD51476	HCV DNazyme subetr
416	13.8	0.4	17	1	ABK02456	Human NOGO Amberzy	c 489	13.8	0.4	17	1	ACD61082	HBV DNazyme subetr
417	13.8	0.4	17	1	ABK046974	Human GRID NCH rib	c 490	13.8	0.4	17	1	ACD54845	HBV DNazyme subetr
418	13.8	0.4	17	1	ABK046974	Human GRID NCH rib	c 491	13.8	0.4	17	1	ACD73351	Mycobacterium gast
c 419	13.8	0.4	17	1	ABK00672	GAPDH CDNA PCR pri	c 492	13.8	0.4	17	1	ACC65076	Murine oligonucleo
420	13.8	0.4	17	1	ABK00672	Human GDMPLP-1 17-m	c 493	13.8	0.4	17	1	ACC65076	Murine oligonucleo
421	13.8	0.4	17	1	ABK010755	Human GDMPLP-1 17-m	c 494	13.8	0.4	17	1	ACC65169	Murine oligonucleo
422	13.8	0.4	17	1	ABK00673	Human GDMPLP-1 17-m	c 495	13.8	0.4	17	1	ACC65958	Murine oligonucleo
423	13.8	0.4	17	1	ABK01880	Human GDMPLP-1 17-m	c 496	13.8	0.4	17	1	ACC65958	Murine oligonucleo
424	13.8	0.4	17	1	ABK007810	Human GDMPLP-1 17-m	c 497	13.8	0.4	17	1	ACC65917	Murine oligonucleo
425	13.8	0.4	17	1	ABK01881	Human GDMPLP-1 17-m	c 498	13.8	0.4	17	1	ADA15895	Primer for amplifi
426	13.8	0.4	17	1	ABK010255	Human GDMPLP-1 17-m	c 499	13.8	0.4	17	1	ADB43213	Tumour suppression
427	13.8	0.4	17	1	ABK02741	Human GDMPLP-1 17-m	c 500	13.8	0.4	17	1	ADB41766	Tumour suppression
c 428	13.8	0.4	17	1	ABK25807	Stress tolerance c	c 501	13.8	0.4	17	1	ADB40208	Tumour suppression
c 429	13.8	0.4	17	1	ABK25808	Stress tolerance c	c 502	13.8	0.4	17	1	ADB41665	Tumour suppression
430	13.8	0.4	17	1	ABK27200	Reduced linolenic	c 503	13.8	0.4	17	1	ADB43678	Tumour suppression
c 431	13.8	0.4	17	1	ABK27199	Stress tolerance c	c 504	13.8	0.4	17	1	ADB42015	Tumour suppression
c 432	13.8	0.4	17	1	ABK25787	Stress tolerance c	c 505	13.8	0.4	17	1	ADC70444	Tumour suppression
c 433	13.8	0.4	17	1	ABK25788	Stress tolerance c	c 506	13.8	0.4	17	1	ADC38460	Human AMPLB scann
c 434	13.8	0.4	17	1	ABK97699	Human NEDD-1 scann	c 507	13.8	0.4	17	1	ADB44767	Tumour suppression
435	13.8	0.4	17	1	ABK97700	Human NEDD-1 scann	c 508	13.8	0.4	17	1	ADB45671	Tumour suppression
436	13.8	0.4	17	1	ABK97698	Human NEDD-1 scann	c 509	13.8	0.4	17	1	ADB45324	Tumour suppression
437	13.8	0.4	17	1	ABK97696	Human NEDD-1 scann	c 510	13.8	0.4	17	1	ADB45499	Tumour suppression
438	13.8	0.4	17	1	ABK97697	Human NEDD-1 scann	c 511	13.8	0.4	17	1	ADD69451	5' anchored (ISSR)
439	13.8	0.4	17	1	ABK74998	Human PAPP-Ea asso	c 512	13.8	0.4	17	1	ADD44223	Carboxypeptidase G
440	13.8	0.4	17	1	ABK90854	Human POSHL1 scann	c 513	13.8	0.4	17	1	ADD44239	Carboxypeptidase G
c 441	13.8	0.4	17	1	ABK90854	Human POSHL1 scann	c 514	13.8	0.4	17	1	ADF64073	Human PCCP1 DNA fr
c 442	13.8	0.4	17	1	ABK90268	Human POSHL1 scann	c 515	13.8	0.4	17	1	ADI48470	Human tumour suppr
c 443	13.8	0.4	17	1	ABK98859	Human POSHL1 scann	c 516	13.8	0.4	17	1	ADI48618	Human tumour suppr
c 444	13.8	0.4	17	1	ABK56440	Human CLC1 gene e	c 517	13.8	0.4	17	1	ADI51804	Human tumour suppr
c 445	13.8	0.4	17	1	ABK55961	Human CLC1 gene e	c 518	13.8	0.4	17	1	ADI49729	Human tumour suppr
446	13.8	0.4	17	1	AAK36054	Human CHLCK DNA am	c 519	13.8	0.4	17	1	ADI49390	Human tumour suppr
c 447	13.8	0.4	17	1	ACN01188	WNV Inozyme subtr	c 520	13.8	0.4	17	1	ADI49542	Human tumour suppr
c 448	13.8	0.4	17	1	ACN01188	WNV Hammerhead Rib	c 521	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 449	13.8	0.4	17	1	ACN05943	WNV minus strand A	c 522	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 450	13.8	0.4	17	1	ACN05943	WNV Inozyme subtr	c 523	13.8	0.4	17	1	ADI49672	Human tumour suppr
451	13.8	0.4	17	1	ACN01465	WNV minus strand Z	c 524	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 452	13.8	0.4	17	1	ACN01285	WNV Inozyme subtr	c 525	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 453	13.8	0.4	17	1	ACN02790	WNV minus strand I	c 526	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 454	13.8	0.4	17	1	ACN05859	WNV minus strand I	c 527	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 455	13.8	0.4	17	1	ACN09716	WNV Inozyme subtr	c 528	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 456	13.8	0.4	17	1	ACN09847	WNV minus strand I	c 529	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 457	13.8	0.4	17	1	ACN01051	WNV minus strand I	c 530	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 458	13.8	0.4	17	1	ACN06089	WNV minus strand I	c 531	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 459	13.8	0.4	17	1	ACN07144	WNV minus strand I	c 532	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 460	13.8	0.4	17	1	ACN01189	WNV minus strand I	c 533	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 461	13.8	0.4	17	1	ACN011320	WNV Amberzyme subs	c 534	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 462	13.8	0.4	17	1	ACN05400	WNV Hammerhead Rib	c 535	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 463	13.8	0.4	17	1	ACN11532	WNV minus strand I	c 536	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 464	13.8	0.4	17	1	ACN09448	WNV minus strand I	c 537	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 465	13.8	0.4	17	1	ACN11653	WNV minus strand H	c 538	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 466	13.8	0.4	17	1	ACN00549	WNV DNazyme subtr	c 539	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 467	13.8	0.4	17	1	ABT37547	G-protein coupled	c 540	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 468	13.8	0.4	17	1	ABT37547	Tumour suppression	c 541	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 469	13.8	0.4	17	1	ABT37508	Tumour suppression	c 542	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 470	13.8	0.4	17	1	ABT37508	Tumour suppression	c 543	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 471	13.8	0.4	17	1	ABT35272	Tumour suppression	c 544	13.8	0.4	17	1	ADI49672	Human tumour suppr

545 13.8 0.4 17 1 ACN64970 Human GDMPLP-1 prob
 546 13.8 0.4 17 1 ACN70900 Human GDMPLP-1 prob
 547 13.8 0.4 17 1 ACN65831 Human GDMPLP-1 prob
 548 13.8 0.4 17 1 ACN63763 Human GDMPLP-1 prob
 549 13.8 0.4 17 1 ACN70901 Human GDMPLP-1 prob
 550 13.8 0.4 17 1 ACN63762 Human GDMPLP-1 prob
 551 13.8 0.4 17 1 ACN73845 Human GDMPLP-1 prob
 552 13.8 0.4 17 1 ACN64971 Human GDMPLP-1 prob
 553 13.8 0.4 17 1 ACN73345 Human GDMPLP-1 prob

ALIGNMENTS

RESULT 1
 ABX79926
 ID ABX79926 standard; cDNA; 33 BP.
 XX
 AC ABX79926;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #251.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedreich's ataxia; myoclonic dystrophy; hyperandrogenemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 DR WPI; 2003-208818/20.
 XX
 PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 PS Example; Col 1089; 588pp; English.
 XX
 CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myoclonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 33 BP; 11 A; 10 C; 11 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30.4; DB 1; Length 33;

Best Local Similarity 96.9%; Pred. No. 5.5;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGCA 32
 RESULT 2
 AAZ44310
 ID AAZ44310 standard; DNA; 30 BP.
 XX
 AC AAZ44310;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Human SCA7 primer 1.
 XX
 KW SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;
 KW repeat expansion detection; RED analysis; detection; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CA2245310-A.
 XX
 PD 19-FEB-1999.
 XX
 PF 19-AUG-1998; 98CA-02245310.
 XX
 PR 19-AUG-1997; 97US-0056170P.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Koob MD, Ranum LP;
 XX
 DR WPI; 2000-098181/09.
 XX
 PT Identifying individuals at risk of developing spinocerebellar ataxia type
 PT 7 by analyzing trinucleotide repeat regions of spinocerebellar ataxia
 PT type 7 gene.
 XX
 PS Disclosure; Page 43; 66pp; English.
 XX
 CC This invention describes a novel method for identifying individuals at
 CC risk for developing spinocerebellar ataxia type 7 (SCA7). The method
 CC comprises analyzing the CAG repeat region of a SCA7 gene to detect CAG
 CC repeats, where individuals at risk have at least 30 CAG repeats and those
 CC not at risk have less than 19 CAG repeats. The method is useful for
 CC identifying individuals at risk of developing SCA7 and also those at risk
 CC of developing SCA1, 2, 3 or 6. The use of genomic DNA in the repeat
 CC expansion detection (RED) analysis allows isolation of any potential
 CC trinucleotide repeat expansion regardless of the expression pattern.
 CC Utilization of different oligonucleotides in the RED assay allows any of
 CC the possible trinucleotide repeats to be detected, and the cyclized nature
 CC of the reaction makes it extremely sensitive. This sequence represents a
 CC primer used to amplify the human SCA7 gene which is described in the
 CC method of the invention.
 XX
 SQ Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30
 RESULT 3
 AAS13781
 ID AAS13781 standard; DNA; 30 BP.
 XX

XX PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
 XX PI Singer RH, Taneja KL;
 XX PT WPI; 1995-336982/43.
 XX DR
 XX PT Detecting tri:nucleotide repeat expansion by in situ hybridisation - with
 PT detection sensitive enough to distinguish between probe bound to expanded
 PT and normal repeat regions, esp. for myotonic dystrophy diagnosis.
 XX XX
 XX PS Disclosure; Page 38; 51pp; English.
 XX XX
 CC The sequences represented by AAQ98457 and AAQ98458 are synthetic probes
 CC for the trinucleotide repeat CTG. These probes can be used in a method of
 CC in situ hybridisation for the detection of a trinucleotide repeat
 CC expansion. These probes were used specifically to identify myotonic
 CC dystrophy (DM). DM is associated with an expanded CTG repeat in the 3'
 CC untranslated region of the Mt-PK gene. These probes are labelled with a
 CC fluorescent label (e.g. fluorescein isothiocyanate) and then used to
 CC treat nucleated cells. The hybridisation of the probe to the expanded
 CC trinucleotide repeat can then be detected by fluorescence microscopy. Due
 CC to the large variation between expanded repeat size, and normal repeat
 CC size in DM (5-27 repeats in non-expanded, 50-2000 repeats in expanded),
 CC the expanded repeat will bind more probes. Only the expanded repeat will
 CC bind enough of the probes to give a detectable fluorescent signal. By
 CC detecting the number of transcripts in a cell of a diagnosed individual,
 CC progress of treatment, and severity of the disease can be monitored. This
 CC method can also be used to diagnose other diseases associated with
 CC trinucleotide repeat expansions, such as fragile X syndrome, muscular
 CC dystrophy and Huntington's disease. For some of these diseases a greater
 CC detection specificity would be required due to the smaller difference in
 CC repeat number between normal and infected individuals
 XX XX
 SQ Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
 Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30
 RESULT 6
 AA224996
 ID AA224996 standard; DNA; 31 BP.
 AC AA224996;
 XX XX
 XX 24-DEC-1999 (first entry)
 DT
 DE Oligonucleotide CAG30 targeted to myotonic-protein kinase gene.
 XX XX
 KW Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
 KW in situ hybridisation; detection; expansion; Fragile X syndrome; ss.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN US5962332-A.
 XX XX
 PD 05-OCT-1999.
 XX XX
 PF 11-DEC-1995; 95US-00570155.
 XX XX
 PR 17-MAR-1994; 94US-00214823.
 PR 07-MAR-1995; 95US-00399499.
 XX XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX PI Taneja KL, Singer RH;
 XX XX

XX DR WPI; 1999-579615/49.
 XX PT Detection of trinucleotide repeats.
 XX PS Disclosure; Col 25; 18pp; English.
 XX XX
 CC Oligonucleotides AA224983-224995 are targeted to the CTG trinucleotide
 CC repeats found in the myotonic-protein kinase (Mt-PK) gene. Excessive
 CC numbers of the trinucleotide repeats in the Mt-PK gene leads to the
 CC disease myotonic dystrophy. The oligonucleotides are used to probe the 5'
 CC -most 7 exons of 14 in the Mt-PK gene. This sequence is used as an
 CC antisense control oligonucleotide for the hybridisation reaction. The
 CC invention relates to a method for the detection of trinucleotide repeat
 CC expansion, e.g. in the Mt-PK gene or FMR1 gene (leading to Fragile X
 CC syndrome) by in situ hybridization
 XX XX
 SQ Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
 Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30
 RESULT 7
 AA31042
 ID AA31042 standard; DNA; 31 BP.
 XX XX
 AC AA31042;
 XX XX
 DT 04-NOV-2004 (revised)
 DT 18-OCT-2001 (first entry)
 XX XX
 DE Human single nucleotide polymorphism (SNP) DB1.
 XX XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX XX
 OS Homo sapiens.
 XX XX
 FH Key Location/Qualifiers
 FT variation 16
 FT /tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX XX
 PN WO200166800-A2.
 XX XX
 PD 13-SEP-2001.
 XX XX
 PF 07-MAR-2001; 2001WO-US007268.
 XX XX
 PR 07-MAR-2000; 2000US-0187510P.
 PR 22-MAY-2000; 2000US-0206129P.
 XX XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX XX
 PI Cargill M, Ireland JS, Lander ES;
 XX XX
 DR WPI; 2001-522952/57.
 XX XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or severity
 PT of a particular phenotype or disorder (e.g. diabetes) associated with a
 PT particular genotype.
 XX XX
 PS Claim 1; Page 124; 145pp; English.
 XX XX
 CC The invention relates to the identification of nucleic acid molecules
 CC (AA129513-AA131314) from the human genome which include polymorphic sites

CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing

CC Revised record issued on 04-NOV-2004 : Correction to Feature Table Key

XX SQ Sequence 31 BP; 16 A; 10 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 29.4; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 6.5;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GCAGCAGCAGCAGCAACCAACACAGCAACAA 1591
 Db 1 GCAGCAGCAGCAGCAACCAACCAACCAACAA 31

RESULT 8

ABZ81777
 ID ABZ81777 standard; DNA; 30 BP.

AC ABZ81777;

XX DT 11-JUN-2003 (first entry)

XX DE Huntington's disease gene mutated exon 1 region.

XX KW Huntington's disease; nontropic; anticonvulsant; huntingtin; human;
 KW gene therapy; mutant; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT mutation replace(5,A)

FT /*tag= a

XX PN WO2003013437-A2.

XX PD 20-FEB-2003.

XX PF 07-AUG-2002; 2002WO-US025352.

XX PR 07-AUG-2001; 2001US-0310757P.

XX PR 08-AUG-2001; 2001US-0310770P.

XX PR 08-AUG-2001; 2001US-0310889P.

XX PR 04-DEC-2001; 2001US-0337219P.

XX PA (UYDE) UNIV DELAWARE.

XX PI Kmiec EB, Parekh-Olmedo H;

XX XX WPI; 2003-256478/25.

XX DR New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.

XX Example 4; Fig 14; 133pp; English.

XX CC The present sequence is that of a portion of a mutated glutamine (CAG)
 CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
 CC gene (see also ABZ81760). The triplet repeat region (see ABZ81770) is
 CC mutated following liposome transfection of neuronal PC12 cells bearing an
 CC HD gene exon 1-GFP fusion gene with phosphorothioate-modified single-
 CC stranded oligonucleotide HD3T/52 (see ABZ81774), which causes a CAG (Gln)
 CC to CAG (Ileu) gene alteration in the HD exon 1 repeats. HD3T/52 is an
 CC example of oligonucleotides of the invention for targeted alteration of

CC the HD gene. Such oligonucleotides can be used for the treatment or
 CC prevention of HD

XX SQ Sequence 30 BP; 9 A; 10 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 28.4; DB 1; Length 30;

Best Local Similarity 96.7%; Pred. No. 8.3;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438

Db 1 CAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 9

ABA00946/c

ID ABA00946 standard; DNA; 28 BP.

XX AC ABA00946;

XX DT 28-APR-2003 (first entry)

XX DE MECT1-MAML2 chimeric protein detection primer, MAML2 Exon 2 antisense.

XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
 KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
 KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour; PCR;
 KW primer; amplify; ss.

XX OS Homo sapiens.

XX PN WO2003004645-A1.

XX PD 16-JAN-2003.

XX PE 03-JUL-2002; 2002WO-US021344.

XX PF 03-JUL-2001; 2001US-0302788P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kaye FJ, Tonon G;

XX DR WPI; 2003-210364/20.

XX PT Screening a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 PT translocation, useful for treating mucoepidermoid carcinoma comprises
 PT detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
 PT a tissue sample.

XX PS Example 4; Page 36; 65pp; English.

XX CC The sequences given in ABA00945-46 are primers which were used to detect
 CC specific MECT1/MAML2 fusion mRNA in mucoepidermoid tumours. The method of
 CC the invention allows for screening of a tissue sample from a subject for
 CC a t(11;19)(q14-21;p12-13) translocation and comprises detecting the
 CC presence of MECT1-MAML2 chimeric nucleic acid or protein in a tissue
 CC sample. The method is useful for diagnosing and treating cancer.

XX CC Including cancer that involves the NOTCH pathway, particularly cancer of
 CC mucoepidermoid carcinoma, the most common malignant salivary gland tumour

XX SQ Sequence 28 BP; 3 A; 6 C; 11 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 28; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 CTCCTGCCAACAGCAAGCGACCCCAATGG 210

Db 28 CTCCTGCCAACAGCAAGCGACCCCAATGG 1

RESULT 10

AAA03952
ID AAA03952 standard; DNA; 29 BP.

XX AC
XX AAA03952;

XX DT
XX 22-MAY-2000 (first entry)

XX DE
XX Polymorphic fragment of hypertension associated gene APOA4.

XX KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
XX KW Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX KW Fabry disease; familial hypercholesterolemia; hereditary spherocytosis;
XX KW polycystic kidney disease; von Willebrand's disease; forensic; human;
XX KW tuberculous sclerosis; hereditary hemorrhagica telangiectasia;
XX KW familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX KW Ehlers-Danlos syndrome; ss.

XX OS Homo sapiens.

XX PN BP95382-A2.

XX PD 10-NOV-1999.

XX PF 07-MAY-1999; 99EP-00250150.

XX PR 07-MAY-1998; 98US-0084641P.

XX PR 03-MAY-1999; 99US-00304232.

XX PA (AFFY-) AFFYMETRIX INC.

XX PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX PI Fan JB, Chakravarti A, Haluska MK;

XX DR WPI; 2000-107928/10.

XX PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX PT hypertension.

XX PS Claim 1; Page 21; 53pp; English.

XX CC The invention provides polymorphic fragments of genes associated with
XX CC hypertension. The nucleic acids including the polymorphic sites can be
XX CC used as probes or primers for expressing variant proteins. Detection of
XX CC the polymorphisms is useful in designing prophylactic and therapeutic
XX CC regimes customized to underlying abnormalities. The polymorphisms can be
XX CC used for association studies for hypertension, and in hypertension
XX CC diagnostic assays. Where the polymorphisms have strong correlation with
XX CC hypertension, within a gene, they are likely to have a causative role in
XX CC hypertension. This information can be used to find the precise role of a
XX CC polymorphism in the disease, and this can be used to identify potential
XX CC drugs which combat the disease. The polymorphisms can be tested for
XX CC association with other diseases e.g. agammaglobulinemia, diabetes
XX CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX CC syndrome, Fabry disease, familial hypercholesterolemia, polycystic
XX CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial
XX CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX CC acute intermittent porphyria. The polymorphic forms can also be used in
XX CC forensics to identify individuals

XX SQ Sequence 29 BP; 11 A; 8 C; 9 G; 0 T; 0 U; 1 Other;

Query Match 0.7%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 22;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGCAGCAGCA 1428

DB 1 CAGCAGCAACAGCAGCAGCAGCAGCA 29

RESULT 11
ABZ81767

ID ABZ81767 standard; DNA; 25 BP.

XX AC
XX ABZ81767;

XX DT
XX 11-JUN-2003 (first entry)

XX DE
XX Huntington's disease gene target region.

XX KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;

XX KW gene therapy; ds.

XX OS Homo sapiens.

XX KW Key Location/Qualifiers

XX FT misc_binding 1..25

XX FT /tag= a

XX FT /bound moiety= "Oligonucleotide"

XX FT /note= "hybridises to bases 1-25 of sequence given in

XX FT ABZ81768"

XX FT /tag= b

XX FT /note= "replaced by T following treatment"

XX PN WO2003013437-A2.

XX PD 20-FEB-2003.

XX PF 07-AUG-2002; 2002WO-US025352.

XX PR 07-AUG-2001; 2001US-0310757P.

XX PR 08-AUG-2001; 2001US-0310770P.

XX PR 08-AUG-2001; 2001US-0310889P.

XX PR 04-DEC-2001; 2001US-0337219P.

XX PA (UYDE) UNIV DELAWARE.

XX PI Kniec EB, Parekh-Olmedo H;

XX DR WPI; 2003-256478/25.

XX PT New single stranded oligonucleotides comprising a DNA domain having at
XX PT least one mismatch with respect to the genetic sequence of the
XX PT Huntington's disease gene to be altered, useful for treating or
XX PT preventing Huntington's disease.

XX PS Example 1; Fig 6a; 133pp; English.

XX CC The present sequence is that of a portion of the glutamine (CAG) triplet
XX CC repeat region of exon 1 of the human Huntington's disease (HD) gene (see
XX CC also ABZ81760). This region of exon 1 is targeted by a DNA-RNA hybrid
XX CC oligonucleotide of the invention (see ABZ81768), resulting in a CAG to
XX CC TAG (stop codon) nucleotide exchange due to sliding of the repeat region,
XX CC a phenomenon that can occur with the methods of this invention. The
XX CC oligonucleotide is an example of oligonucleotides of the invention for
XX CC targeted alteration of the HD gene. Such oligonucleotides can be used for
XX CC the treatment or prevention of HD

XX SQ Sequence 25 BP; 8 A; 9 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGC 1433

DB 1 CAGCAGCAGCAGCAGCAGCAGCAGC 25

RESULT 12

ABZ81768/c

ID ABZ81768 standard; RNA; 25 BP.

XX AC
XX ABZ81768;

XX 11-JUN-2003 (first entry)
XX Huntington's disease gene targeting oligonucleotide.
DE Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
XX gene therapy; ds.
KW Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. .25
FT misc_binding /*tag= a
FT /bound_motety= "HD gene exon 1 triplet repeat"
FT /note="hybridises to bases 1-25 of sequence given in
FT ABZ81767"
XX
XX WO2003013437-A2.
XX
XX 20-FEB-2003.
XX
XX 07-AUG-2002; 2002WO-US025352.
XX
XX 07-AUG-2001; 2001US-0310757P.
PR 08-AUG-2001; 2001US-0310770P.
XX 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX
XX (UYDE) UNIV DELAWARE.
PA
XX Kmiec EB, Parekh-Olmedo H;
PI
XX WPI; 2003-256478/25.
DR
XX New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
XX
XX Example 1; Fig 6a; 133pp; English.
XX
XX The present sequence is that of a portion of a 52-mer RNA/DNA chimeric
CC oligonucleotide of the the glutamine (CAG) that is targeted to triplet
CC repeat region (see ABZ81767) of exon 1 of the human Huntington's disease
CC (HD) gene. This targeting results in a CAG to TAG (stop codon) nucleotide
CC exchange due to sliding of the repeat region, a phenomenon that can occur
CC with the methods of this invention. The oligonucleotide is an example of
CC claimed oligonucleotides of the invention for targeted alteration of the
CC HD gene. Such oligonucleotides can be used for the treatment or
CC prevention of HD
XX
XX Sequence 25 BP; 0 A; 8 C; 9 G; 0 T; 8 U; 0 Other;
SQ
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGC 1433
DB 25 CAGCAGCAGCAGCAGCAGCAGCAGC 1
RESULT 13
ABN87602
ID ABN87602 standard; DNA; 24 BP.
XX
XX AC ABN87602;
XX
XX 07-AUG-2002 (first entry)
XX
XX Human copine 127.5 PCR primer 1 SEQ ID NO:3.
DE
XX Human; copine 127.5; cell membrane protein function disorder; PCR primer;

XX ss.
XX Homo sapiens.
XX
XX CN1331112-A.
XX
XX 16-JAN-2002.
XX
XX 30-JUN-2000; 2000CN-00116931.
XX
XX 30-JUN-2000; 2000CN-00116931.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX WPI; 2002-316396/36.
XX
XX Copine 127.5 polypeptide and its encoding polynucleotide, for treating
PT e.g. cell membrane protein function disorder.
XX
XX Example 2; Page 18 (Disclosure); 35pp; Chinese.
XX
XX The present invention describes human copine 127.5 (I). Also described is
CC a method for producing (I) using DNA recombination technology. (I) can be
CC used in the treatment of cell membrane protein function disorders. The
CC present sequence represents a PCR primer for (I), which is used in an
CC example from the present invention
XX
XX Sequence 24 BP; 12 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No.20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2281 GAATCAATTGACCCACACAGAGAA 2304
DB 1 GAATCAATTGACCCACACAGAGAA 24
RESULT 14
ADN97255
ID ADN97255 standard; DNA; 24 BP.
XX
XX AC ADN97255;
XX
XX 01-JUL-2004 (first entry)
XX
XX Primer of the invention #57.
DE
XX DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
XX forensic identification; marijuana; primer; ss.
XX
XX Unidentified.
XX
XX WO2004008841-A2.
XX
XX 29-JAN-2004.
XX
XX 21-JUL-2003; 2003WO-US022887.
XX
XX 19-JUL-2002; 2002US-0397179P.
XX
XX (UYAR-) UNIV ARIZONA.
XX (KEIM/) KEIM P S.
XX (ZINN/) ZINNAMON K.
XX
XX Keim PS, Zinnamon K;
XX WPI; 2004-143139/14.
XX
XX New isolated nucleic acid for amplification of a short tandem repeat
PT located in DNA isolated from Cannabis sativa L species, useful for

PT forensic identification of marijuana or for linking a marijuana sample to
XX its plant source.

XX Example 11; SEQ ID NO 122; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa
CC using short tandem repeat markers. The nucleic acid is useful for
CC forensic identification of marijuana or for linking a marijuana sample to
CC its plant source. The present sequence represents a primer of the
CC invention.

XX Sequence 24 BP; 8 A; 8 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1433

DB 1 AGCAGCAGCAGCAGCAGCAGC 24

RESULT 15

ADN97164
ID ADN97164 standard; DNA; 24 BP.

XX AC ADN97164;

XX AC (first entry)

DT 01-JUL-2004

XX Primer of the invention #3.

XX DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
KW forensic identification; marijuana; primer; ss.

XX Synthetic.

XX WO2004008841-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022887.

XX 19-JUL-2002; 2002US-0397179P.

XX (UYAR-) UNIV ARIZONA.

XX (KEIM/) KEIM P S.

XX (ZINN/) ZINNAMON K.

XX Keim PS, Zinamon K;

XX WPI; 2004-143139/14.

XX New isolated nucleic acid for amplification of a short tandem repeat

XX located in DNA isolated from Cannabis sativa L species, useful for

XX forensic identification of marijuana or for linking a marijuana sample to

XX its plant source.

XX Disclosure; SEQ ID NO 31; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa

XX using short tandem repeat markers. The nucleic acid is useful for

XX forensic identification of marijuana or for linking a marijuana sample to

XX its plant source. The present sequence represents a primer of the

XX invention.

XX Sequence 24 BP; 8 A; 8 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1433

DB 1 AGCAGCAGCAGCAGCAGCAGC 24

RESULT 16

ADR68635/c

ID ADR68635 standard; DNA; 24 BP.

XX AC ADR68635;

XX 04-NOV-2004 (first entry)

XX DNA G-quadruplex structure-fixing compound-related oligonucleotide #12.

XX G-quadruplex structure; isomer; racemate; enantiomer; diastereoisomer;
KW cytotatic; muscular-Gen; dermatological; vasotropic; endocrine-Gen;
KW telomerase inhibitor; anticancer agent; genetic disorder;
KW Bloom's syndrome; Werner's syndrome; Rothmund-Thomson syndrome;
KW ataxia telangiectasia; ss.

XX Unidentified.

XX FR2850970-A1.

XX 13-AUG-2004.

XX 07-FEB-2003; 2003FR-00001478.

XX 07-FEB-2003; 2003FR-00001478.

XX (AVET) AVENTIS PHARMA SA.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX (MUSE-) MUSEUM NAT HISTOIRE NATURELLE.

XX (CURI-) INST CURIE.

XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX (UYRE-) UNIV REIMS CHAMPAGNE-ARDENNE.

XX Hittinger A, Caulfield T, Maillet P, Bouchard H, Mandine E;

XX Belmokhtar C, Mergny JL, Guittat L, Riou JF, Gomez D;

XX WPI; 2004-583573/57.

XX New quaternary aromatic nitrogen heterocycle derivatives that fix the G-

XX quadruplex structure of DNA or RNA are telomerase inhibitors, useful in

XX the treatment of cancers and some genetic disorders.

XX Disclosure; Page 25; 57pp; French.

XX This invention relates to novel compounds that fix the G-quadruplex

XX structure of DNA or RNA, their isomers, racemates, enantiomers,

XX diastereoisomers, and their salts. The invention may be useful for the

XX production of compounds with a cytostatic, muscular-Gen, dermatological,

XX vasotropic or endocrine-Gen activity acting as telomerase inhibitors. The

XX compounds are useful as anticancer agents and for treatment of genetic

XX disorders such as Bloom's syndrome, Werner's syndrome, Rothmund-Thomson

XX syndrome and ataxia telangiectasia. The present sequence is that of an

XX oligonucleotide which is related to the novel compounds of the invention.

XX Sequence 24 BP; 0 A; 8 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGC 1432

DB 24 CAGCAGCAGCAGCAGCAGCAGC 1

RESULT 17

ADM48412/c

ID ADM48412 standard; DNA; 29 BP.

XX

```
AC ADM48412;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Probe #7 used to illustrate the method of the invention.
XX
XX KW Detection; protein-protein interaction; protein-drug interaction; probe;
XX ss.
XX
XX OS Unidentified.
XX
XX PN US2003215825-A1.
XX
XX PD 20-NOV-2003.
XX
XX PF 12-NOV-2002; 2002US-00291986.
XX
XX PR 09-APR-2002; 2002AU-00001597.
XX
XX PA (TONG/) TONG S.
XX
XX PI Tong S;
XX
XX DR WPI; 2004-106890/11.
XX
XX PT Detecting molecular target in sample utilizing molecular interaction
XX between molecular targets, bead-bound probes and support-bound probes,
XX useful for detecting interaction between protein and drug.
XX
XX PS Disclosure; Fig 13C; 41pp; English.
XX
XX CC The present invention relates to a novel method of detecting a molecular
XX target in a sample by attaching to bead a first molecular probe to form a
XX bead-bound probe, attaching to support at predefined area a second
XX molecular probe to form support-bound probe, introducing sample to the
XX bead-bound probe and support-bound probe so that the molecular target is
XX sandwiched between support and beads and detecting presence of beads at
XX predefined area on support which indicates the presence of the molecular
XX target in the sample. The method is useful for detecting interaction
XX between two proteins. It is useful for detecting interaction between a
XX protein and a drug. The method is also useful for detecting the
XX interactions between several drugs and several proteins. The present
XX sequence is a probe used to illustrate the method of the invention.
XX
XX SQ Sequence 29 BP; 0 A; 7 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAGCAGCAGC 1448
DB 29 CAGCAGCAGCAGCAGCAGCAGCAGC 5

RESULT 18
ABA00945
ID ABA00945 standard; DNA; 23 BP.
XX
XX AC ABA00945;
XX
XX DT 28-APR-2003 (first entry)
XX
XX DE MECT1-MAML2 chimeric protein detection primer, MECT1 Exon 1 Sense.
XX
XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
XX q14-q21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
XX cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour; PCR;
XX primer; amplify; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2003004645-A1.

XX
XX PD 16-JAN-2003.
XX
XX PF 03-JUL-2002; 2002WO-US021344.
XX
XX PR 03-JUL-2001; 2001US-0302788P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Kaye FJ, Tonon G;
XX
XX DR WPI; 2003-210364/20.
XX
XX PT Screening a tissue sample from a subject for a t(11;19)(q14-q21;p12-q13)
XX translocation, useful for treating mucoepidermoid carcinoma comprises
XX detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
XX a tissue sample.
XX
XX PS Example 4; Page 36; 65pp; English.
XX
XX CC The sequences given in ABA00945-46 are primers which were used to detect
XX specific MECT1/MAML2 fusion mRNA in mucoepidermoid tumours. The method of
XX the invention allows for screening of a tissue sample from a subject for
XX a t(11;19)(q14-q21;p12-q13) translocation and comprises detecting the
XX presence of MECT1-MAML2 chimeric nucleic acid or protein in a tissue
XX sample. The method is useful for diagnosing and treating cancer,
XX including cancer that involves the NOTCH pathway, particularly cancer of
XX mucoepidermoid carcinoma, the most common malignant salivary gland tumour
XX
XX SQ Sequence 23 BP; 8 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGAGAGATGCGGACTTCGAACA 32
DB 1 CGAGAGATGCGGACTTCGAACA 23

RESULT 19
ADC59319
ID ADC59319 standard; DNA; 23 BP.
XX
XX AC ADC59319;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Oligonucleotide, #1, based on human polynucleotide #1.
XX
XX KW Human; ss; polyglutamine disease; genealogical polyglutamine disease;
XX nootropic; anticonvulsant.
XX
XX OS Homo sapiens.
XX
XX PN JF2002360268-A.
XX
XX PD 17-DEC-2002.
XX
XX PF 03-AUG-2001; 2001JP-00236788.
XX
XX PR 04-AUG-2000; 2000JP-00236839.
XX
XX PR 06-APR-2001; 2001JP-00108723.
XX
XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX (DAUC ) DAICHI PHARM CO LTD.
XX
XX DR WPI; 2003-516153/49.
XX
XX PT A genealogical line diagnostic marker for polyglutamine disease, useful
XX in the diagnosis, prevention and/or treatment, comprises a polyglutamine
XX related gene and its encoded polypeptide.
XX
```



```
PS Claim 3; SEQ ID NO 11; 72pp; Japanese.
XX
CC The invention discloses polyglutamine disease related genes and their
CC encoded polypeptides. Also claimed is a recombinant vector,
CC transformants, preparation of the polynucleotides and resultant
CC polypeptides, diagnostic methods and a kit. The genes and encoded
CC polypeptides are useful in the diagnosis, prevention and treatment of
CC genealogical polyglutamine disease. The sequence presented is an
CC oligonucleotide which is based on one of theDNAs encoding a polypeptide
CC of the invention.
XX
SQ Sequence 23 BP; 4 A; 12 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1369 GCCTTCTCTCTCTACTACTACACCC 1391
DB 1 GCCTTCTCTCTCTACTACTACACCC 23
RESULT 20
AD043735/C
XX AD043735 standard; DNA; 27 BP.
XX
XX AD043735;
XX
XX 29-JUL-2004 (first entry)
XX
XX PCR primer used to amplify SEAP for cloning into pFerX8 and pFerX9.
XX
XX transfection; eukaryotic cell; eukaryotic locus;
XX ferritin heavy chain locus; PCR; primer; ss;
XX secreted alkaline phosphatase; SEAP.
XX
XX Synthetic.
XX
XX WO2004037982-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033433.
XX
XX 24-OCT-2002; 2002US-0421252P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Prentice H;
XX
XX WPI; 2004-357431/33.
XX
XX New genetic vector comprising distal 5' flanking sequences and proximal
XX 5' regulatory sequences, an insertion site and proximal 3' regulatory
XX sequences, useful for transfecting and expressing a protein within
XX eukaryotic cells.
XX
XX Example 2; Page 23; 51pp; English.
XX
XX The specification describes a genetic vector for stable transfection and
XX expression of a desired protein within eukaryotic cells. The vector
XX comprises distal 5' flanking sequences of a eukaryotic locus, proximal 5'
XX regulatory sequences of a eukaryotic locus, at least a first insertion
XX site for a first heterologous coding sequence, and proximal 3' regulatory
XX sequences effective for transcription termination of a eukaryotic locus.
XX These sequences are operably joined in a 5' to 3' orientation, with
XX optional linker sequences between adjacent sequences. The distal flanking
XX sequences and proximal 5' regulatory sequences and the proximal 3'
XX regulatory sequences are derived from a ferritin heavy chain locus, and
XX have a total length of between 1000 and 10000 bases. The genetic vector
XX is useful for stably transfecting and expressing a desired protein within
XX eukaryotic cells. PCR primers AD043734-AD043735 were used to amplify
XX secreted alkaline phosphatase (SEAP) for insertion into pFerX8 and
XX
PS Claim 3; SEQ ID NO 11; 72pp; Japanese.
XX
CC The invention discloses polyglutamine disease related genes and their
CC encoded polypeptides. Also claimed is a recombinant vector,
CC transformants, preparation of the polynucleotides and resultant
CC polypeptides, diagnostic methods and a kit. The genes and encoded
CC polypeptides are useful in the diagnosis, prevention and treatment of
CC genealogical polyglutamine disease. The sequence presented is an
CC oligonucleotide which is based on one of theDNAs encoding a polypeptide
CC of the invention.
XX
SQ Sequence 23 BP; 4 A; 12 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1369 GCCTTCTCTCTCTACTACTACACCC 1391
DB 1 GCCTTCTCTCTCTACTACTACACCC 23
RESULT 20
AD043735/C
XX AD043735 standard; DNA; 27 BP.
XX
XX AD043735;
XX
XX 29-JUL-2004 (first entry)
XX
XX PCR primer used to amplify SEAP for cloning into pFerX8 and pFerX9.
XX
XX transfection; eukaryotic cell; eukaryotic locus;
XX ferritin heavy chain locus; PCR; primer; ss;
XX secreted alkaline phosphatase; SEAP.
XX
XX Synthetic.
XX
XX WO2004037982-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033433.
XX
XX 24-OCT-2002; 2002US-0421252P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Prentice H;
XX
XX WPI; 2004-357431/33.
XX
XX New genetic vector comprising distal 5' flanking sequences and proximal
XX 5' regulatory sequences, an insertion site and proximal 3' regulatory
XX sequences, useful for transfecting and expressing a protein within
XX eukaryotic cells.
XX
XX Example 2; Page 23; 51pp; English.
XX
XX The specification describes a genetic vector for stable transfection and
XX expression of a desired protein within eukaryotic cells. The vector
XX comprises distal 5' flanking sequences of a eukaryotic locus, proximal 5'
XX regulatory sequences of a eukaryotic locus, at least a first insertion
XX site for a first heterologous coding sequence, and proximal 3' regulatory
XX sequences effective for transcription termination of a eukaryotic locus.
XX These sequences are operably joined in a 5' to 3' orientation, with
XX optional linker sequences between adjacent sequences. The distal flanking
XX sequences and proximal 5' regulatory sequences and the proximal 3'
XX regulatory sequences are derived from a ferritin heavy chain locus, and
XX have a total length of between 1000 and 10000 bases. The genetic vector
XX is useful for stably transfecting and expressing a desired protein within
XX eukaryotic cells. PCR primers AD043734-AD043735 were used to amplify
XX secreted alkaline phosphatase (SEAP) for insertion into pFerX8 and
XX
CC pFerX9, vectors of the invention. SEAP was used as a reporter gene.
XX
SQ Sequence 27 BP; 1 A; 9 C; 10 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 22.4; DB 1; Length 27;
Best Local Similarity 95.8%; Pred. No. 51;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1432
DB 24 CAGCAGCAGCAGCAGCAGCAGCAGCTG 1
RESULT 21
ADC59320/C
ID ADC59320 standard; DNA; 22 BP.
XX
XX ADC59320;
XX
XX 18-DEC-2003 (first entry)
XX
XX Oligonucleotide, #2, based on human polynucleotide #1.
XX
XX Human; ss; polyglutamine disease; genealogical polyglutamine disease;
XX nontropic; anticonvulsant.
XX
XX Homo sapiens.
XX
XX JP2002360268-A.
XX
XX 17-DEC-2002.
XX
XX 03-AUG-2001; 2001JP-00236788.
XX
XX 04-AUG-2000; 2000JP-00236839.
XX
XX 06-APR-2001; 2001JP-00108723.
XX
XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX
XX (DAUC-) DAIICHI PHARM CO LTD.
XX
XX WPI; 2003-516153/49.
XX
XX A genealogical line diagnostic marker for polyglutamine disease, useful
XX in the diagnosis, prevention and/or treatment, comprises a polyglutamine
XX related gene and its encoded polypeptide.
XX
XX Claim 26; SEQ ID NO 12; 72pp; Japanese.
XX
XX The invention discloses polyglutamine disease related genes and their
XX encoded polypeptides. Also claimed is a recombinant vector,
XX transformants, preparation of the polynucleotides and resultant
XX polypeptides, diagnostic methods and a kit. The genes and encoded
XX polypeptides are useful in the diagnosis, prevention and treatment of
XX genealogical polyglutamine disease. The sequence presented is an
XX oligonucleotide which is based on one of theDNAs encoding a polypeptide
XX of the invention.
XX
SQ Sequence 22 BP; 3 A; 3 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1631 GCCCAATCTCTACCAAGCCAGC 1652
DB 22 GCCCAATCTCTACCAAGCCAGC 1
RESULT 22
ADC38187
ID ADC38187 standard; DNA; 25 BP.
XX
XX ADC38187;
```

```
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:536.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
FN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 536; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 3 GCAGCAGCAGCAACAGCAGCAG 24
RESULT 23
ADC38189
ID ADC38189 standard; DNA; 25 BP.
XX ADC38189;
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:538.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
FN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 536; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 3 GCAGCAGCAGCAACAGCAGCAG 24
RESULT 23
ADC38189
ID ADC38189 standard; DNA; 25 BP.
XX ADC38189;
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:538.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
FN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 538; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 1 GCAGCAGCAGCAACAGCAGCAG 22
RESULT 24
ADC38186
ID ADC38186 standard; DNA; 25 BP.
XX ADC38186;
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:535.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
FN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 535; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 1 GCAGCAGCAGCAACAGCAGCAG 22
```

```
PR 01-NOV-2001; 2001US-0334773P.
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 538; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 1 GCAGCAGCAGCAACAGCAGCAG 22
RESULT 24
ADC38186
ID ADC38186 standard; DNA; 25 BP.
XX ADC38186;
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:535.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
FN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 535; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
DB 1 GCAGCAGCAGCAACAGCAGCAG 22
```

CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.

XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450

Db 4 GCAGCAGCAGCAACAGCAGCAG 25

RESULT 25

ADC38188

ID ADC38188 standard; DNA; 25 BP.

XX AC ADC38188;

XX 18-DEC-2003 (first entry)

XX Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:537.

XX human; angiomotin-like protein 1; AMLP1; cytosstatic; gene therapy;
XX AMLP1a; ss.

XX Synthetic.

OS Homo sapiens.

XX WO200307931-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035129.

XX 01-NOV-2001; 2001US-0334773P.

XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX Shannon M, Phan T;

XX WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiomotin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 537; 172pp; English.

XX The present invention describes the human angiomotin-like protein 1
XX (AMLP1). human AMLP1 has cytosstatic activity, and can be used in gene
XX therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLP1. The present sequence represents a scanning
XX oligonucleotide for human AMLP1a, which is used in an example from the
XX present invention.

XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 22; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450

Db 2 GCAGCAGCAGCAACAGCAGCAG 23

RESULT 26

ABS71093/c

ID ABS71093 standard; DNA; 26 BP.

XX AC ABS71093;

XX 27-NOV-2002 (first entry)

XX Human GPCR ligand Bv8 cDNA PCR primer hBv8-F1.

XX G-protein coupled receptor; GPCR; ZAQ; human; ZAQ; ZAQ; rat; ZAQ1;
XX rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GPR73; Bv8 protein;
XX digestive disorder; central nervous system disorder; CNS; diarrhoea;
XX bowel inflammation; constipation; food absorption disorder; nootropic;
XX Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
XX antiinflammatory; antiarrhoeic; neuroleptic; neuroprotective; PCR;
XX primer; ss.

XX Homo sapiens.

XX WO200262944-A2.

XX 15-AUG-2002.

XX 01-FEB-2002; 2002WO-JP000852.

XX 02-FEB-2001; 2001JP-00026820.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;

XX Hinuma S;

XX WPI; 2002-627537/67.

XX Screening of compounds modifying the binding of G-protein coupled
XX receptor protein ZAQ and related proteins to their ligands for use in
XX treatment and diagnosis of digestive disorders.
XX Example 3; Page 117; 197pp; Japanese.

XX The present invention relates to a screening method for compounds for
XX their ability to modify the binding of G-protein coupled receptor (GPCR)
XX protein ZAQ and related proteins (human ZAQ, human ZAQ, rat ZAQ1
XX (rZAQ1), rZAQ2, human and mouse ISE (mISE) receptor, and mouse GPR73) to
XX their ligands (the mature form of human, mouse or rat Bv8 protein). The
XX receptor protein and ligand are contacted in the presence or absence of
XX the test compound. The compounds are useful in a drug composition for the
XX treatment, and prevention of digestive and central nervous system (CNS)
XX disorders, including bowel inflammation, diarrhoea, constipation, food
XX absorption disorders, Alzheimer's disease, Parkinson's disease and
XX schizophrenia. The present sequence represents a PCR primer used in the
XX examples of the present invention

XX Sequence 26 BP; 1 A; 9 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 21.2; DB 1; Length 26;

Best Local Similarity 88.5%; Pred. No. 69;

Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1407 AACAGCAGCAGCAGCAGCAGCAG 1432

Db 26 AACAGCAGCAGCAGCAGCAGCAGTAG 1

RESULT 27

ABZ30010/c

ID ABZ30010 standard; DNA; 26 BP.

XX AC ABZ30010;

XX 30-JAN-2003 (first entry)

XX

PR 27-SEP-1999; 99US-0156135P.
 XX 23-AUG-2000; 2000US-0227436P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 XX WPI; 2001-273485/28.
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 PS Claim 101; Page 53; 338pp; English.
 XX
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 Db 21 CAGCAGCAGCAGCAGCAGCAG 1
 |||||
 RESULT 30
 ABS78296/c
 ID ABS78296 standard; DNA; 21 BP.
 AC ABS78296;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #780.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 WO200253141-A2.
 XX
 11-JUL-2002.
 XX
 14-DEC-2001; 2001WO-US048458.
 XX
 14-DEC-2000; 2000US-0255534P.
 XX
 (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;

XX WPI; 2002-566690/60.
 XX
 PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 33; 276pp; English.
 XX
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 Db 21 CAGCAGCAGCAGCAGCAGCAG 1
 |||||
 RESULT 31
 ABL38849/c
 ID ABL38849 standard; DNA; 21 BP.
 XX
 AC ABL38849;
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 240.
 XX
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT modified_base 1..21
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 PN WO200197843-A2.
 XX
 PD 27-DEC-2001.
 XX
 22-JUN-2001; 2001WO-US020154.
 XX
 22-JUN-2000; 2000US-0213346P.
 XX
 (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Weiner G, Hartmann G;
 XX
 WPI; 2002-154611/20.
 XX
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.

XX Disclosure; Page 156; 312pp; English.

PS The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx

CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the

CC exemplification of the invention

XX

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 32

ABK10202/c

ID ABK10202 standard; DNA; 21 BP.

AC ABK10202;

XX

DT 21-MAY-2002 (first entry)

XX

DE Double stranded DNA isolation (CTG)7 repeat sequence.

XX

KW Single stranded DNA isolation; DNA purification; CTG repeat; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT repeat_region 1..21 /tag= a

FT /rpt_type= TANDEM

FT repeat_unit 1..3 /tag= b

FT /note= "CTG type repeat"

XX

PN WO200210182-A2.

XX

PD 07-FEB-2002.

XX

PF 18-JUL-2001; 2001WO-US022782.

XX

PR 02-AUG-2000; 2000US-0222686P.

XX

PA (PEKE) PE CORP NY.

XX

PI Chiesa C, Schroth GP, Egholm M;

XX

DR WPI; 2002-188719/24.

XX

PT Isolating one strand of double-stranded nucleic acid, by contacting

PT double stranded nucleic acid having first and second strands with

PT competitor oligo to form first strand-oligo complex and isolating the

PT complex.

XX

PS Disclosure; Page 12; 61pp; English.

XX

CC This invention relates to a novel method for isolating one strand of

CC double-stranded target nucleic acid. The method comprises contacting a

CC double stranded target DNA molecule with a competitor oligonucleotide

CC capable of hybridizing to the first strand of the double stranded

CC molecule. The method is performed under conditions in which the first

CC strand dissociates from the second and hybridizes with the competitor

CC oligonucleotide to form a heteroduplex. The method of the invention is

CC useful for separating a strand from a double-stranded target nucleic

CC acid. The method is rapid, efficient and specific for isolating a single

CC strand from a double-stranded nucleic acid. Because the method provides

CC easy and efficient recovery of the single strand from a double-stranded

CC advantageously used to purify a first strand from a double-stranded

CC nucleic acid that is a polymerase chain reaction (PCR) amplification

CC product from a pool of related or unrelated sequences in high yield for

CC subsequent use. The method also permits capture and/or recovery of the

CC first strand of a double-stranded target nucleic acid from biological

CC samples or other samples containing large molecule contaminants. The

CC present sequence represents a double stranded (CTG)7 DNA molecule used to

CC isolate double stranded DNA molecules in an example of a similar method

CC to that of the invention

XX

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 33

ACH03118/c

ID ACH03118 standard; DNA; 21 BP.

XX

AC ACH03118;

XX

DT 25-SEP-2003 (first entry)

XX

DE Immunostimulatory nucleic acid #753.

XX

KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;

KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; SS.

XX

OS Synthetic.

XX

PN US2003050268-A1.

XX

PD 13-MAR-2003.

XX

PF 29-MAR-2002; 2002US-00112653.

XX

PR 29-MAR-2001; 2001US-0279642P.

XX

PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX

PI Krieg AM, Berg DJ;

XX

DR WPI; 2003-521815/49.

XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,

PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.

XX

PS Disclosure; Page 29; 229pp; English.

XX

CC The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of

CC developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 DB 21 CAGCAGCAGCAGCAGCAGCAG 1
 RESULT 34
 ADB37082/c
 ID ADB37082 standard; DNA; 21 BP.
 XX
 AC ADB37082;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #696.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 PN US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 16; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 DB 21 CAGCAGCAGCAGCAGCAGCAG 1
 RESULT 35
 ADC38190
 ID ADC38190 standard; DNA; 25 BP.

XX
 AC ADC38190;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:539.
 XX
 KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1a; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 PT New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 539; 172pp; English.
 XX
 CC The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1430 CAGCAGCAGCAGCAGCAGCAG 1450
 DB 1 CAGCAGCAGCAGCAGCAGCAG 21
 RESULT 36
 ADC38185
 ID ADC38185 standard; DNA; 25 BP.
 XX
 AC ADC38185;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:534.
 XX
 KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1a; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX

PF 01-NOV-2002; 2002WO-US035129.
 XX
 XX 01-NOV-2001; 2001US-0334773P.
 XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX Shannon M, Phan T;
 FI WPI; 2003-430501/40.
 XX
 XX New isolated nucleic acid molecule encoding a human angiotensin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 534; 172pp; English.
 XX
 XX The present invention describes the human angiotensin-like protein 1
 CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
 CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLPI. The present sequence represents a scanning
 CC oligonucleotide for human AMLPI, which is used in an example from the
 CC present invention.
 XX
 XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.6%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1429 GCAGCAGCAGCAACAGCAGCA 1449
 Db 5 GCAGCAGCAGCAACAGCAGCA 25
 RESULT 37
 ABL61611
 ID ABL61611 standard; DNA; 24 BP.
 XX
 AC ABL61611;
 XX
 XX 13-MAY-2002 (first entry)
 DT Porcine GPR8-related PCR primer #3.
 DE
 DE Porcine GPR8-related PCR primer #3.
 XX
 XX Anorectic; GPR8 ligand; central nervous system; obesity; pig;
 KW appetite-stimulating agent; prolactin; porcine; PCR primer; ss.
 XX
 OS Sus scrofa.
 XX
 PN WO200198494-A1.
 XX
 XX 27-DEC-2001.
 PD
 XX 20-JUN-2001; 2001WO-JP005257.
 PF
 XX 21-JUN-2000; 2000JP-00191089.
 PR 06-SEP-2000; 2000JP-00275013.
 PR 13-APR-2001; 2001JP-00116000.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Mori M, Shimomura Y, Harada M, Kurihara M, Kitada C, Asami T;
 PI Mateumoto Y, Adachi Y, Watanabe T, Sugo T, Abe M;
 XX WPI; 2002-139790/18.
 DR
 XX Ligand to GPR8 and encoded gene, useful in developing receptor-binding
 PT assay system, diagnosis and screening candidate compounds for central
 PT nervous system function-regulating drugs to treat e.g. obesity.
 XX
 XX Example 30; Page 184; 221pp; Japanese.

XX The present invention relates to GPR8 ligands. The ligands as well as
 CC their precursor proteins and DNAs are useful in developing receptor-
 CC binding assay systems, diagnosis and screening candidate compounds for
 CC central nervous system function-regulating drugs as preventives or
 CC remedies for obesity, appetite-stimulating agents and prolactin
 CC production promoters or inhibitors. The present PCR primer was used to
 CC illustrate the invention
 XX
 SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 Query Match 0.6%; Score 20.8; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 62;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1418 CAGCAGCAGCAGCAGCAGCA 1441
 Db 1 CAGCGCAGCAGCAGCAGCTAA 24
 RESULT 38
 ABK94601
 ID ABK94601 standard; DNA; 24 BP.
 XX
 AC ABK94601;
 XX
 XX 28-AUG-2002 (first entry)
 DT
 DE G-protein-coupled receptor DNA PCR primer #17.
 XX
 XX Human; rat; primer; ss; G protein-coupled receptor; anorectic; anabolic;
 KW obesity; appetite enhancement; prolactin production; eating disorder;
 KW PCR; pig; mouse.
 XX
 OS Sus scrofa.
 XX
 PN WO200244368-A1.
 XX
 XX C6-JUN-2002.
 PD
 XX 29-NOV-2001; 2001WO-JP010418.
 PF
 XX 30-NOV-2000; 2000JP-00364801.
 PR 26-MAR-2001; 2001JP-00087482.
 PR 15-MAY-2001; 2001JP-00145434.
 PR 06-SEP-2001; 2001JP-00270838.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Terao Y, Shintani Y, Harada M, Shimomura Y, Mori M;
 FI WPI; 2002-471832/50.
 XX
 XX New rat and mouse brain-originated G protein-coupled receptor proteins
 PT TGR26, useful in diagnosis and developing drugs for prevention or
 PT treatment of obesity or an eating disorder.
 XX
 XX Example 11; Page 244; 312pp; Japanese.
 FS
 XX The invention relates to G protein-coupled receptor proteins and their
 CC associated nucleic acids. The sequences are used in diagnosis of diseases
 CC relating to function of the protein and can be used for treating obesity,
 CC enhancing appetite or inhibiting prolactin production by administering
 CC the compounds or their salts that can alter binding of the G protein-
 CC coupled receptors. The proteins and encoded DNAs are useful in diagnosis
 CC of and developing drugs for prevention or treatment of obesity and eating
 CC disorders. This sequence represents a PCR primer used in production of
 CC DNA encoding a G protein-coupled receptor protein
 XX
 SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
 Query Match 0.6%; Score 20.8; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 62;

DT	28-APR-2003	(first entry)
XX	Histidine tag encoding DNA.	
XX	Genetic information; glyph; molecular biology; histidine tag; ds.	
KW	Synthetic.	
OS		
XX		
Key	Location/Qualifiers	
FH	1..24	
FT	/tag= a	
FT		
XX		
PN	WO200282264-A2.	
XX		
PD	17-OCT-2002.	
XX		
PF	05-APR-2002; 2002WO-US010825.	
XX		
PR	06-APR-2001; 2001US-0282022P.	
XX	(SEED/) SEED B.	
PA		
XX	Seed B;	
PI		
XX		
DR	WFI; 2003-058598/05.	
P-	PSDB; ABP71241.	
XX		
PT	Displaying genetic information represented by set of glyphs, by receiving	
PT	entered command to display glyphs, identifying glyph assigned to the	
PT	entered command, and displaying identified glyph.	
XX		
XX	Example 3; Page 37; 50pp; English.	
XX		
CC	The invention relates to displaying genetic information represented by a	
CC	set of glyphs. The method involves receiving an entered command to	
CC	display one of the set of glyphs, identifying the glyph of the set	
CC	assigned to the entered command, and displaying the identified glyph,	
CC	where the glyph is displayed at a location on a display screen with a	
CC	cursor. Another method for displaying a double-stranded codon and an	
CC	amino acid encoded by the codon is also provided. The methods provide	
CC	a simple and quick way for displaying and genetic information that has been	
CC	modified by a standard molecular biology technique. The present sequence	
CC	represents a DNA fragment encoding a histidine tag	
XX		
SQ	Sequence 24 BP; 8 A; 12 C; 4 G; 0 T; 0 U; 0 Other;	
Query Match	0.6%; Score 20.8; DB 1; Length 24;	
Best Local Similarity	91.7%; Pred. No. 62;	
Matches	22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	977 CACGACCAGCAGCAGCAGCACCG 1000	
Dd	1 CACGACCAGCAGCAGCAGCACCG 24	
RESULT 41		
ADC51835		
ID	ADC51835 standard; DNA; 24 BP.	
XX		
AC	ADC51835;	
XX		
DT	18-DEC-2003 (first entry)	
XX		
DE	GPR8 PCR primer, SEQ ID 46.	
XX		
KW	Body weight; GPR8L; brain; hyperphagia; obesity; anorectic; GPR8; PCR;	
KW	primer; ss.	
XX		
OS	Unidentified.	
XX		
PN	WO2003057236-A1.	
XX		
PD	17-JUL-2003.	

```
XX PF 27-DEC-2002; 2002WO-JP013781.
XX XX
XX PR 28-DEC-2001; 2001JP-00403260.
XX PR 28-MAR-2002; 2002JP-00093096.
XX XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX PA
XX XX
XX PI Mateumoto H, Noguchi J, Harada M, Mori M;
XX XX
XX DR WPI; 2003-569538/53.
XX XX
XX PT Composition comprising peptide of brain origin binding to orphan G-
XX PT protein coupled receptor GPR8 for treatment and prevention of obesity and
XX PT hyperphagia.
XX XX
XX PS Example 30; SEQ ID NO 46; 277pp; Japanese.
XX CC
XX CC The present invention relates to novel compositions for inhibiting body
XX CC weight gain, for lowering body weight, for inhibiting fat weight gain,
XX CC and for suppressing appetite, which contain as active component a peptide
XX CC ligand (GPR8L, ADC51805) of brain origin. The compositions can be used
XX CC for treatment and prevention of hyperphagia and obesity (including
XX CC malignant mastocytosis, exogenous obesity, hyperinsulinemic obesity,
XX CC hyperplasmic obesity, hypophyseal obesity, hypoplasmic obesity,
XX CC hypothyroid obesity, hypothalamic obesity, symptomatic obesity, infant
XX CC obesity, upper body obesity, alimentary obesity, hypogonadal obesity,
XX CC systemic mastocytosis, simple obesity and central obesity). The present
XX CC sequence was used to illustrate the invention.
XX XX
XX SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 62;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1418 CAGCAGCAGCAGCAGCAGCAGCA 1441
Db 1 CAGCGCGCAGCAGCAGCAGCTAA 24
XX
RESULT 42
ID ABK88725/c
XX AC
XX AC ABK88725;
XX XX
XX DT 07-OCT-2002 (first entry)
XX XX
XX DE Human Pur alpha anti-sense strand, phosphorothioate oligonucleotide #4.
XX KW Human; apoptotic cell death; proteinaceous transcription factor;
XX KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
XX KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
XX KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
XX KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
XX KW immune system dysfunction; anti-tumour; cytostatic; Pur alpha;
XX KW phosphorothioate; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..22
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate internucleotide linkages"
XX XX
XX PN WO200244363-A1.
XX XX
XX PD 06-JUN-2002.
XX XX
XX PF 28-NOV-2001; 2001WO-NZ000287.
XX XX

PR 28-NOV-2000; 2000US-00724809.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX PA
XX PI Lasham A, Watson JD;
XX XX
XX DR WPI; 2002-557540/59.
XX XX
XX PT Modulating p53-mediated apoptotic cell death in a population of cells, by
XX PT modulating the amount of a transcriptional regulator of apoptosis
XX PT available to bind to a target polynucleotide in the cells.
XX XX
XX PS Example 2; Page 57; 62pp; English.
XX CC
XX CC The present invention relates to methods for modulating apoptotic cell
XX CC death using proteinaceous transcription factors that regulate the
XX CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
XX CC and p53). The methods involve modulating the amount of a transcriptional
XX CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
XX CC in the cells, where TRA is a member of the Y-box nucleic acid binding
XX CC family of polypeptides (e.g. YB-1). The methods of the invention are
XX CC useful for modulating apoptotic cell death in a population of cells,
XX CC where the cells are selected from tumour cells, cells of the immune
XX CC system, embryonic cells, cells of the nervous system, or cells infected
XX CC with intracellular pathogens. The methods are also useful for increasing
XX CC the sensitivity of tumour cells to a DNA-damaging agent, and for
XX CC increasing sensitivity to apoptosis in a population of cells harbouring
XX CC intracellular pathogens. The methods are useful for screening an
XX CC apoptosis modulatory agent that modulates the binding of TRA. The methods
XX CC for regulating apoptosis can be used therapeutically and prophylactically
XX CC for various disorders such as cancer, viral and retroviral infections,
XX CC neurodegenerative disorders, and immune system dysfunction. The present
XX CC sequence represents a phosphorothioate oligonucleotide to the anti-sense
XX CC strand of human Pur alpha
XX XX
XX SQ Sequence 22 BP; 0 A; 5 C; 9 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20.4; DB 1; Length 22;
XX Best Local Similarity 95.5%; Pred. No. 56;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1397 CAACAGCAGCAGCAGCAGCAGC 1418
Db 22 CACCAGCAGCAGCAGCAGCAGC 1
XX
RESULT 43
ID AAD37201 standard; DNA; 20 BP.
XX AC
XX AC AAD37201;
XX XX
XX DT 21-AUG-2002 (first entry)
XX XX
XX DE Human MEKK4 antisense oligonucleotide, ISIS #23136.
XX XX
XX KW Human; MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1;
XX KW MAP3K4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKKK4; cytostatic;
XX KW prophylaxis; immunological; hyperproliferative disorder; cancer; therapy;
XX KW antisense; inflammatory; phosphorothioate backbone; ss.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base 1..5
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotides"
```

```
FT modified_base 2 /*tag= d
FT /*mod_base= m5c
FT modified_base 5
FT /*tag= e
FT /*mod_base= m5c
FT modified_base 8
FT /*tag= f
FT /*mod_base= m5c.
FT modified_base 11
FT /*tag= g
FT /*mod_base= m5c
FT modified_base 14
FT /*tag= h
FT /*mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /*mod_base= OTHER
FT modified_base 17
FT notes= "2'-methoxyethyl nucleotides"
FT modified_base 17
FT /*tag= i
FT /*mod_base= m5c
FT modified_base 20
FT /*tag= j
FT /*mod_base= m5c
FT
FT
XX WO200227033-A1.
XX
XX
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US030549.
XX
XX 29-SEP-2000; 2000US-00676436.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Gaarde WA, Monia BP, Wyatt JR;
XX WPI; 2002-416486/44.
XX
XX New antisense compound targeted to nucleic acid encoding mitogen-
XX activated protein kinase 4, useful for treating immunologic disorder,
XX inflammatory disorder or cancer.
XX
XX Claim 3; Page 93; 132pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of MEKK4 (also referred as mitogen-
XX activated protein kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK
XX kinase kinase 4; MAPKKK4; MTK1). The antisense oligos are useful for
XX inhibiting the expression of MEKK4 in cells or tissues. They are also
XX useful for treating an animal having a disease or condition associated
XX with MEKK4 such as immunological, inflammatory, hyperproliferative
XX disorder or cancer. Sequences of the invention are also useful for
XX diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX They are also useful in antisense therapy. The present sequence is an
XX antisense oligonucleotide targeted to human MEKK4 DNA. This sequence is
XX used in the exemplification of the invention
XX
XX Sequence 20 BP; 6 A; 7 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GCAGCAGCAGCAGCAGCAGC 20
|||||
RESULT 44
ABZ30516/c
ID ABZ30516 standard; DNA; 20 BP.

XX AC ABZ30516;
XX
XX 30-JAN-2003 (first entry)
XX
XX Candida albicans GRACE strain PCR primer SEQ ID NO 4667.
XX
XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
XX signal transduction; DNA replication; cell division; growth;
XX proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
XX Candida albicans.
XX
XX WO200253728-A2.
XX
XX 11-JUL-2002.
XX
XX 26-DEC-2001; 2001WO-US049486.
XX
XX 29-DEC-2000; 2000US-0259128P.
XX
XX 20-FEB-2001; 2001US-00792024.
XX
XX 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX
XX Constructing strains for identifying gene products as effective targets
XX for therapeutic intervention, by inactivating in the strain one allele of
XX a gene and placing other allele of the gene under conditional expression.
XX
XX Claim 36; SEQ ID NO 4667; 167pp + Sequence Listing; English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of a PCR
XX primer used in the method of the invention. Note: The sequence data for
XX this patent is not represented in the printed specification but is based
XX on sequence information supplied to Derwent by the European Patent Office
XX
XX Sequence 20 BP; 0 A; 4 C; 7 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1553 CAACAACAGCAGCAGCAGCA 1572
Db 20 CAACAACAGCAGCAGCAGCA 1
|||||
RESULT 45
ABZ31489/c
```

ID ABZ31489 standard; DNA; 20 BP.
AC ABZ31489;
DT 30-JAN-2003 (first entry)
XX
XX Candida albicans GRACE strain PCR primer SEQ ID NO 5708.
XX
XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
XX Candida albicans.
OS
XX WO200253728-A2.
PN
XX 11-JUL-2002.
PD
XX 26-DEC-2001; 2001WO-US049486.
PF
XX 29-DEC-2000; 2000US-0259128P.
PR
XX 20-FEB-2001; 2001US-0079202A.
PR
XX 22-AUG-2001; 2001US-0314050P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlssen KL;
PI
XX WPI; 2002-566694/60.
DR
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
PT
XX
XX Claim 36; SEQ ID NO 5708; 167pp + Sequence Listing; English.
PS
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1555 ACAACAGCAGCAGCAGCAGC 1574
|||||
Db 20 ACAACAGCAGCAGCAGCAGC 1

RESULT 46

AAQ14196
ID AAQ14196 standard; DNA; 21 BP.
XX
AC AAQ14196;
XX
DT 02-JAN-1992 (first entry)
XX
XX Oligonucleotide probe incorporating disulphide linker.
DE
XX ss.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH misc_feature 8
FT /*tag= a
FT /note= "n = O2-P-O-CH2-CH2-O-CH2-CH2-S-S-CH2-CH2-O- CH2-
FT CH2-O-P-O3"
FT
XX WO9114696-A.
PN
XX 03-OCT-1991.
PD
XX 29-MAR-1990; 90US-00502361.
PF
XX 29-MAR-1990; 90US-00502361.
PR
XX (GILE-) GILEAD SCI INC.
PA
XX Latham JA, Lin KY, Matteucci M;
PI
XX WPI; 1991-310523/42.
DR
XX New oligo:nucleotide- transport agent di:sulphide conjugate(s) - for
PT inhibiting nucleotide expression in therapy and diagnosis of endogenous
PT nucleotide sequences in cells.
PT
XX Example; Page 37; 67pp; English.
PS
XX The oligonucleotide has a disulphide linker incorporated into the probe
CC which acts as a hybridisation-triggered crosslinking agent. This will
CC permit novel diagnostic assay modifications such as the use of
CC crosslinker to increase probe discrimination and incorporation of a
CC denaturing wash step to reduce background. Also carrying out
CC hybridisation and crosslinking at or near the melting temperature of the
CC hybrid DNA will reduce secondary structure in the target DNA and increase
CC probe specificity. See also AAQ14195
XX
SQ Sequence 21 BP; 6 A; 7 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
|||||
Db 1 CAGCAGCAGCAGCAGCAGCAG 21

RESULT 47
ADC38191
ID ADC38191 standard; DNA; 25 BP.
XX
AC ADC38191;
XX

DT 18-DEC-2003 (first entry)
XX

DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:540.
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX
OS Synthetic.

```

OS Homo sapiens.
XX WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-NOV-2002; 2002WO-US035129.
XX
XX PR 01-NOV-2001; 2001US-0334773P.
XX
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX PI Shannon M, Phan T;
XX
XX DR WPI; 2003-430501/40.
XX
XX PT New isolated nucleic acid molecule encoding a human angiominotin-like
XX protein, useful for treating or preventing a disorder associated with
XX PT decreased or increased expression or activity of AMLP1.
XX
XX PS Example 2; SEQ ID NO 540; 172pp; English.
XX
XX CC The present invention describes the human angiominotin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX CC compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX CC oligonucleotide for human AMLPIa, which is used in an example from the
XX present invention.
XX
XX SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1431 AGCAGCAGCAACAGCAGCAG 1450
XX |
XX 1 AGCAGCAGCAACAGCAGCAG 20

RESULT 48
ADC38184
ID ADC38184 standard; DNA; 25 BP.
XX
XX AC ADC38184;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human AMLPIa scanning 25-mer oligonucleotide SEQ ID NO:533.
XX
XX KW human; angiominotin-like protein 1; AMLPI; cytostatic; gene therapy;
XX KW AMLPIa; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-NOV-2002; 2002WO-US035129.
XX
XX PR 01-NOV-2001; 2001US-0334773P.
XX
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX PI Shannon M, Phan T;
XX
XX DR WPI; 2003-430501/40.
XX
XX PT New isolated nucleic acid molecule encoding a human angiominotin-like

Query Match 0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1431 AGCAGCAGCAACAGCAGCAG 1448
XX |
XX 6 GCAGCAGCAGCAACAGCAGC 25

RESULT 49
ADN97247
ID ADN97247 standard; DNA; 24 BP.
XX
XX AC ADN97247;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Primer of the invention #52.
XX
XX KW DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
XX KW forensic identification; marijuana; primer; ss.
XX
XX OS Unidentified.
XX
XX PN WO2004008841-A2.
XX
XX PD 29-JAN-2004.
XX
XX PF 21-JUL-2003; 2003WO-US022887.
XX
XX PR 19-JUL-2002; 2002US-0397179P.
XX
XX PA (UYAR-) UNIV ARIZONA.
XX PA (KEIM/) KEIM P S.
XX PA (ZINN/) ZINNAMON K.
XX
XX PI Keim PS, Zinnamon K;
XX
XX DR WPI; 2004-143139/14.
XX
XX PT New isolated nucleic acid for amplification of a short tandem repeat
XX located in DNA isolated from Cannabis sativa L species, useful for
XX forensic identification of marijuana or for linking a marijuana sample to
XX its plant source.
XX
XX PS Example 10; SEQ ID NO 114; 79pp; English.
XX
XX CC The present invention relates to DNA fingerprinting for Cannabis Sativa
XX using short tandem repeat markers. The nucleic acid is useful for
XX forensic identification of marijuana or for linking a marijuana sample to
XX its plant source. The present sequence represents a primer of the
XX invention.
XX
XX SQ Sequence 24 BP; 8 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 88;

```

```

PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX PS Example 2; SEQ ID NO 533; 172pp; English.
XX
XX CC The present invention describes the human angiominotin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX CC compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX CC oligonucleotide for human AMLPIa, which is used in an example from the
XX present invention.
XX
XX SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1429 GCAGCAGCAGCAACAGCAGC 1448
XX |
XX 6 GCAGCAGCAGCAACAGCAGC 25

RESULT 49
ADN97247
ID ADN97247 standard; DNA; 24 BP.
XX
XX AC ADN97247;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Primer of the invention #52.
XX
XX KW DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
XX KW forensic identification; marijuana; primer; ss.
XX
XX OS Unidentified.
XX
XX PN WO2004008841-A2.
XX
XX PD 29-JAN-2004.
XX
XX PF 21-JUL-2003; 2003WO-US022887.
XX
XX PR 19-JUL-2002; 2002US-0397179P.
XX
XX PA (UYAR-) UNIV ARIZONA.
XX PA (KEIM/) KEIM P S.
XX PA (ZINN/) ZINNAMON K.
XX
XX PI Keim PS, Zinnamon K;
XX
XX DR WPI; 2004-143139/14.
XX
XX PT New isolated nucleic acid for amplification of a short tandem repeat
XX located in DNA isolated from Cannabis sativa L species, useful for
XX forensic identification of marijuana or for linking a marijuana sample to
XX its plant source.
XX
XX PS Example 10; SEQ ID NO 114; 79pp; English.
XX
XX CC The present invention relates to DNA fingerprinting for Cannabis Sativa
XX using short tandem repeat markers. The nucleic acid is useful for
XX forensic identification of marijuana or for linking a marijuana sample to
XX its plant source. The present sequence represents a primer of the
XX invention.
XX
XX SQ Sequence 24 BP; 8 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 88;

```

```
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAG 1432
DB 1 AGCAGCAGCAGCAGCAGCAGGAG 23

RESULT 50
ABZ81769
ID ABZ81769 standard; DNA; 21 BP.
XX AC
XX ABZ81769;
XX
DT 11-JUN-2003 (first entry)
XX
DE Huntington's disease gene mutated exon 1 region.
XX
KW Huntington's disease; nontropic; anticonvulsant; huntingtin; human;
KW gene therapy; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(10,C)
FT /*tag= a
XX
PN WO2003013437-A2.
XX
PD 20-FEB-2003.
XX
PF 07-AUG-2002; 2002WO-US025352.
XX
PR 07-AUG-2001; 2001US-0310757P.
PR 08-AUG-2001; 2001US-0310770P.
PR 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX
PA (UYDE ) UNIV DELAWARE.
XX
PI Kmiec BB, Parekh-Olmedo H;
XX
XX WPI; 2003-256478/25.
XX
PT New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
XX
PS Example 1; Fig 6b; 133pp; English.
XX
CC The present sequence is that of a portion of a mutated glutamine (CAG)
CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC gene (see also ABZ81760). The triplet repeat region (see ABZ81767) is
CC mutated following treatment with an RNA/DNA chimeric oligonucleotide (see
CC ABZ81768) that causes a CAG (Gln) to TAG (stop) gene alteration in the HD
CC exon 1 repeats due to sliding of the repeat region, a phenomenon that can
CC occur with the methods of this invention. The RNA/DNA chimeric
CC oligonucleotide is an example of oligonucleotides of the invention for
CC targeted alteration of the HD gene. Such oligonucleotides can be used for
CC the treatment or prevention of HD
XX
SQ Sequence 21 BP; 7 A; 6 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 69;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
DB 1 CAGCAGCAGTAGCAGCAGCAGCAG 21
```

```
RESULT 51
AAF76808
ID AAF76808 standard; DNA; 22 BP.
XX AC
XX AAF76808;
XX
DT 14-MAY-2001 (first entry)
XX
DE Codon-optimised HPV6 E2 fragment 6PM.
XX
KW Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO200114416-A2.
XX
PD 01-MAR-2001.
XX
PF 21-AUG-2000; 2000WO-US022932.
XX
PR 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Neepser MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX
XX WPI; 2001-218428/22.
XX
PT Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells.
XX
PS Example 6; Fig 23; 119pp; English.
XX
CC The present sequence is an oligomer which was used in the assembly of one
CC of a number of synthetic polynucleotides that encode a human
CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC mutated HPV proteins have reduced protein function as compared to wild
CC type proteins but maintain immunogenicity. The proteins comprise codons
CC for optimised expression in humans. The polynucleotides are useful as a
CC vaccine which provides effective immunoprophylaxis against papillomavirus
CC infection through stimulation of neutralising antibody and cell-mediated
CC immunity
XX
SQ Sequence 22 BP; 9 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1497 CTCAACACAGCAGCAGCAGCAGC 1517
DB 2 CGCAACACAGCAGCAGCAGCAGC 22

RESULT 52
ABX03797/c
ID ABX03797 standard; cDNA; 24 BP.
XX AC
XX ABX03797;
XX
DT 09-JAN-2003 (first entry)
XX
DE DNA encoding secreted protein signal peptide sequence #6.
XX
KW Differential display method; leucine-rich motif; transmembrane protein;
KW secreted protein; secreted protein signal peptide; ss.
XX
OS Unidentified.
```

XX PN WO200259259-A2.
 XX PD 01-AUG-2002.
 XX PF 23-JAN-2002; 2002WO-IL000071.
 XX PR 23-JAN-2001; 2001US-0263158P.
 XX PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 XX PI Wreschner DH;
 XX DR WPI; 2002-599769/64.
 XX DR P-PSDB; ABG98326.
 XX PT Differential display method for identifying secreted or transmembrane
 PT protein, comprises contacting a DNA with a first primer that hybridizes
 PT to a sequence coding for a leucine-rich motif and with a second
 PT oligonucleotide primer.
 XX PS Disclosure; Fig 2; 37pp; English.
 XX CC The invention relates to a differential display comprising contacting
 CC cDNA with a first primer that hybridises to an oligonucleic sequence
 CC coding for a leucine-rich motif, and with a second oligonucleotide primer
 CC to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
 CC at least 2 samples, synthesising cDNA from the RNA of each sample,
 CC contacting the cDNA with a first primer that hybridises to an
 CC oligonucleic sequence coding for a leucine-rich motif, and with a second
 CC oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA
 CC -hybrid molecules, detecting amplified products and comparing the
 CC amplified products from each sample to identify distinctive amplified
 CC products coding for at least one secreted or transmembrane protein. The
 CC method is useful for discovering novel secreted and/or transmembrane
 CC proteins which are important for cell processes and play an important
 CC role in determining its phenotype, and which act as mediators for the
 CC transfer of signals from external environment into the cell itself, thus
 CC modulating gene expression. Sequences ABX03792-ABX03869 represent DNA
 CC encoding secreted protein signal peptide sequences
 XX SQ Sequence 24 BP; 0 A; 9 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1403 CAGCAGCAGCAGCAGCAG 1423
 DB 21 CAGCAGCAGCAGCAGCAGCG 1
 RESULT 53
 ADN06499
 ID ADN06499 standard; DNA; 24 BP.
 XX AC ADN06499;
 XX DT 15-JUL-2004 (first entry)
 XX DE Human FLAP related microsatellite marker SEQ ID NO:147.
 KW leukotriene synthesis inhibitor; myocardial infarction;
 KW acute coronary syndrome; antiatherosclerotic; cardiant; antianginal;
 KW leukotriene biosynthesis inhibitor; leukotriene receptor antagonist;
 KW 5-lipoxygenase activating protein; FLAP; human; chromosome 13;
 KW chromosome 13q12; polymorphism; 5-lipoxygenase gene promoter;
 KW 5-LO gene promoter; diabetes; hypertension; hypercholesterolemia;
 KW obesity; inflammatory marker; low density lipoprotein; cholesterol;
 KW high density lipoprotein; angina; atherosclerosis; microsatellite marker;
 KW ss.
 XX OS Homo sapiens.

OS Synthetic.
 XX PN WO2004035741-A2.
 XX PD 29-APR-2004.
 XX PF 16-OCT-2003; 2003WO-US032556.
 XX PR 17-OCT-2002; 2002US-0419433P.
 XX PR 21-FEB-2003; 2003US-0449331P.
 XX PA (DECO-) DECODE GENETICS EHF.
 XX PI Helgadottir A, Gurney ME, Gulcher JR;
 XX DR WPI; 2004-357211/33.
 XX PT Use of leukotriene synthesis inhibitor for manufacture of a medicament
 PT for treatment for myocardial infarction or susceptibility to myocardial
 PT infarction in individual.
 XX PS Disclosure; SEQ ID NO 147; 306pp; English.
 XX CC The present invention describes using a leukotriene synthesis inhibitor
 CC (I) for the manufacture of a medicament for the treatment of myocardial
 CC infarction or susceptibility to myocardial infarction in an individual.
 CC Also described is a method (M1) for the treatment of acute coronary
 CC syndrome (ACS) in an individual comprising administering (I). (I) has
 CC antiatherosclerotic, cardiant and antianginal activities, and can be used
 CC as a leukotriene biosynthesis inhibitor, and a leukotriene receptor
 CC antagonist. (I) can be used for the manufacture of a medicament for the
 CC treatment of myocardial infarction or susceptibility to myocardial
 CC infarction in an individual who has at least one risk factor chosen from
 CC an at-risk haplotype for myocardial infarction, an at-risk haplotype in
 CC the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a
 CC FLAP nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-
 CC LO) gene promoter; in an individual who has at least one risk factor
 CC chosen from diabetes, hypertension, hypercholesterolemia, elevated
 CC lip(a), obesity, past or current smoker; in an individual having elevated
 CC inflammatory marker chosen from C-reactive protein (CRP), serum amyloid
 CC A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue
 CC necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
 CC soluble intervascular adhesion molecule (sICAM), E-selectin, matrix
 CC metalloproteinase type-1, matrix metalloproteinase type-2, matrix
 CC metalloproteinase type-3 and matrix metalloproteinase type-9; in an
 CC individual having increased low density lipoprotein (LDL) cholesterol
 CC and/or decreased high density lipoprotein (HDL) cholesterol; in an
 CC individual having increased leukotriene synthesis; in an individual
 CC having previous myocardial infarction or acute coronary syndrome (ACS)
 CC event, stable angina; or in an individual who has atherosclerosis or who
 CC requires treatment to restore blood flow in arteries. (M1) is useful for
 CC treating an individual suffering from acute coronary syndrome chosen from
 CC unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-
 CC elevation myocardial infarction (STEMI). The human FLAP gene is located
 CC on chromosome 13, more specifically to 13q12. The present sequence
 CC represents a microsatellite marker used in the exemplification of the
 CC present invention.
 XX SQ Sequence 24 BP; 16 A; 7 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1570 GCAGCAACACACACACACACACACAC 1593
 DB 1 GAAACAAACACACACACACACACAC 24
 RESULT 54
 ADS94518
 ID ADS94518 standard; DNA; 24 BP.
 XX XX

```

AC ADS94518;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human 5-lipoxygenase activating protein (FLAP) gene PCR primer #144.
XX
XX human; 5-lipoxygenase activating protein; FLAP; chromosome 13q12;
KW single nucleotide polymorphism; SNP; myocardial infarction; PCR; primer;
KW microsatellite marker; ss.
XX
OS Homo sapiens.
XX
XX WO2004035746-A2.
XX
XX 29-APR-2004.
XX
XX 16-OCT-2003; 2003WO-US032805.
XX
XX 17-OCT-2002; 2002US-0419432P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Helgadottir A, Gulcher JR, Manolescu A;
XX
XX WPI; 2004-348442/32.
XX
XX Novel FLAP (5-lipoxygenase activating protein) nucleic acid useful for
XX diagnosing myocardial infarction and for identifying agent that is useful
XX for treating myocardial infarction.
XX
XX Example; SEQ ID NO 147; 230pp; English.
XX
XX The invention comprises nucleic acid sequences of the human 5-
XX lipoxygenase activating protein (FLAP) gene - present on chromosome
XX 13q12. In particular the invention relates to polymorphisms identified
XX within this gene. The DNA sequences of the invention are useful for
XX diagnosing susceptibility to myocardial infarction and identifying agents
XX that alter expression of FLAP. The present DNA sequence represents a PCR
XX primer that is used to amplify a microsatellite marker from the human
XX FLAP gene.
XX
XX Sequence 24 BP; 16 A; 7 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1570 GCAGCAACACACAGCAACCAACA 1593
DB 1 GAAACACACACACACACACCAACA 24
RESULT 55
AAAX97150/c
ID AAAX97150 standard; DNA; 20 BP.
XX
XX AAAX97150;
XX
XX 13-SEP-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
OS Chlamydia pneumoniae.
XX
XX WO99271105-A2.
XX
XX 03-JUN-1999.
XX
XX

```

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PF 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
XX Page 1881; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotides sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX
XX Sequence 20 BP; 1 A; 3 C; 7 G; 9 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1454 CAGCAACAGCAACAGCAAC 1472
DB 19 CAGCAACAGCAACAGCAAC 1
RESULT 56
AAAF76807/c
ID AAFA76807 standard; DNA; 23 BP.
XX
XX AAFA76807;
XX
XX 14-MAY-2001 (first entry)
XX
XX Codon-optimised HPV6 E2 fragment 6PL.
XX
XX Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
XX Human papillomavirus.
OS Synthetic.
XX
XX WO200114416-A2.
XX
XX C1-MAR-2001.
XX
XX 21-AUG-2000; 2000WO-US022932.
XX
XX 25-AUG-1999; 99US-0150728P.
PR C7-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Neepser MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX WPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
XX protein or mutated HPV protein useful as anti-HPV vaccines, comprises
XX optimized-codons for expression of the viral proteins in human host
XX cells.

```


XX Example 6; Fig 23; 119pp; English.

XX The present sequence is an oligomer which was used in the assembly of one

CC of a number of synthetic polynucleotides that encode a human

CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The

CC mutated HPV proteins have reduced protein function as compared to wild

CC type proteins but maintain immunogenicity. The proteins comprise codons

CC for optimised expression in humans. The polynucleotides are useful as a

CC vaccine which provides effective immunoprophylaxis against papillomavirus

CC infection through stimulation of neutralising antibody and cell-mediated

CC immunity

XX

SQ Sequence 23 BP; 0 A; 5 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 19; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1499 CAACAACAGCAACAGCAGC 1517

Db 22 CAACAACAGCAACAGCAGC 4

RESULT 57

AAA54149/c

ID AAA54149 standard; cDNA; 22 BP.

AC AAA54149;

XX

DT 08-FEB-2001 (first entry)

XX

XX Antisense oligonucleotide (WH6) directed against preproendothelin-1.

DE

XX Preproendothelin; endothelin; antisense oligonucleotide; therapy;

KW treatment; inhibition; syntheisis; lung disease; pulmonary hypertension;

KW obliterative bronchiolitis; asthma; obstructive pulmonary disease; human;

KW ss.

XX

OS Homo sapiens.

XX

XX W0200055314-A2.

XX

PD 21-SEP-2000.

XX

PF 17-MAR-2000; 2000WO-US040074.

XX

XX 18-MAR-1999; 99US-0125000P.

XX

PA (UNTH-) UNITED THERAPEUTICS CORP.

XX

XX Corder R, Smith APL, Higenbottam TW, Rothblatt M, Vane SJ;

PI Lees DDM;

PI

XX WPI; 2000-647072/62.

XX

XX Antisense oligonucleotides complementary to human preproendothelin-1 mRNA

PT and capable of inhibiting synthesis of preproendothelin-1 useful for

PT treating lung diseases such as pulmonary hypertension and asthma.

XX

PS Claim 26; Fig 19; 54pp; English.

XX

XX Antisense oligonucleotides directed against human preproendothelin-1 can

CC be used to inhibit the synthesis of preproendothelin-1 and endothelin-1.

CC Combinations of active antisense oligonucleotides achieve a greater

CC effect than individual antisense oligonucleotides. The antisense

CC oligonucleotides have applications for treating lung disease such as

CC pulmonary hypertension, obliterative bronchiolitis, asthma or chronic

CC obstructive pulmonary disease, they are also useful for treating diseases

CC caused or aggravated by excess production of endothelin. The antisense

CC oligonucleotides are described in GENESSEQ records AAA54136-A54157 and

CC AAA54192-A54205. This antisense oligonucleotide is designated WH6 and

CC corresponds to nucleotides 939-960 of preproendothelin-1

XX SQ Sequence 22 BP; 5 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 807 TGGCCAACTCTGCCCTCTCCAC 828

Db 22 TGGCCGACTCTGCACTCTCCAC 1

RESULT 58

AAC85525/c

ID AAC85525 standard; cDNA; 23 BP.

AC AAC85525;

XX

XX 16-MAY-2001 (first entry)

XX

DE Primer ZC21.076.

XX

KW Splice variant; zdint2; mammalian adhesion protease peptide; MAPP;

KW testis; ovary; prostate; small intestine; colon; stomach; thyroid;

KW spinal cord; lymph node; trachea; heart; wound healing; apoptosis;

KW neurogenesis; tumor proliferation; ischemia reperfusion; inflammation;

KW immunologic recognition; gamete maturation; platelet aggregation;

KW infarction; brain; cancer; Alzheimer's disease; multiple sclerosis;

KW congestive heart failure; PCR; polymerase chain reaction; amplify;

KW primer; ss.

XX

OS Synthetic.

XX

XX W0200109293-A2.

XX

PD 08-FEB-2001.

XX

PF 02-AUG-2000; 2000WO-US021085.

XX

PR 03-AUG-1999; 99US-00368070.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

XX Sheppard PO, Baidur N, Bishop PD;

XX

XX WPI; 2001-202662/20.

XX

XX Mammalian adhesion protease peptides useful for delivery of therapeutic

PT agents, for identifying agonists and antagonists and treating disorders

PT of brain, heart tissue and platelet aggregation.

XX

PS Example 1; Page 105; 106pp; English.

XX

CC This primer sequence was used to clone the full length cDNA encoding

CC mammalian adhesion protease peptide (MAPP). Analysis of tissue

CC distribution of MAPP cDNA showed a transcript of approx. 4.4kb with a

CC strong signal in testes, ovary, prostate, small intestine and colon, and

CC a fainter signal in stomach, thyroid, spinal cord, lymph node and

CC trachea. Also there were two transcripts, approx. 4kb and 4.4kb, both

CC showing medium strength signal in heart tissue

XX

SQ Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.8; DB 1; Length 23;

Best Local Similarity 90.9%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1421 CAGCAGCAGCAGCAGCAGCAAC 1442

Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 59

```
ABV72153/c
ID ABV72153 standard; DNA; 23 BP.
XX
AC ABV72153;
XX
XX 05-DEC-2002 (first entry)
XX
XX PCR primer ZC21076 used to amplify cDNA encoding zdint2.
XX
XX Human; isoform; zdint2; mammalian adhesion protease peptide; MAPP;
XX
XX disintegrin-like family member; disintegrin protease; DP; PCR; primer;
XX
XX anticoagulation; fertilization; muscle fusion; neurogenesis; ss.
XX
XX Homo sapiens.
XX
XX US6420154-B1.
XX
XX 16-JUL-2002.
XX
XX 02-AUG-2000; 2000US-00632098.
XX
XX 03-AUG-1999; 99US-0146968P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Baidur N, Bishop PD;
XX
XX WPI; 2002-626081/67.
XX
XX New Isolated Mammalian Adhesion Protease Peptides (zdint2), which have
XX
XX homology to disintegrin-like family members, useful for preventing,
XX
XX diagnosing and treating fertility, muscular and neurogenic disorders.
XX
XX Example 1; Col 81-82; 42pp; English.
XX
XX PCR primers ABV72153-54 were used to amplify cDNA encoding human zdint2.
XX
XX zdint2 is a mammalian adhesion protease peptide (MAPP), and has homology
XX
XX to disintegrin-like family members (ADAMs, SVMPs and MDCs), referred to
XX
XX as disintegrin proteases (dps). MAPPs have been found to be involved in
XX
XX anticoagulation, fertilization, muscle fusion, and neurogenesis. Zdint2
XX
XX may be used in the prevention, diagnosis and treatment of diseases
XX
XX associated with inappropriate MAPP expression. The proteins may be
XX
XX administered to treat disorders associated with decreased expression by
XX
XX rectifying mutations or deletions in a patient's genome that affect the
XX
XX activity of MAPP by expressing inactive proteins or to supplement the
XX
XX patients own production of MAPPs
XX
XX Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 18.8; DB 1; Length 23;
XX
XX Best Local Similarity 90.9%; Pred. No. 1.1e+02;
XX
XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
XX
XX ||||| ||||| ||||| ||||| |||||
XX
XX 23 CAGTAGTAGCAGCAGCAGCAAC 2
XX
XX RESULT 60
XX
XX AAV52748/c
XX
XX ID AAV52748 standard; DNA; 20 BP.
XX
XX AC AAV52748;
XX
XX 02-NOV-1998 (first entry)
XX
XX DE Angiotensin-converting enzyme PCR 5'-primer SEQ ID NO:1.
XX
XX KW Angiotensin-converting enzyme; ACE; human; heart; PCR primer; detection;
XX
XX screening; cardiovascular disease; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX FN US5800990-A.
XX
XX PD 01-SEP-1998.
XX
XX PF 06-DEC-1995; 95US-00568271.
XX
XX PR 06-DEC-1995; 95US-00568271.
XX
XX PA (COLS ) UNIV COLORADO.
XX
XX PI Perryman MB, Raynolds MV;
XX
XX DR WPI; 1998-494763/42.
XX
XX PT Detecting mutation(s) in angiotensin-converting enzyme gene - to assess
XX
XX cardiovascular disease risk.
XX
XX PS Example 1; Col 9; 12pp; English.
XX
XX

ABV72153/c
ID ABV72153 standard; DNA; 23 BP.
XX
AC ABV72153;
XX
XX 05-DEC-2002 (first entry)
XX
XX PCR primer ZC21076 used to amplify cDNA encoding zdint2.
XX
XX
XX Human; isoform; zdint2; mammalian adhesion protease peptide; MAPP;
XX
XX disintegrin-like family member; disintegrin protease; DP; PCR; primer;
XX
XX anticoagulation; fertilization; muscle fusion; neurogenesis; ss.
XX
XX Homo sapiens.
XX
XX US6420154-B1.
XX
XX 16-JUL-2002.
XX
XX 02-AUG-2000; 2000US-00632098.
XX
XX 03-AUG-1999; 99US-0146968P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Baidur N, Bishop PD;
XX
XX WPI; 2002-626081/67.
XX
XX New Isolated Mammalian Adhesion Protease Peptides (zdint2), which have
XX
XX homology to disintegrin-like family members, useful for preventing,
XX
XX diagnosing and treating fertility, muscular and neurogenic disorders.
XX
XX Example 1; Col 81-82; 42pp; English.
XX
XX PCR primers ABV72153-54 were used to amplify cDNA encoding human zdint2.
XX
XX zdint2 is a mammalian adhesion protease peptide (MAPP), and has homology
XX
XX to disintegrin-like family members (ADAMs, SVMPs and MDCs), referred to
XX
XX as disintegrin proteases (dps). MAPPs have been found to be involved in
XX
XX anticoagulation, fertilization, muscle fusion, and neurogenesis. Zdint2
XX
XX may be used in the prevention, diagnosis and treatment of diseases
XX
XX associated with inappropriate MAPP expression. The proteins may be
XX
XX administered to treat disorders associated with decreased expression by
XX
XX rectifying mutations or deletions in a patient's genome that affect the
XX
XX activity of MAPP by expressing inactive proteins or to supplement the
XX
XX patients own production of MAPPs
XX
XX Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 18.8; DB 1; Length 23;
XX
XX Best Local Similarity 90.9%; Pred. No. 1.1e+02;
XX
XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
XX
XX ||||| ||||| ||||| ||||| |||||
XX
XX 23 CAGTAGTAGCAGCAGCAGCAAC 2
XX
XX RESULT 60
XX
XX ADH62525/c
XX
XX ID ADH62525 standard; DNA; 23 BP.
XX
XX AC ADH62525;
XX
XX 25-MAR-2004 (first entry)
XX
XX DE Human MAPP DNA specific PCR primer, ZC21076.
XX
XX MAPP; disintegrin protease; diagnosis; tumour; gene therapy; PCR; primer;
XX
XX mammalian adhesion protease peptide; ss.
XX
XX Homo sapiens.
XX
XX
```

CC The following methods have been developed for detecting small deletions,
 CC insertions or point mutations in an angiotensin-converting enzyme (ACE)
 CC gene of a human patient: (1) a method comprising: (a) isolating an ACE
 CC genomic DNA sequence from the patient, where the sequence spans intron
 CC 25, using oligonucleotide primers in the 3' region of exon 25 and the 5',
 CC region of exon 26; (b) hybridising the genomic sequence with a detectable
 CC probe specific for the corresponding sequence with no mutations; and (c)
 CC detecting mismatches between the genomic sequence and the probe; (2) a
 CC method comprising: (a) isolating an ACE genomic DNA sequence as in (1);
 CC (b) amplifying the sequence; (c) hybridising the amplification products
 CC with a probe as in (1); and (d) detecting mismatches between the
 CC amplification products and the probe; (3) a method comprising: (a)
 CC isolating an ACE genomic DNA sequence as in (1); (b) denaturing the
 CC genomic sequence to obtain single-stranded DNA; (c) hybridising the
 CC single-stranded DNA with a probe as in (1); and (d) detecting mismatches
 CC between the single-stranded DNA and the probe; (4) a method comprising:
 CC (a) isolating an ACE genomic DNA sequence as in (1); (b) amplifying the
 CC sequence; (c) denaturing the amplification products to obtain single-
 CC stranded DNA; (d) hybridising the single-stranded DNA with a probe as in
 CC (1); and (e) detecting mismatches between the single-stranded DNA and the
 CC probe. The methods are used for assessing the patient's risk of
 CC developing cardiovascular disease. The present sequence represents a PCR
 CC primer for ACE

XX SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GCAGCAACAGCAGCAGCAGC 1421
 DB 20 GCAGCAACAGCAGCGGCAGC 1

RESULT 62
 AAA55806/c
 ID AAA55806 standard; DNA; 20 BP.

XX AC AAA55806;

XX DT 01-SEP-2000 (first entry)

XX DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:51.

XX KW Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.

XX OS Homo sapiens.

XX EN WO200023112-A1.

XX XX 27-APR-2000.

XX XX 19-OCT-1999; 99WO-US024278.

XX XX 19-OCT-1998; 98US-0104804P.

XX PA (METH-) METHYLGENE INC.

XX PI Besterman JM, Macleod AR, Siders WM;

XX DR WPI; 2000-339532/29.

XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.

XX PS Disclosure; Page 29; 99pp; English.

XX CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention

XX SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
 DB 20 CGCAGCAGCAGCAGCAGCA 1

RESULT 63

AAH43116/c

ID AAH43116 standard; DNA; 20 BP.

XX AC AAH43116;

XX DT 19-SEP-2001 (first entry)

XX DE Antisense oligo, target HDAC-2 121-141.

XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
 KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
 KW fungal infections; ss.

XX OS Synthetic.

XX PN WO200138322-A1.

XX XX 31-MAY-2001.

XX XX 22-NOV-2000; 2000WO-IB001881.

XX XX 23-NOV-1999; 99US-0167035P.

XX PA (METH-) METHYLGENE INC.

XX PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

XX DR WPI; 2001-432601/46.

XX PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
 PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
 PT restenosis or fungal infections.

XX PS Disclosure; Page 40; 147pp; English.

XX CC The sequences given in AAH43115-21 are oligonucleotides which are

CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
DB 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 64
AAC89545/c
ID AAC89545 standard; DNA; 20 BP.
XX
AC AAC89545;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-2 antisense sequence SEQ ID NO: 15.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX

PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX

PS Example 1; Page 24; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
DB 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 65
AAC89536/c
ID AAC89536 standard; DNA; 20 BP.
XX
AC AAC89536;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-2 PCR primer SEQ ID NO: 6.
XX

KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX

PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX

PS Disclosure; Page 12; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
DB 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 66

AAS20967/c
ID AAS20967 standard; DNA; 20 BP.
XX

AC AAS20967;
XX

DT 09-APR-2002 (first entry)
XX

DE PCR primer Snrpn-U relating to gene imprinting invention.
XX

KW Human; genomic imprinting; pluripotent mouse embryonic germ cell line;
KW EG; methylated CpG island; DNA methylation; gene imprinting;
KW post-translational modification of histone; cancer; birth defect;
KW diabetes; aberrant imprinting; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190313-A2.
XX

XX WO200285309-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013143.
 XX 24-APR-2001; 2001US-0286036P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX Claim 15; SEQ ID NO 1318; 763pp; English.
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
 DB 20 CTGCAGCAGCAGCAGCAGCA 1
 RESULT 69
 ADP20499
 ID ADP20499 standard; DNA; 20 BP.
 XX AC
 XX ADP20499;
 XX 26-AUG-2004 (first entry)
 DT
 KW Immunoregulator; antisense oligonucleotide; cancer; tumour cell vaccine;
 KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;

DE Transcription factor AP-2 antisense oligonucleotide seqid 46.
 XX cytosolic; AP-2-Inhibitor-Alpha; AP-2 alpha; AP-2 alpha modulator;
 KW AP-2 alpha associated disorder; hyperproliferative disorder; human;
 KW transcription factor; antisense oligonucleotide; antisense technology;
 KW ss.
 XX Homo sapiens.
 XX OS
 XX US2004109848-A1.
 XX 10-JUN-2004.
 XX 09-DEC-2002; 2002US-00315962.
 XX 09-DEC-2002; 2002US-00315962.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Dean NM, Freier SM, Dobie KW;
 XX WPI; 2004-440306/41.
 XX New compounds targeted to nucleic acid molecules encoding AP-2 alpha and
 PT inhibits the expression of AP-2 alpha, useful for treating AP-2 alpha-
 PT associated disease or condition, particularly a hyperproliferative
 PT disorder.
 XX Example 15; SEQ ID NO 46; 58pp; English.
 XX The invention describes a compound (1) 8-80 nucleobases in length
 CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
 CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
 CC (19868 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
 CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
 CC comprising contacting the cells or tissues with (1); screening for a
 CC modulator of AP-2 alpha by contacting a preferred target segment of a
 CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
 CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
 CC alpha expression, which modulate the expression of AP-2 alpha; a
 CC diagnostic method for identifying a disease state; and a kit or assay
 CC device comprising (1). The compound is useful for treating an animal
 CC having a disease or condition associated with AP-2 alpha, particularly a
 CC hyperproliferative disorder. The compounds may be used for diagnostics,
 CC therapeutics prophylaxis and as research reagents; or as tools in
 CC differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion or the entire complement of genes expressed within
 CC cells and tissues. This sequence represents a human transcription factor
 CC AP-2 antisense oligonucleotide.
 XX Sequence 20 BP; 6 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1411 GCAGCAGCAGCAGCAGCAGC 1430
 DB 1 GCAGCAGCAGCAGCAGTAGC 20
 RESULT 70
 AAA63144/C
 ID AAA63144 standard; DNA; 18 BP.
 XX AC
 XX AAA63144;
 XX 07-DEC-2000 (first entry)
 DT
 XX Antisense oligonucleotide for use in RNase H mapping assay SEQ ID NO: 48.
 DE Immunoregulator; antisense oligonucleotide; cancer; tumour cell vaccine;
 KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;

KW XX SS.
 OS Mus sp.
 XX WO200034467-A1.
 XX 15-JUN-2000.
 PD XX
 XX 24-NOV-1999; 99WO-US028096.
 XX XX
 PR 04-DEC-1998; 98US-00205995.
 XX (ANTI-) ANTIGEN EXPRESS INC.
 XX Xu M, Qiu G, Humphreys R;
 XX WPI; 2000-423417/36.
 XX Cancer cell vaccine for treating malignancies, autoimmune disorders and
 PT isolating autodeterminant peptides comprises a regulator of invariant
 PT chain protein expression or immunoregulatory function.
 XX Claim 21; Page 47; 94pp; English.
 XX The present sequence is an antisense oligonucleotide which was used in an
 CC RNase mapping experiment. This enables the identification of sites within
 CC the 11 RNA strand which hybridise to antisense DNA. These sites can then
 CC be used as targets for antisense strands which may, using gene therapy,
 CC be used as tumour cell vaccines (for example to treat carcinomas, lung,
 CC melanoma, leukaemia, lymphomas, stomach, breast, colon or rectum, lung,
 CC prostate, bladder, pancreas, brain and ovarian cancers), or they can be
 CC used to treat autoimmune diseases including rheumatoid arthritis,
 CC diabetes mellitus and thyroiditis
 XX Sequence 18 BP; 0 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1400 CAGCAGCAACAGCAGCAG 1417
 DB 18 CAGCAGCAACAGCAGCAG 1
 RESULT 71
 AAS13717/C
 ID AAS13717 standard; DNA; 18 BP.
 XX AC AAS13717;
 XX DT 08-MAY-2002 (first entry)
 XX DE Simple sequence repeat, SSR, #14.
 XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW cereal profiling; grass profiling; seed batch purity testing.
 XX Poae.
 OS NZ509193-A.
 XX 25-MAY-2001.
 XX 03-JAN-2001; 2001NZ-00509193.
 XX 24-DEC-1999; 99AU-00004906.
 PR 04-MAY-2000; 2000AU-00007310.
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UYSC-) UNIV SOUTHERN CROSS.
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UYAD-) UNIV ADELAIDE.

PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX Forster JW, Jones ES;
 XX WPI; 2001-512563/56.
 XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
 PT core elements isolated from ryegrass and fescue, useful for selecting of
 PT genes in grass or cereal breeding or profiling grass or cereal species
 PT varieties.
 XX Claim 6; Page 51; 72pp; English.
 XX The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a
 CC method for DNA profiling grass or cereal species varieties by assessing
 CC variation between SSR varieties and testing the purity of grass or cereal
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs
 CC may be used in the selection of genes in grass or cereal breeding, for
 CC profiling grass or cereal species varieties, for testing the purity of
 CC grass or cereal seed batches, and for DNA profiling to establish the
 CC distinct identity, uniformity and/or stability of a cultivar. The present
 CC sequence is a ryegrass or fescue SSR
 XX Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1411 GCAGCAGCAGCAGCAGCA 1428
 DB 18 GCAGCAGCAGCAGCAGCA 1
 RESULT 72
 ADN97239
 ID ADN97239 standard; DNA; 18 BP.
 XX AC ADN97239;
 XX DT 01-JUL-2004 (first entry)
 XX DE Primer of the invention #47.
 XX DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
 KW forensic identification; marijuana; primer; ss.
 XX Unidentified.
 OS WO2004008841-A2.
 XX 29-JAN-2004.
 XX 21-JUL-2003; 2003WO-US022887.
 XX 19-JUL-2002; 2002US-0397179P.
 PR (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P S.
 PA (ZINN/) ZINNAMON K.
 XX Keim PS, Zinamon K;
 XX

DR WPI; 2004-143139/14.
XX
PT New isolated nucleic acid for amplification of a short tandem repeat
PT located in DNA isolated from Cannabis sativa L species, useful for
PT forensic identification of marijuana or for linking a marijuana sample to
PT its plant source.
XX
PS Example 9; SEQ ID NO 106; 79pp; English.
XX
CC The present invention relates to DNA fingerprinting for Cannabis Sativa
CC using short tandem repeat markers. The nucleic acid is useful for
CC forensic identification of marijuana or for linking a marijuana sample to
CC its plant source. The present sequence represents a primer of the
CC invention.
XX
SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427
DB 1 AGCAGCAGCAGCAGCAGC 18
|||||

RESULT 73
ADO26674/c
ID ADO26674 standard; DNA; 18 BP.
XX
AC ADO26674;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:67.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26675.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 67; 86pp; English.
XX
CC The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct

CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism of interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism of interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGC 1426
DB 18 CAGCAGCAGCAGCAGCAGC 1
|||||

RESULT 74
ADO26644
ID ADO26644 standard; DNA; 18 BP.
XX
AC ADO26644;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:37.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26645.
XX
PT Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 37; 86pp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism or interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism or interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426

DB 1 CAGCAGCAGCAGCAGCAG 18

RESULT 75

ADO26638/c

ID ADO26638 standard; DNA; 18 BP.

XX AC ADO26638;

XX AC 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:31.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

XX P-PSDB; ADO26639.

XX Constructing synthetic polynucleotide for modulating the quality of a
 CC selected phenotype displayed by an organism comprises replacing a first
 CC codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 31; 86bp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism or interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism or interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX SQ Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428

DB 18 GCAGCAGCAGCAGCAGCA 1

RESULT 76

ADO26610

ID ADO26610 standard; DNA; 18 BP.

XX AC ADO26610;

XX AC 12-AUG-2004 (first entry)

XX DT 12-AUG-2004 (first entry)

XX XX

CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX
 SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427
 |||||
 Db 1 AGCAGCAGCAGCAGCAGC 18

RESULT 78
 ADO26614/c
 ID ADO26614 standard; DNA; 18 BP.

XX
 AC ADO26614;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic leader sequence encoding DNA SEQ ID NO:7.
 XX
 KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
 XX
 OS Synthetic.
 XX
 PN WO2004042059-A1.
 XX
 PD 21-MAY-2004.
 XX
 PF 10-NOV-2003; 2003WO-AU001487.
 XX
 PR 08-NOV-2002; 2002US-0425163P.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Frazer IH;
 XX
 DR WPI; 2004-411519/38.
 XX
 DR P-PSDB; ADO26615.
 XX
 PT Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.
 XX
 PS Example 1; SEQ ID NO 7; 86pp; English.

CC The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism of interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism of interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that

CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX
 SQ Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427
 |||||
 Db 18 AGCAGCAGCAGCAGCAGC 1

RESULT 79
 ADR06261
 ID ADR06261 standard; DNA; 18 BP.

XX
 AC ADR06261;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Short tandem (microsatellite) repeat #1.
 XX
 KW amplification data; DNA marker; biological sample identification;
 KW microorganism detection; virus detection; bacteria detection;
 KW fungi detection; protozoa detection; HIV-1;
 KW human T-cell lymphotropic virus type 1; HTLV-1; Hepatitis B virus; HBV;
 KW Hepatitis C virus; HCV; Herpes Simplex virus; paternity screening;
 KW genetic screening; prenatal diagnosis; presymptomatic diagnosis;
 KW disease carrier detection; forensic chemical analysis;
 KW short tandem repeat; microsatellite repeat; ds.
 XX
 OS Unidentified.

XX
 PN US2004157220-A1.
 XX
 PD 12-AUG-2004.
 XX
 PF 10-FEB-2003; 2003US-00360854.
 XX
 PR 10-FEB-2003; 2003US-00360854.
 XX
 PA (KURN/) KURNOOL P.
 PA (WUBB/) WU B.
 PA (BANK/) BANKS P.
 XX
 PI Kurnool P, Wu B, Banks P;
 XX
 DR WPI; 2004-614752/59.
 XX
 PT Identifying biological sample of mammal, involves obtaining amplification
 PT data indicative of amplification of DNA markers of genomic DNA of mammal,
 PT generating indicia indicative of amplification data, associating indicia
 PT with sample.
 XX

PS Example; Page 19; 39pp; English.

XX The invention describes a method of identifying (M1) a biological sample
CC comprising a biological material of a mammal. The method involves
CC obtaining amplification data indicative of amplification of at least two
CC DNA markers of genomic DNA of the mammal, generating indicia indicative
CC of the amplification data, and associating the indicia with the
CC biological sample, where the indicia is used to identify the biological
CC sample. (M1) is useful: in identifying biological sample of a subject
CC undergoing diagnosis to determine whether the subject is afflicted with a
CC particular disease or disorder; for identifying a biological sample of a
CC subject, undergoing screening for genetic lesions or mutations; for
CC identifying a biological sample of a subject, being diagnosed for the
CC presence of target microorganism chosen from virus, bacteria, fungi or
CC protozoa, where the virus includes HIV-1, human T-cell lymphotropic
CC virus type 1 (HTLV-1), Hepatitis B virus (HBV), Hepatitis C virus (HCV)
CC and Herpes Simplex, the bacteria includes Mycobacterium tuberculosis,
CC Rickettsia rickettsii, Ehrlichia chaffeensis, Borrelia burgdorferi and
CC Yersinia pestis, the fungi includes Cryptococcus neoformans, Pneumocystis
CC carinii and Histoplasma capsulatum, and the protozoa is chosen from
CC Trypanosoma cruzi, Leishmania sp., Plasmodium, Entamoeba histolytica,
CC Babesia microti, Giardia lamblia, Cyclospora sp. and Eimeria sp.; in
CC identifying a biological sample of a subject undergoing paternity
CC screening, genetic screening, prenatal diagnosis, presymptomatic
CC diagnosis, disease carrier detection or forensic chemical analysis; in
CC identifying a biological sample during the screening of the plant to
CC detect the presence of the target microorganism, or during carrier
CC detection analysis or forensic chemical analysis of a plant; and in
CC diagnostic medicines, for identification of genetically inherited
CC diseases in humans, family relationship analysis and microbial typing.
CC (M1) enables simultaneous analysis and tracking of biological samples.
CC The molecular barcode of the genomic DNA of the sample can be determined
CC at any time during the collection or processing of a biological sample.
CC This sequence represents an example of a short tandem or microsatellite
CC repeat that can be used in DNA fingerprinting to identify a biological
CC material.

SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1409 CAGCAGCAGCAGCAGCAG 1426

DB 1 CAGCAGCAGCAGCAGCAG 18

RESULT 80

AAV68372/c

ID AAV68372 standard; DNA; 20 BP.

XX AAV68372;

DT 10-MAR-1999 (first entry)

DE Adapter primer oligonucleotide #11 for CAG repeat analysis.

XX CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
KW nucleic acid analysis; variation assessment; neurological disease;
KW Huntington's chorea; PCR suppression; ss.

XX Synthetic.

XX WO9849345-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US008616.

XX 29-APR-1997; 97US-0045078P.

XX (UYBO-) UNIV BOSTON.

XX Smith CL;

XX WPI; 1998-594983/50.

XX Analysing nucleic acid samples - using amplification primers which
PT contain CAG or CTG tri-nucleotide repeats for differential display of
PT samples from different sources.

XX Example; Page 31; 44pp; English.

XX This sequence represents an adapter primer oligonucleotide. It was used
CC to isolate CAG repeat containing sequences from the human genome to test
CC the method of the invention. The method is for analysing nucleic acids in
CC a sample, and comprises: (a) providing a sample containing nucleic acid,
CC a first oligonucleotide primer comprising a CTG repeat, a second
CC oligonucleotide primer comprising a CAG repeat and a polymerase and PCR
CC reagents; (b) preparing said nucleic acid so that it is amplifiable; (c)
CC amplifying the nucleic acid with the first and second primers; and (d)
CC detecting the amplified product. The method is used to distinguish
CC between the expression of genes in two or more biological samples, e.g.
CC body fluids, cells, solid tissue or solid and liquid foods. It can be
CC used in medical diagnostics, e.g. to differentiate between normal and
CC diseased tissue or to assess the variation within monozygotic twin pairs.
CC The method allows the isolation and analysis of genome subsets containing
CC CAG repeats which are known to be important in a number of neurological
CC diseases including Huntington's chorea. The method uses PCR suppression,
CC in which only fragments which contain a target repeat are efficiently
CC amplified. This allows accurate identification of differentially
CC expressed genes in various cell types. Genome complexity is reduced by
CC the new method which targets genomic subsets containing CAG repeats

SQ Sequence 20 BP; 1 A; 6 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.5%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1409 CAGCAGCAGCAGCAGCAG 1426

DB 20 CAGCAGCAGCAGCAGCAG 3

RESULT 81

AAV68373/c

ID AAV68373 standard; DNA; 20 BP.

XX AAV68373;

DT 10-MAR-1999 (first entry)

DE Adapter primer oligonucleotide #12 for CAG repeat analysis.

XX CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
KW nucleic acid analysis; variation assessment; neurological disease;
KW Huntington's chorea; PCR suppression; ss.

XX Synthetic.

XX WO9849345-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US008616.

XX 29-APR-1997; 97US-0045078P.

XX (UYBO-) UNIV BOSTON.

XX Smith CL;

XX WPI; 1998-594983/50.

XX

Analysing nucleic acid samples - using amplification primers which contain CAG or CTG trinucleotide repeats for differential display of samples from different sources.

Example; Page 31; 44pp; English.

This sequence represents an adapter primer oligonucleotide. It was used to isolate CAG repeat containing sequences from the human genome to test the method of the invention. The method is for analysing nucleic acids in a sample, and comprises: (a) providing a sample containing nucleic acid, a first oligonucleotide primer comprising a CTG repeat, a second oligonucleotide primer comprising a CAG repeat and a polymerase and PCR reagents; (b) preparing said nucleic acid so that it is amplifiable; (c) amplifying the nucleic acid with the first and second primers; and (d) detecting the amplified product. The method is used to distinguish between the expression of genes in two or more biological samples, e.g. body fluids, cells, solid tissue or solid and liquid foods. It can be used in medical diagnostics, e.g. to differentiate between normal and diseased tissue or to assess the variation within monozygotic twin pairs. The method allows the isolation and analysis of genome subsets containing CAG repeats which are known to be important in a number of neurological diseases including Huntington's chorea. The method uses PCR suppression, in which only fragments which contain a target repeat are efficiently amplified. This allows accurate identification of differentially expressed genes in various cell types. Genome complexity is reduced by the new method which targets genomic subsets containing CAG repeats

Sequence 20 BP; 1 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match	0.5%	Score 18;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 96;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 82
ADC65856/C
ID ADC65856 standard; DNA: 20 BP.

XX ADC65856;

DT 18-DEC-2003 (first entry)

Mouse TGF-beta receptor II targeted antisense oligonucleotide #55.

XX mouse; antisense oligonucleotide; KW

KW hyperproliferative disorder; breast cancer; autoimmune disorder;
KW transforming growth factor beta receptor II; TGF-beta receptor II;
KW hypermatoid arthritis; 2'-O-methoxyethyl gapmer;
KW phosphorothioate backbone; ss; murine.

XX Mus musculus.

XX PN WO2003000656-A2.

XX PD 03-JAN-2003.

XX PF 19-JUN-2002:

XX
PR 21-JUN-2001: 2001US-00888361XX
PA (TSTS-) TSTS PHARM TNC

XX
PT Murray SF. Watt JR.

XX WPT: 2003-175279/17

XX New compound having a sequence targeted to a nucleic acid encoding
PT Transforming growth factor beta-receptor II, useful for preparing a
PT composition for treating hyperproliferative disorder e.g., lung, liver,

PT colon or gastric cancer.
XX
PS Claim 3; SEQ ID NO 152; 141pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acid encoding transforming growth factor beta (TGF-beta)
CC receptor II. The antisense oligonucleotides of the invention are useful
CC for treating: hyperproliferative disorders (e.g. breast cancer), or an
CC autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
CC represents a 2'-O-methoxyethyl gapped oligonucleotide with a
CC phosphorothioate backbone that is targeted to mouse TGF-beta receptor II.
XX
XX Sequence 20 BP; 1 A; 4 C; 6 G; 9 T; 0 U; 0 Other;

Query Match	0.5%	Score 18;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 96;		
Matches 18;	Conservative 0;	Mismatches	0;	Indels 0;
Gaps	0;			

Qy 1602 AGCAGCAGCAACAACCAT 1619
Db 20 AGCAGCAGCAACAACCAT 3

RESULT 83
ADD69519/c
ID ADD69519 standard: DNA: 20 BP.

XX AC ADD69519:

XX
DT 15-JAN-20XX
DE
TSSR-related PCR primer 6.

inter-simple sequence repeats

KW animal; Basmati rice; ss.
XX

OS Unidentified.
XX

PN WO2003085133-A2.
XX

PD 16-OCT-2003.
XX

PF 09-JAN-2003; 2003WO-1B00000
XXPR 08-APR-2002; 2002IN-CH00002
XX

PA (DNAF-) CENT DNA FINGERPRINTING
XX

PI Nagaraju JG;
XX

DR WPI; 2003-804317/75.
XX

PT New set of inter-simple
PT genotyping eukaryotes. use

PT animal systems.
XX

PS Disclosure; Page 19; 60pp;
XX

CC The invention relates to a
CC (ISSR)-PCR primers for gen

invention may be useful to animal systems, in particular

CC from non-Basmati rice vari
CC from evolved Basmati rice

CC
XX
ISSR-related PCR primer of

sequence 20 BP; 1 A; 6 C;

.Query Match	0.5%
Best Local Similarity	100.0%

Matches 18; Conservative

Q7 1410 AGCAGCAGCAGCAGCAG

```

Db      |||||
20 AGCAGCAGCAGCAGCAGC 3

RESULT 84
ABZ75647/c
ID ABZ75647 standard; DNA; 21 BP.
XX
AC ABZ75647;
XX
XX 15-MAY-2003 (first entry)
XX
DE Template (CTGA)6-A3 for second strand synthesis by HIV RT.
XX
KW DNA polymerization; drug susceptibility; HIV; reverse transcriptase; RT;
KW ds.
XX
OS Synthetic.
XX
XX WO2002103039-A1.
XX
PD 27-DEC-2002.
XX
XX 14-JUN-2002; 2002WO-SE001155.
XX
PR 14-JUN-2001; 2001US-0297773P.
XX
PA (CAVI-) CAVIDI TECH AB.
XX
PI Kaellander C, Pettersson I, Gronowitz S, Shao X;
XX
DR WPI; 2003-167535/16.
XX
PT Measuring DNA-dependent DNA polymerization in a biological sample, useful
PT for drug susceptibility testing, comprises measuring the amount of a
PT incorporated modified deoxynucleoside triphosphate with the aid of a
PT labeled antibody.
XX
PS Example 1; Page 33; 36pp; English.
XX
CC The invention relates to measuring DNA-dependent DNA polymerization in a
CC biological sample and involves measuring the amount of incorporated
CC modified deoxynucleoside triphosphate with the aid of the label of a
CC bound antibody. The method is useful in measuring DNA polymerization for
CC drug susceptibility testing. Sequences ABZ75637-647 represent different
CC templates used for second strand synthesis by HIV reverse transcriptase
CC (RT)
XX
SQ Sequence 21 BP; 3 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      0.5%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 85
ABK70327
ID ABK70327 standard; DNA; 21 BP.
XX
AC ABK70327;
XX
XX 15-JUL-2002 (first entry)
XX
DE Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #15.
XX
KW Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KW insulin-like growth factor binding protein-2; hormone-regulated tumour;
KW breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KW hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;

```

```

KW ODN; endocrine tumour therapy; ss.
XX Synthetic.
XX WO200222642-A1.
XX PD 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US028748.
XX
XX 14-SEP-2000; 2000US-0232641P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Satoshi K, Nelson C, Rennie PS;
XX WPI; 2002-339861/37.
XX
XX Composition for treating hormone-regulated cancer, particularly of
XX prostate or breast, comprises oligonucleotide antisense to insulin-like
XX growth factor binding protein-2.
XX
XX Claim 3; Page 12; 36pp; English.
XX
XX The present invention relates to a new composition for treating hormone-
XX regulated cancer. The composition comprises an antisense oligonucleotide
XX that inhibits expression of IGFBP-2 (insulin-like growth factor binding
XX protein-2). The molecules of the invention are used to delay progression
XX of hormone-regulated tumours, particularly of breast or prostate, to the
XX hormone-independent state, to delay metastatic progression to the bone of
XX IGF-1-sensitive cancers and to treat hormone-responsive cancers by
XX inducing apoptosis, after hormonal withdrawal. The present nucleic acid
XX sequence represents one of a collection (ABK70313-ABK70375) of antisense
XX IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
XX prostate and other endocrine tumour therapy
XX
SQ Sequence 21 BP; 6 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 1 CAGTAGCAGCAGCAGCAGCGG 21

RESULT 86
ABX94818
ID ABX94818 standard; DNA; 22 BP.
XX
AC ABX94818;
XX
XX 11-JUL-2003 (first entry)
XX
DE Human cysteine-rich FGF receptor (CFR) PCR primer CFR-For1.
XX
KW Human; antibody; murine antibody NM58-49/69; cysteine-rich FGF receptor;
KW glycoprotein receptor; proliferating cell; stomach carcinoma; vaccine.
KW CFR-1 protein; human antibody 103/51; immunoglobulin M; cytostatic; gut;
KW antibacterial; antiinflammatory; receptor antagonism; cancer; stomach;
KW cesophagus; rectum; liver; gall bladder; pancreas; lung; bronchus;
KW breast; cervix; prostate; heart; ovary; uterus; metaplasia of oesophagus;
KW Helicobacter pylori-associated gastritis; tubular adenoma; tumour marker;
KW villous adenoma; Barrett dysplasia; cervical intraepithelial neoplasia;
KW anticancer agent; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /+tag= a
XX /mod_base= OTHER

```

FT /note= "This nucleotide is depicted as o in the
specification"

FN WO2003011907-A2.

PN 13-FEB-2003.

PD 23-JUL-2002; 2002WO-DE002699.

PF 24-JUL-2001; 2001DE-01036009.

PP 09-MAR-2002; 2002DE-01010425.

PR (MUELLER) MUELLER-HERMELINK H K.

PA (VOLLMEYER) VOLLMEYER H.

PP (HENSEL) HENSEL F.

PI Mueller-Hermelink HK, Vollmers H, Henseel F;

PN WPI; 2003-256436/25.

PP New glycoprotein receptor on surface of cancer cells, useful for
treatment and diagnosis of cancer and for drug screening, also new
specific antibody.

PT Disclosure; Page 21; 49pp; German.

PP This invention describes a novel glycoprotein receptor, present on the
surface membrane of strongly proliferating cells, especially stomach
carcinoma, having at least one determinant that corresponds with a
determinant of CCR-1 protein and binding specifically to human antibody
103/51 and/or the murine antibody 58/47-69 (immunoglobulin M). The
products of the invention have cytostatic, antibacterial and
anti-inflammatory activity and can be used in a vaccine or for receptor
antagonism. The novel receptor is used for therapeutic in vivo generation
of antibodies, for treatment and prevention of cancer (of oesophagus,
stomach, gut, rectum, liver, gall bladder, pancreas, lung, bronchi,
breast, cervix, prostate, heart, ovary and/or uterus), for treating a
wide range of precancerous states (e.g. Helicobacter pylori-associated
gastritis, tubular or villous adenoma, Barrett dysplasia/metaplasia of
oesophagus, cervical intraepithelial neoplasia etc.), for diagnosis (as a
tumour marker) and for identifying potential anticancer agents from their
ability to bind selectively to the glycoprotein receptor. This sequence
represents a PCR primer used to amplify the human cysteine-rich FGF
receptor (CPR) described in the disclosure of the invention

PP Sequence 22 BP; 7 A; 7 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.5%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1426 GCAGCAGCAGCAGCAGCAGCA 1446
DB 2 GCAGCTTCAGCAGCAGCAGCA 22

RESULT 87

AAT39475

ID AAT39475 standard; DNA; 19 BP.

XX AC AAT39475;

DT 21-MAY-1997 (first entry)

XX DE Steroidogenesis acute regulatory protein sense PCR primer 1.

XX Human; steroidogenesis; acute regulatory protein; hStAR; analysis;
mutation; detection; prenatal; genetic defect; congenital; protein;
lipoid adrenal hyperplasia; treatment; prevention; gene;
replacement therapy; hypercholesterolaemia; primer; PCR;
polymerase chain reaction; ss.

OS Synthetic.

XX WO9629338-A1.

PN 26-SEP-1996.

PD 22-MAR-1996; 96WO-US003896.

PF 23-MAR-1995; 95US-00410540.

PP (REGC) UNIV CALIFORNIA.

PA (TYPE-) UNIV PENNSYLVANIA.

PI Miller WL, Lin D, Strauss JF;

PN WPI; 1996-443130/44.

PP Isolated human steroidogenesis acute regulatory protein gene - used for
detection of mutation(s) of this gene that cause congenital lipoid
adrenal hyperplasia.

PT Disclosure; Page 4; 89pp; English.

PP The present sequence is a PCR primer (nt 66-84) for the human
steroidogenesis acute regulatory protein (hStAR) cDNA. The hStAR gene can
be analysed for mutations to detect (e.g. prenatally) genetic defects
associated with congenital lipoid adrenal hyperplasia (CAH), or its
transmission to children. CAH can be treated by protein or gene
replacement therapy, which can also be used to prevent or treat
hypercholesterolaemia. A human adrenal cortex cDNA library was screened
with a mouse StAR probe to isolate a 1.6 Kb insert, including an ORF for
a 285 residue protein. When it was cloned into pSPORT and expressed in
COS-1 cells cotransfected with pP450scab P4DX, it increased the level
of pregnenolone synthesis from cholesterol or 20-alpha-hydroxycholesterol

PP Sequence 19 BP; 5 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
DB 1 GCAGCAGCAGCAGCAGCAG 19

RESULT 88

ADH70599/c

ID ADH70599 standard; DNA; 19 BP.

XX AC ADH70599;

DT 25-MAR-2004 (first entry)

XX DE Human Vbeta gene repeat sequence #389.

XX human; T-cell associated disease; Vbeta; autoimmune disease;
degenerative nervous system disease; graft versus host disease;
hypersensitivity disease; infectious disease; neoplastic disease;
Addison's disease; atrophic gastritis;
degenerative nervous system disease; multiple sclerosis;
Alzheimer's disease; hypersensitivity; Goodpasture's syndrome;
allergy; type II hypersensitivity; infectious disease; viral infection;
type IV hypersensitivity; leprosy; parasitic infection; schistosoma;
HIV; fungal infection; Candida; parasitic infection; schistosoma;
filaria; bacterial infection; Mycobacterium; neoplastic disease;
lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
breast cancer; ds.

OS Homo sapiens.

XX US2002150891-A1.

PN 17-OCT-2002.

XX The sequences given in AAH3115-21 are oligonucleotides which are
 CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
 CC may be used in combination with an inhibitor of histone deacetylase
 CC enzyme function, to give an improved inhibitory effect, thereby reducing
 CC the amount of inhibitor required to obtain a given inhibitory effect.
 CC Compounds containing these oligonucleotides may be used to treat cell
 CC proliferation conditions such as cancer, restenosis or psoriasis. They
 CC can also be used to treat protozoal and fungal infections
 XX
 SQ Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
 Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 93
 AAH56611/c
 ID AAH56611 standard; DNA; 20 BP.

XX
 AC AAH56611;

XX
 DT 06-SEP-2001 (first entry)

XX
 DE Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:259.

XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.

XX Streptococcus pyogenes.

OS
 XX WO200136625-A2.

PN
 XX 25-MAY-2001.

PD
 XX 20-NOV-2000; 2000WO-CA001347.

PF
 XX 18-NOV-1999; 99US-0166249P.

PR
 XX (GENE-) GENESENSE TECHNOLOGIES INC.

PA
 XX Wright JA, Young AH, Dugourd D;

XX
 PI WPI; 2001-355633/37.

XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
 PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.

XX
 PS Claim 3; Page 48; 110pp; English.

XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (i) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibiting expression of groES or groEL. (i) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (i) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the

CC microorganism or to a cell infected with the microorganism, (i). (i) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (i) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 XX

SQ Sequence 20 BP; 1 A; 4 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY ,1456 GCACAGCAACAGCAACAG 1474
 Db 19 GAAACAGCAACAGCAACAG 1

RESULT 94

AAAC89537/c

ID AAC89537 standard; DNA; 20 BP.

XX
 AC AAC89537;

XX
 DT 08-MAR-2001 (first entry)

DE Human HDAC-2 PCR primer SEQ ID NO: 7.

XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-P; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; PCR primer; ss.

XX Homo sapiens.

OS
 XX WO200071703-A2.

PN
 XX 30-NOV-2000.

PD
 XX 03-MAY-2000; 2000WO-IB001252.

PF
 XX 03-MAY-1999; 99US-0132287P.

PR
 XX (METH-) METHYLGENE INC.

PA
 XX Macleod AR, Li Z, Besterman JM;

XX
 PI WPI; 2001-016407/02.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX Disclosure; Page 12; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia

XX
 SQ Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
 |||||
 Db 20 GCAGCAGCAGCAGCAGG 2

RESULT 95
 AAC89546/c
 ID AAC89546 standard; DNA; 20 BP.
 XX AC
 XX AAC89546;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Human HDAC-2 antisense sequence SEQ ID NO: 16.
 XX
 XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200071703-A2.
 PN
 XX 30-NOV-2000.
 PD
 XX 03-MAY-2000; 2000WO-IB001252.
 PF
 XX 03-MAY-1999; 99US-0132287P.
 PR
 XX (METH-) METHYLGENE INC.
 PA
 XX Macleod AR, Li Z, Besterman JM;
 PI
 XX WPI; 2001-016407/02.
 DR
 XX
 XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
 XX
 XX Example 1; Page 24; 125pp; English.
 XX
 CC The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 20 BP; 0 A; 9 C; 5 G; 4 T; 2 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
 |||||
 Db 20 GCAGCAGCAGCAGCAGG 2

RESULT 96
 ABZ86068/c
 ID ABZ86068 standard; DNA; 20 BP.
 XX AC
 XX ABZ86068;
 XX
 DT 17-OCT-2003 (first entry)
 DT
 XX Human oligonucleotide sequence.
 DE
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 DN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 PF
 XX 23-APR-2002; 2002WO-US013135.
 PR
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 DR
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Claim 15; SEQ ID NO 1310; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
 |||||
 Db 20 CGCAGCAGCAGCAGCAGC 2

RESULT 97
 ABZ85596/c
 ID ABZ85596 standard; DNA; 20 BP.
 XX AC
 XX ABZ85596;
 XX
 DT 17-OCT-2003 (first entry)
 DT
 XX Human oligonucleotide sequence.
 DE
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPITG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 838; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antinflammatory steroid and ubiquinone. A composition of the invention
 CC has antinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1533 CCCACAGCAGCAGCAGCA 1551
 DB 19 CCCACAGCAGCAGCAGCA 1
 RESULT 98
 ABZ86071/c
 ID ABZ86071 standard; DNA; 20 BP.
 XX AC ABZ86071;
 XX 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antinflammatory steroid; ubiquinone; antinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPITG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 1313; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antinflammatory steroid and ubiquinone. A composition of the invention
 CC has antinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGC 1427
 DB 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 99
 ABZ86075/c
 ID ABZ86075 standard; DNA; 20 BP.
 XX AC ABZ86075;
 XX 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antinflammatory steroid; ubiquinone; antinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Claim 15; SEQ ID NO 1317; 872pp; English.
 XX
 CC The invention relates to a novel pharmacological composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
 Db 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 100
 ABD22298/c
 ID ABD22298 standard; DNA; 20 BP.
 XX
 AC ABD22298;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human stanniocalcin-derived oligo SEQ ID 1310.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-093058/08.
 XX
 PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 1310; 763pp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
 Db 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 101
 ABD22301/c

ID ABD22301 standard; DNA; 20 BP.
XX ABD22301;
AC
XX 29-JUL-2004 (first entry)
DT
DE Human stannocalcin-derived oligo SEQ ID 1313.
XX
XX Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI; 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antiseize
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1313; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC of availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 20 CAGCAGCAGCAGCAGCAGC 2
RESULT 102
ID ABD22305/c
AC ABD22305 standard; DNA; 20 BP.
XX
XX ABD22305;
XX
XX 29-JUL-2004 (first entry)
DT
XX Human stannocalcin-derived oligo SEQ ID 1317.
XX
XX Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI; 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antiseize
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1317; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC of availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427

Db 20 CAGCAGCAGCAGCAGCAGC 2

RESULT 103

ABD21826/C

ID ABD21826 standard; DNA; 20 BP.

XX ABD21826;

DT 29-JUL-2004 (first entry)

XX Human stannocalcin-derived oligo SEQ ID 838.

DE Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

PN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI WPI; 2003-093058/08.

DR Pharmaceutical composition for treating asthma, has antisense

XX oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 838; 763bp; English.

PS This invention describes a novel composition (a) a first active agent,

XX comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1533 CCCAAGCAGCAGCAGCAGCA 1551

Db 19 CCCAAGCAGCAGCAGCAGCA 1

RESULT 104

ADP20520

ID ADP20520 standard; DNA; 20 BP.

XX ADP20520;

DT 26-AUG-2004 (first entry)

XX Transcription factor AP-2 antisense oligonucleotide seqid 67.

XX Cytostatic; AP-2-Inhibitor-Alpha; AP-2 alpha; AP-2 alpha modulator;

XX AP-2 alpha associated disorder; hyperproliferative disorder; human;

XX transcription factor; antisense oligonucleotide; antisense technology;

XX ss.

XX Homo sapiens.

XX US2004109848-A1.

XX 10-JUN-2004.

XX 09-DEC-2002; 2002US-00315962.

XX 09-DEC-2002; 2002US-00315962.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean NM, Freier SM, Dobie KW;

XX WPI; 2004-440306/41.

XX New compounds targeted to nucleic acid molecules encoding AP-2 alpha and

PT inhibits the expression of AP-2 alpha, useful for treating AP-2 alpha-

PT associated disease or condition, particularly a hyperproliferative

PT disorder.

XX Example 15; SEQ ID NO 67; 58pp; English.

XX The invention describes a compound (I) 8-80 nucleobases in length

CC

CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
CC (19868 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
CC comprising contacting the cells or tissues with (i); screening for a
CC modulator of AP-2 alpha by contacting a preferred target segment of a
CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
CC alpha expression, which modulate the expression of AP-2 alpha; a
CC diagnostic method for identifying a disease state; and a kit or assay
CC device comprising (i). The compound is useful for treating an animal
CC having a disease or condition associated with AP-2 alpha, particularly a
CC hyperproliferative disorder. The compounds may be used for diagnostics,
CC therapeutics prophylaxis and as research reagents; or as tools in
CC differential and/or combinatorial analyses to elucidate expression
CC patterns of a portion or the entire complement of genes expressed within
CC cells and tissues. This sequence represents a human transcription factor
CC AP-2 antisense oligonucleotide.

XX
SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCGCAGCAGCAGCAGCAG 19

RESULT 105
AAA37188/c

ID AAA37188 standard; DNA; 21 BP.

XX AC AAA37188;

XX DT 08-AUG-2000 (first entry)

XX DE Human PRO1315 forward PCR primer SEQ ID NO:105.

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
KW PCR primer; hybridisation; probe; ss.

XX OS Homo sapiens.

XX PN WO200012708-A2.

XX PD 09-MAR-2000.

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0098936P.

PR 09-SEP-1998; 98US-0098959P.

PR 09-SEP-1998; 98US-0098988P.

PR 09-SEP-1998; 98US-00989602P.

PR 10-SEP-1998; 98US-00989642P.

PR 10-SEP-1998; 98US-00989741P.

PR 10-SEP-1998; 98US-00989754P.

PR 10-SEP-1998; 98US-00989763P.

PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106082P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.


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PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2000-237871/20.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Example 34; Page 402; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGGAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 106
AAC73260
ID AAC73260 standard; DNA; 21 BP.
XX
XX AAC73260;
XX
XX 02-FEB-2001 (first entry)
XX
XX SNP flanking sequence #48 used in multiplexing PCR/SBE assay.
XX
XX Oligonucleotide array; genotyping; single base extension reaction; SBE;
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KW polymorphic locus; single nucleotide polymorphism; ss.
XX Unidentified.
XX WO2000058516-A2.
XX
XX 05-OCT-2000.
XX
XX 27-MAR-2000; 2000WO-US008069.
XX
XX 26-MAR-1999; 99US-0126473P.
XX 23-JUN-1999; 99US-0140359P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (AFFY-) AFFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
XX Example 7; Page 52; 70pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one such polymorphic locus
CC used in the present invention. The amplified nucleic acid product is then
CC used as a template in a SBE reaction with an extension primer. The SBE
CC reaction products are used to form the oligonucleotide array. Note: This
CC sequence includes a SNP represented by the degenerate codon in the
XX sequence
XX
SQ Sequence 21 BP; 8 A; 5 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1404 AGCAACAGCAGCAGCAGCAGC 1424
Db 1 AGGACAGCAGCAGCAGCAGC 21

RESULT 107
AAF54275/c
ID AAF54275 standard; DNA; 21 BP.
XX
XX AAF54275;
XX
XX 02-APR-2001 (first entry)
XX
XX Primer #26 used in the identification of proteins.
XX
XX Secreted; transmembrane; gene therapy; ss.
XX Unidentified.
XX WO2000078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
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PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162508P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski EJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Example 34; Page 416; 787bp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
XX Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGCAGCAACAGCAGCAGC 2
RESULT 108
ACD68312/C
ID ACD68312 standard; DNA; 21 BP.
XX
XX ACD68312;
AC
AC 17-SEP-2003 (first entry)
DT
DE
DE Novel human secreted and transmembrane protein related primer #23.
XX
XX Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW cartilage disorder; sports injury; arthritis; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003073130-A1.
FN
XX
XX 17-APR-2003.
PD
XX
XX 11-DEC-2001; 2001US-00015869.
PF
XX
XX 01-SEP-1998; 98US-0098716P.
PR

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PR 20-OCT-1998; 98US-0104987P.
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PR 28-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106454P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
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PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
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PR 18-NOV-1998; 98US-0108904P.
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PR 16-APR-1999; 99US-0129674P.
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PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
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PR 15-SEP-1999; 99WO-US021194.
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PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 24-FEB-2000; 2000WO-US004342.
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PR 15-MAR-2000; 2000WO-US005841.
PR 17-MAR-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US008666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-585293/55.
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-
PT insulinemia.
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGCAGCAACAGCAGCAGC 2
|||||
|||||

RESULT 109
ACH04114/c
ID ACH04414 standard; DNA; 21 BP.
XX
AC ACH04414;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; vulnary;
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis; primer.
XX
OS Homo sapiens.
XX
PN US2003044841-A1.
XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
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PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
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PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
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PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
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PR 16-APR-1999; 99US-0129674P.
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PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-492259/46.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating various cardiac insufficiency
XX disorders, bone and/or cartilage disorders such as sports injuries and
XX arthritis.
XX
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XX Best Local Similarity 94.78; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX Db 20 CAGGAGCAACAGCAGCAGC 2
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XX RESULT 110
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XX AC ACD67958;
XX
XX DT 17-SEP-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein related primer #23.
XX
XX KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
XX tissue typing; chromosome identification; vaccine; PCR; primer; sb.
XX
XX OS Homo sapiens.
XX
XX PN US2003073129-A1.
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XX PD 17-APR-2003.
XX
XX PF 04-SEP-2001; 2001US-00946374.
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PA (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Deasnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams RM, Wood WI;
XX
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DR WPI; 2003-585292/55.

XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Example 34; Page 235; 561pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I), having at least 80% sequence identity to a sequence
CC selected from any one of the 123 amino acid sequences given in

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGCAGCAACAGCAGCAGC 2

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XX ADC17974;
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XX 18-DEC-2003 (first entry)
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XX Human PRO PCR primer #26.
DE
XX Human; PRO; PCR; ss; protein electrophoresis; chromosome mapping;
KW gene mapping; genetic disorder; primer.
XX Homo sapiens.
OS
XX US2003064925-A1.
PN
XX 03-APR-2003.
PD
XX 10-DEC-2001; 2001US-00013907.
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PR 17-SEP-1998; 98US-0100710P.

CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic
CC agents. The polynucleotides are useful as hybridisation probes for a cDNA

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
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Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 112

ADD70620/C

ID ADD70620 standard; DNA; 21 BP.

XX AC ADD70620;

XX DT 15-JAN-2004 (first entry)

XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.

XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.

XX OS Homo sapiens.

XX PN US2003099625-A1.

XX PD 29-MAY-2003.

XX PF 12-DEC-2001; 2001US-00015386.

XX PR 01-SEP-1998; 98US-0098716P.

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PR 03-NOV-1998; 98US-0108822P.
PR 03-NOV-1998; 98US-0108823P.
PR 03-NOV-1998; 98US-0

PT hypo-insulinemia, sports injuries and arthritis.
XX Example 34; SEQ ID NO 105; 557pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimaeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
CC the invention.
XX
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Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 20 CAGGAGCAACGACGACGAC 2
RESULT 114
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ID ADD70143 standard; DNA; 21 BP.
XX
XX ADD70143;
AC
DT 15-JAN-2004 (first entry)
XX
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
DE
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia; ss.
OS
XX Homo sapiens.
XX
XX US2003054406-A1.
PN
XX
XX 20-MAR-2003.
PD
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XX 06-DEC-2001; 2001US-00006818.
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PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams FM, Wood WI;
XX WPI; 2003-708344/67.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
XX Example 34; SEQ ID NO 105; 549pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCACAGCAGCAGC 1418
Db 20 CAGGAGCACAGCAGCAGC 2

RESULT 115
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ID ADD38264 standard; DNA; 21 BP.
XX
AC ADD38264;
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DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassemia; ss.
XX
OS Homo sapiens.
XX
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PD 22-MAY-2003.
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XX 07-DEC-2001; 2001US-00012755.
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PR 01-SEP-1999; 99WO-US020111.
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PR 22-MAY-2000; 2000WO-US013705.
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PR 02-JUN-2000; 2000WO-US015264.
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PR 01-JUN-2001; 2001WO-US017800.

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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
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XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WFI; 2003-787000/74.
XX
XX Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.
XX
XX Example 34; SEQ ID NO 105; 556pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX AC ADD39220;
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XX DT 15-JAN-2004 (first entry)
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XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
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XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
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XX OS Homo sapiens.
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XX PN US2003096954-A1.
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XX PD 22-MAY-2003.
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PR 29-JUN-2001; 2001WO-US021066.
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PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PI Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Fan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-765477/72.
DR

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XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
PT PRO1244, PRO1246, useful for treating cancerous tumors, cardiac  
PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.  
XX  
PS Example 34; SEQ ID NO 105; 555pp; English.  
CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity  
Query Match 0.5%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 20 CAGGAGCAACAGCAGCAGC 2  
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AC ADD40174;  
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DT 15-JAN-2004 (first entry)  
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.  
XX  
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.  
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XX US2003082627-A1.  
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XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755104/71.
XX
XX New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT insufficiency disorders.
XX
XX Example 34; SEQ ID NO 105; 550pp; English.
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CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX Homo sapiens.
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PI Williams PM, Wood WI;
XX
XX WPI; 2003-708395/67.
XX
XX
PT Novel secreted and transmembrane PRO polypeptides useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide and as therapeutic agents e.g. vaccines.
XX
XX
PS Example 34; SEQ ID NO 105; 555pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
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XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Deanovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PW, Wood WI;
XX
DR WPI; 2003-765493/72.
XX
XX New isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis and tumors.
XX
XX Example 34; SEQ ID NO 105; 555pp; English.
PS
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
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Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. NO. 1.4e+02;
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KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX
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XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-765413/72.
DR
XX
PT Novel isolated PRO polypeptides useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis and tumors.
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX Homo sapiens.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755105/71.
XX
XX Novel secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX
XX Example 34; SEQ ID NO 105; 548bp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 20 CAGGAGCAACAGCAGCAGC 2
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ID ADF29901 standard; DNA; 21 BP.
XX
XX ADF29901;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
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XX OS Homo sapiens.
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KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
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PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.

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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Deanoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2004-021098/02.
DR
XX
XX New secreted and transmembrane PRO nucleic acid, for use in molecular
PT biology, chromosome and gene mapping, in generating antisense RNA and
PT DNA, in various diagnostic assays and in gene therapy.
XX
XX Example 34; SEQ ID NO 105; 552pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
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ID ADF25789 standard; DNA; 21 BP.
XX
AC ADF25789;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX
OS Homo sapiens.
XX
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XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2004-041394/04.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
XX biological activity of cell, as molecular weight markers in protein
XX electrophoresis, for treating arthritis, tumor.
XX
XX Example 34; SEQ ID NO 105; 552pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
XX
XX Query Match 0.5%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX ADF24688;
DT 12-FEB-2004 (first entry)
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XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
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XX Humane; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX
XX Homo sapiens.
XX
XX US2003198993-A1.
XX
XX 23-OCT-2003.
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XX 06-DEC-2001; 2001US-00007236.
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XX 01-SEP-1998; 98US-0098716P.
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XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
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PR	14-OCT-1998;	98US-0104257P.	PR	08-NOV-2000;	98US-0162506P.

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PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019892.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2004-041347/04.
XX
XX PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
XX PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
XX cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Example 34; SEQ ID NO 105; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
CC
CC
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 20 CAGCAGCAACAGCAGCAGC 2
RESULT 129
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ID ADF29424 standard; DNA; 21 BP.
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XX 12-FEB-2004 (first entry)
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XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX
XX Homo sapiens.
XX
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XX 30-OCT-2003.
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PR (GETH ) GENENTECH INC.
PR Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PR Cao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PR Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PR Williams PM, Wood WJ;
PR WPI; 2004-041478/04.
PR
PR New isolated PRO polypeptide useful for tissue typing, modulating the
PR biological activity of a cell, as molecular weight markers in protein
PR electrophoresis, and for treating e.g. arthritis, or tumor.
PR
PR Example 34; SEQ ID NO 105; 551bp; English.
PR
PR the invention relates to an isolated PRO polypeptide (secreted or
PR transmembrane protein) having at least 80% amino acid sequence identity
PR
PR Query Match 0.5%; Score 17.4; DB 1; Length 21;
PR Best Local Similarity 94.7%; Pred. No. 1.4e+02;
PR Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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PR DB 20 CAGGAGCACAGCAGCAGC 2
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PR DT
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PR XX
PR KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
PR immune response; cardiac insufficiency disorder; calcium flux;
PR umbilical vein endothelial cell; bone disorder; cartilage disorder;
PR arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
PR Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
PR dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
PR XX Homo sapiens.
PR OS
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PR PR 10-SEP-1998; 98US-0099808P.
PR PR 10-SEP-1998; 98US-0099812P.
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PR 30-SEP-1998; 98US-0102571P.
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PR 07-OCT-1998; 98US-0103328P.
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PR 07-OCT-1998; 98US-0103401P.
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PR 08-OCT-1998; 98US-0103711P.
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PR 20-OCT-1998; 98US-0105000P.
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PR 22-OCT-1998; 98US-0105266P.
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PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
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PR 27-OCT-1998; 98US-0106082P.
PR 28-OCT-1998; 98US-0106083P.
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PR 30-OCT-1998; 98US-0106464P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
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PR 18-NOV-1998; 98US-0108848P.
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PR 18-NOV-1998; 98US-0108951P.
PR 18-NOV-1998; 98US-0108952P.
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PR 18-NOV-1998; 98US-0108904P.
PR 30-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0114223P.
PR 05-JAN-1999; 98US-0129674P.
PR 15-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 23-JUN-1999; 98US-0141037P.
PR 26-JUL-1999; 98US-0145698P.
PR 01-SEP-1999; 98US-0145698P.
PR 15-SEP-1999; 98US-0145698P.
PR 30-SEP-1999; 98US-0145698P.
PR 02-DEC-1999; 98US-0145698P.
PR 16-DEC-1999; 98US-0145698P.
PR 05-JAN-2000; 98US-0145698P.
PR 06-JAN-2000; 98US-0145698P.
PR 11-FEB-2000; 98US-0145698P.
PR 18-FEB-2000; 98US-0145698P.
PR 24-FEB-2000; 98US-0145698P.
PR 02-MAR-2000; 98US-0145698P.
PR 15-MAR-2000; 98US-0145698P.
PR 17-MAR-2000; 98US-0145698P.
PR 23-MAY-2000; 98US-0145698P.
PR 30-MAY-2000; 98US-0145698P.
PR 02-JUN-2000; 98US-0145698P.
PR 23-AUG-2000; 98US-0145698P.
PR 24-AUG-2000; 98US-0145698P.
PR 08-NOV-2000; 98US-0145698P.
PR 10-NOV-2000; 98US-0145698P.
PR 01-DEC-2000; 98US-0145698P.
PR 28-FEB-2001; 98US-0145698P.
PR 01-MAR-2001; 98US-0145698P.
PR 20-JUN-2001; 98US-0145698P.
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PR 04-JUL-2001; 98US-0145698P.
PR 04-SEP-2001; 98US-0145698P.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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XX WPI; 2004-041280/04.
DR
XX New isolated PRO polypeptides useful for treating diseases such as cancer
PT and diabetes.
PT
XX Example 34, SEQ ID NO 105; 551pp; English.
XX
PS The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1400 CAGGAGCAACGACGACG 1418
Db 20 CAGGAGCAACGACGACG 2
RESULT 131
ADH02993/c
ID ADH02993 standard; DNA; 21 BP.
XX
XX AC ADH02993;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX
XX OS Homo sapiens.
XX
XX US2003216562-A1.
XX
XX PD 20-NOV-2003.
XX
XX PF 12-DEC-2001; 2001US-00015390.
XX
XX PR 01-SEP-1998; 98US-0098716P.
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PR 17-SEP-1998; 98US-0100684P.
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PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
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PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
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PR 26-OCT-1998; 98US-0105694P.
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PR 03-NOV-1998; 98US-0106856P.
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PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
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PR 18-NOV-1998; 98US-0108904P.
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PR 06-JAN-2000; 2000WO-US000376.
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PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2004-021867/02.
XX Novel isolated PRO polypeptide useful for treating tumor, kidney
XX disorders, diabetes mellitus, thalassemias.
XX Example 34; SEQ ID NO 105; 552pp; English.
PS

XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1400 CAGCAGCAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2
RESULT 132
ADH03947/c
ID ADH03947 standard; DNA; 21 BP.
XX AC ADH03947;
XX DT 11-MAR-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX OS Homo sapiens.
XX US2003220471-A1.
XX 27-NOV-2003.
XX 06-DEC-2001; 2001US-00006746.
XX 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2004-010888/01.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX Example 34; SEQ ID NO 105; 554pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. Pro is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are

CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
 CC the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1400 CAGGAGCAACAGCAGCAGC 1418
 Db 20 CAGGAGCAACAGCAGCAGC 2
 RESULT 133
 ADH03470/c
 ID ADH03470 standard; DNA; 21 BP.
 XX
 AC ADH03470;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
 XX
 KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2003224478-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 21-AUG-2002; 2002US-00226254.
 XX
 PR 29-OCT-1999; 99US-0162506P.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2004-022072/02.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules, useful in gene therapy, or preparing a medicament for treating
 PT a condition that is responsive to the PRO polypeptide or anti-PRO
 PT antibody, e.g. cancer.
 XX
 PS Example 34; SEQ ID NO 105; 557pp; English.
 XX

CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
 CC host cell comprising the vector, producing PRO, a chimaeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. PRO is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
 CC the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1400 CAGGAGCAACAGCAGCAGC 1418
 Db 20 CAGGAGCAACAGCAGCAGC 2
 RESULT 134
 ADH04424/c
 ID ADH04424 standard; DNA; 21 BP.
 XX
 AC ADH04424;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
 XX
 KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2004005626-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 07-DEC-2001; 2001US-00011795.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 28-SEP-1998; 98US-0102167P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
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PR 26-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105293P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 28-OCT-1998; 98US-0106022P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 28-OCT-1998; 98US-0106248P.
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PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 18-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
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PR 30-DEC-1998; 98US-0114223P.
PR 03-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
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PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 10-NOV-1998; 98US-0106934P.
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PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
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PR 17-NOV-1998; 98US-0108802P.
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PR 18-NOV-1998; 98US-0108852P.
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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US02111.
PR 15-SEP-1999; 99WO-US02119.
PR 23-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
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PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 24-AUG-2000; 2000WO-US023328.
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PR 04-SEP-2001; 2001US-00946374.

XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2004-108212/11.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
XX Example 34; SEQ ID NO 105; 562pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 136
ADJ94624/c
ID ADL94624 standard; DNA; 21 BP.
XX
XX AC ADL94624;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX Homo sapiens.
XX
XX US2004073015-A1.
XX
XX 15-APR-2004.
XX
XX 12-DEC-2001; 2001US-00015395.
XX
XX 23-SEP-1998; 98US-0101477P.
XX 20-JUL-1999; 99US-0144758P.
XX 01-SEP-1999; 99WO-US020111.
XX 18-OCT-1999; 99US-00403297.
XX 18-FEB-2000; 2000WO-US004342.
XX 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2004-315422/29.
XX
XX New PRO polynucleotides and polypeptides, useful in promoting wound
PT healing and in diagnosing and treating cancer, neurodegenerative
PT diseases, stroke, hypertension or diabetes mellitus.
```

XX Example 34; SEQ ID NO 105; 550pp; English.

PS The invention relates to an isolated PRO polypeptide (secreted or

CC transmembrane protein) having at least 80% amino acid sequence identity

CC to an amino acid sequence chosen from 123 fully defined sequences as

CC given in the specification (including their extracellular domains either

CC or without their associated signal peptides. Also include are the

CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a

CC host cell comprising the vector, producing PRO, a chimeric molecule

CC comprising PRO fused to a heterologous amino acid sequence, and an anti-

CC PRO antibody. PRO is useful as molecular weight markers for protein

CC electrophoresis and also for chromosome identification. PRO is also

CC useful for tissue typing. PRO and PRO NA are useful as hybridisation

CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is

CC useful for generating transgenic animals or knock-out animals which are

CC useful in development and screening useful reagents. PRO NA is also

CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are

CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410

CC polypeptides are useful for suppressing immune response. PRO1246

CC polypeptide is useful for treating cardiac insufficiency disorders.

CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and

CC PRO1561 polypeptide are useful for stimulating calcium flux in human

CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474

CC polypeptides are useful for treating bone and/or cartilage disorders

CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418

CC polypeptides are useful for treating diabetes in skeletal muscle cells

CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for

CC treating Berger disease or other nephropathies associated with Schonlein-

CC Henoch purpura, coeliac disease, dermatitis, herpiformis or Crohn's

CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1306, PRO1418,

CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present

CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of

CC the invention.

XX

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAGCAACGACGAGC 1418

DB 20 CAGGAGCAACGACGAGC 2

RESULT 137

ADO61397/c

ID ADO61397 standard; DNA; 21 BP.

AC ADO61397;

XX 26-AUG-2004 (first entry)

DE Human ATP1A2 DNA PCR primer #1.

XX Human; Na/K pump alpha 2 subunit; Na/K human pump; ATPase; ATP1A2;

KW chromosome 1; migraine disorder; migraine;

KW alternating hemiplegia of childhood; hemiplegia; PCR; primer; ss;

KW antimigraine.

XX Homo sapiens.

OS WO2004046377-A2.

PN 03-JUN-2004.

PD 12-NOV-2003; 2003WO-EF012635.

PF 15-NOV-2002; 2002IT-RM000576.

PR (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.

PA

XX

PI Casari G, De Fusco M, Marconi R;

XX WPI; 2004-420637/39.

XX New alpha 2 subunit of the Na/K pump, useful in diagnosing and treating

PT pathologies associated with migraine or with alternating hemiplegia of

PT childhood.

XX Claim 6; SEQ ID NO 1; 39pp; English.

PS The invention relates to a nucleic acid comprising at least one segment

CC of the gene encoding a functional portion of the gene-regulating region

CC of the alpha 2 subunit of the Na/K pump (ATPase, ATP1A2), for use in the

CC diagnosis of or in genetic therapy of pathologies associated with

CC migraine or with alternating hemiplegia of childhood. The invention also

CC relates to a method for detecting in an individual at least one mutation

CC in the gene encoding the alpha 2 subunit of the Na/K human pump (ATPase,

CC ATP1A2) located on chromosome 1, associated with migraine disorders, at

CC least one pair of oligonucleotides for the exponential amplification

CC reaction of at least one segment of the gene encoding the alpha 2 subunit

CC of the Na/K human pump (ATPase, ATP1A2), in which the segment encodes a

CC functional portion or a gene-regulating portion of the subunit and a

CC method for identifying an agonist or antagonist agent of the Na/K human

CC pump (ATPase, ATP1A2) or its functional portion or a gene-regulating

CC portion of the subunit. The nucleic acids, proteins and methods are

CC useful in diagnosing and treating pathologies associated with migraine or

CC with alternating hemiplegia of childhood. This sequence represents a PCR

CC primer used to amplify human ATP1A2 DNA of the invention.

XX

SQ Sequence 21 BP; 0 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2296 ACAGAGAAACCCAAAGCAA 2314

DB 21 ACAGAGAAAGCCAAAGCAA 3

RESULT 138

ADC37823

ID ADC37823 standard; DNA; 17 BP.

XX ADC37823;

AC ADC37823;

XX 18-DEC-2003 (first entry)

DT Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:172.

DE human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;

KW AMLP1a; ss.

XX Synthetic.

OS Homo sapiens.

XX WO2003037931-A2.

PN 08-MAY-2003.

PD 01-NOV-2002; 2002WO-US035129.

PF 01-NOV-2001; 2001US-0334773P.

PR (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX Shannon M, Phan T;

PI WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiotensin-like

PT protein, useful for treating or preventing a disorder associated with

PT decreased or increased expression or activity of AMLP1.

PT

XX Example 2; SEQ ID NO 172; 172bp; English.
PS The present invention describes the human angiomin-like protein 1
CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLPI. The present sequence represents a scanning
CC oligonucleotide for human AMLPI, which is used in an example from the
CC present invention.
XX Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1401 AGCAGCAACAGCAGCAG 1417
Db 1 AGCAGCAACAGCAGCAG 17
|||||

RESULT 139
ADC37821
ID ADC37821 standard; DNA; 17 BP.
AC ADC37821;
XX 18-DEC-2003 (first entry)
XX Human AMLPIa scanning 17-mer oligonucleotide SEQ ID NO:170.
XX human; angiomin-like protein 1; AMLPI; cytostatic; gene therapy;
KW AMLPIa; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX 08-MAY-2003.
XX 01-NOV-2002; 2002WO-US035129.
XX 01-NOV-2001; 2001US-0334773P.
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiomin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLPI.
XX Example 2; SEQ ID NO 170; 172bp; English.
XX The present invention describes the human angiomin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX oligonucleotide for human AMLPI, which is used in an example from the
XX present invention.
XX Sequence 17 BP; 6 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1432 GCAGCAGCAACAGCAGC 1448
Db 1 GCAGCAGCAACAGCAGC 17
|||||

RESULT 140
ADC37818
ID ADC37818 standard; DNA; 17 BP.
XX ADC37818;
AC ADC37818;
XX 18-DEC-2003 (first entry)
XX Human AMLPIa scanning 17-mer oligonucleotide SEQ ID NO:167.
XX human; angiomin-like protein 1; AMLPI; cytostatic; gene therapy;
KW AMLPIa; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX 08-MAY-2003.
XX 01-NOV-2002; 2002WO-US035129.
XX 01-NOV-2001; 2001US-0334773P.
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiomin-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLPI.
XX Example 2; SEQ ID NO 167; 172bp; English.
XX The present invention describes the human angiomin-like protein 1
XX (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
XX therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMLPI. The present sequence represents a scanning
XX oligonucleotide for human AMLPI, which is used in an example from the
XX present invention.
XX Sequence 17 BP; 6 A; 6 C; 5 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAACAGCAGC 1445
Db 1 GCAGCAGCAACAGCAGC 17
|||||

RESULT 141
ADC37819
ID ADC37819 standard; DNA; 17 BP.
XX ADC37819;
AC ADC37819;
XX 18-DEC-2003 (first entry)
XX Human AMLPIa scanning 17-mer oligonucleotide SEQ ID NO:168.
XX human; angiomin-like protein 1; AMLPI; cytostatic; gene therapy;
KW

SQ Sequence 17 BP; 7 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCA 1416
 Db 1 CAGCAGCAACAGCAGCA 17

RESULT 144
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 DT 14-SEP-1998 (first entry)
 XX
 DE Protein kinase catalytic subunit PCR primer 265.
 XX
 KW Severe combined immunodeficiency disease; SCID; horse; diagnosis;
 KW DNA-dependent protein kinase; PCR; primer; ds.
 XX
 KW Synthetic.
 OS Equus caballus.
 OS
 XX WO9821367-A1.
 XX
 XX 22-MAY-1998.
 PD
 XX 14-NOV-1997; 97WO-US021066.
 XX
 XX 15-NOV-1996; 96US-0031261P.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Meeks K;
 PI
 XX WPI; 1998-297967/26.
 DR
 XX DNA-dependent protein kinase catalytic subunit - useful for determining
 PT equine severe combined immunodeficiency alleles.
 XX
 XX Example 3; Page 19; 98pp; English.
 PS
 XX Primer 265 was used in an RT-PCR strategy to clone and sequence equine
 CC DNA-dependent protein kinase catalytic subunit transcripts. Primer 265,
 CC and other primers used in the RT-PCR (see also AAV30171-93), are based on
 CC a published human DNA-dependent protein kinase catalytic subunit
 CC sequence. cDNA template was derived from 2 fibroblast cell lines, 0176
 CC (from a normal, non-Arabian horse) and 1821 (from a SCID foal). Sequence
 CC analysis showed that in SCID horses, a 5 bp deletion is present
 CC corresponding to nucleotide 9454 of the 12,381 nucleotide coding sequence
 CC of the human transcript. This results in premature termination of the
 CC catalytic subunit at amino acid 3160 (see AAW56642) of the polypeptide.
 CC Primers 405 and 392 (see AAV30192-93) can be used to screen for mutant
 CC SCID allele. Methods are provided for identifying carriers of the
 CC mutation and for differentiating SCID homozygotes, heterozygotes and
 CC normal horses
 XX

SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 GGGAGATCTCTCTGCA 271
 Db 1 GGGAGATCTCTCTGCA 17

RESULT 145
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Complementary oligo of sequence containing a mixture of CAG/CAA codons.
 XX

AAH19623
 ID AAH19623 standard; DNA; 18 BP.
 XX
 AC AAH19623;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Oligonucleotide containing a mixture of CAG/CAA codons.
 XX
 KW Polyglutamine region; polypeptide aggregation; aggregation disruption;
 KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
 KW spinocerebellar ataxia; multiple myeloma; amyloidosis; anticonvulsant;
 KW spongiform encephalopathy; neuroprotective; neurotropic; antiparkinsonian;
 XX ss.
 XX
 XX Synthetic.
 OS
 XX WO200123412-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 27-SEP-2000; 2000WO-US041008.
 PF
 XX 27-SEP-1999; 99US-00405048.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 XX Housman DE, Preisinger EA, Kazantsev AG;
 PI
 XX WPI; 2001-300097/31.
 DR
 XX Screening for agents which disrupt aggregation of polypeptides for
 PT treating aggregation-associated disorders e.g. Alzheimer's disease, by
 PT using aggregation-disposed polypeptides or cell expressing the
 PT polypeptides.
 XX
 XX Example 1; Page 25; 42pp; English.
 PS
 XX The present sequence was used to generate a polypeptide with extended
 CC polyglutamine regions. This was performed in an example illustrating a
 CC method for identifying a compound which disrupts polypeptide aggregation.
 CC The method is carried out using a cell which has been genetically
 CC modified to express aggregation-disposed polypeptides, or using purified
 CC aggregation-disposed polypeptides. The compounds identified by this
 CC method are useful for treating disorders associated with such polypeptide
 CC aggregation, including Huntington's disease, Alzheimer's disease,
 CC Parkinson's disease, spinocerebellar ataxia, multiple myeloma,
 CC amyloidosis, and spongiform encephalopathies like Creutzfeldt-Jakob
 CC disease and kuru in humans. The present sequence was annealed to its
 CC complement to generate double stranded duplex DNA with trinucleotide
 CC extensions
 XX
 SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1397 CAACAGCAGCAACAGCA 1413
 Db 1 CAACAGCAGCAACAGCA 17

RESULT 146
 AAH19624/C
 ID AAH19624 standard; DNA; 18 BP.
 XX
 AC AAH19624;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Complementary oligo of sequence containing a mixture of CAG/CAA codons.
 XX

KW Polyglutamine region; polypeptide aggregation; aggregation disruption;
 KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
 KW spinocerebellar ataxia; multiple myeloma; amyloidosis; anticonvulsant;
 KW spongiform encephalopathy; neuroprotective; neurotropic; antiparkinsonian;
 KW ss.
 XX
 OS Synthetic.
 XX
 XX WO200123412-A2.
 XX
 XX
 PD 05-APR-2001.
 XX
 XX
 PF 27-SEP-2000; 2000WO-US041008.
 XX
 XX
 PR 27-SEP-1999; 99US-00405048.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX Houseman DE, Preisinger EA, Kazantsev AG;
 XX
 XX WPI; 2001-300097/31.
 XX
 XX Screening for agents which disrupt aggregation of polypeptides for
 PT treating aggregation-associated disorders e.g. Alzheimer's disease, by
 PT using aggregation-disposed polypeptides or cell expressing the
 PT polypeptides.
 XX
 XX Example 1; Page 25; 42pp; English.
 XX
 CC The present sequence was used to generate a polypeptide with extended
 CC polyglutamine regions. This was performed in an example illustrating a
 CC method for identifying a compound which disrupts polypeptide aggregation.
 CC The method is carried out using a cell which has been genetically
 CC modified to express aggregation-disposed polypeptides, or using purified
 CC aggregation-disposed polypeptides. The compounds identified by this
 CC method are useful for treating disorders associated with such polypeptide
 CC aggregation, including Huntington's disease, Alzheimer's disease,
 CC Parkinson's disease, spinocerebellar ataxia, multiple myeloma,
 CC amyloidosis, and spongiform encephalopathies like Creutzfeldt-Jakob
 CC disease and kuru in humans. The present sequence was annealed to its
 CC complement to generate double stranded DNA with trinucleotide
 CC extensions
 XX
 XX Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1451 CAGCAGCAACGCAACA 1467
 |||||
 Db 18 CAGCAGCAACGCAACA 2
 RESULT 147
 ABK11198
 ID ABK11198 standard; DNA; 18 BP.
 XX
 XX AC ABK11198;
 XX
 XX 05-JUN-2002 (first entry)
 XX
 XX Oligonucleotide #1 used to generate DNA with trinucleotide extensions.
 DE
 KW Inhibition of protein-protein interaction; Alzheimer's disease;
 KW polyglutamine-containing transcription factor; hexamerisation of p53;
 KW homodimerisation of jun; expanded trinucleotide repeat; CAG repeat;
 KW Huntington's disease; HD; Primal and bulbar muscular atrophy; SBMA;
 KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1;
 KW spinocerebellar ataxia type 2; spinocerebellar ataxia type 6;
 KW spinocerebellar ataxia type 7; Machado-Joseph disease; MJD/SCA3;
 KW neurotropic; anticonvulsant; cerebroprotective; neuroprotective; ss.
 XX

OS Synthetic.
 XX WO200216644-A1.
 XX
 PD 28-FEB-2002.
 XX
 XX 20-AUG-2001; 2001WO-US026097.
 XX
 XX 18-AUG-2000; 2000US-0226502P.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX Kazantsev A, Thompson L, Houseman DE;
 XX
 XX WPI; 2002-280948/32.
 XX
 XX Novel agent for inhibiting protein-protein interaction useful to treat
 PT Alzheimer's disease, has two domains which bind first, second proteins
 PT with seven consecutive glutamine residues and a domain separating two
 PT domains.
 XX
 XX Disclosure; Page 8; 40pp; English.
 XX
 CC The present invention relates to therapeutic agents comprising a first
 CC domain (D1) that binds a protein having at least seven consecutive
 CC glutamine (Glu) residues, a second domain (D2) that binds another protein
 CC having at least 7 consecutive Glu residues, and a third domain (D3) that
 CC separates D1 from D2. The therapeutic agents of the invention are useful
 CC for inhibiting protein-protein interactions (e.g. aggregation,
 CC dimerisation or other physiologically significant association), and can
 CC be used for treating Alzheimer's disease, and disorders in which
 CC polyglutamine-containing transcription factors or coactivators are
 CC desirably active (e.g. disorders associated with homodimerisation of jun
 CC or hexamerisation of p53). The therapeutic agents can also be used to
 CC treat various disorders, including those associated with expanded
 CC trinucleotide (CAG) repeats. For example such disorders can include
 CC Huntington's disease (HD), Primal and bulbar muscular atrophy (SBMA),
 CC dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1, type
 CC 2, type 6 or type 7, or Machado-Joseph disease (MJD/SCA3). The present
 CC sequence represents an oligonucleotide used to generate double stranded
 CC DNA with trinucleotide extensions
 XX
 XX Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1397 CAACAGCAGCAACAGCA 1413
 |||||
 Db 1 CAACAGCAGCAACAGCA 17
 RESULT 148
 ABK11199/C
 ID ABK11199 standard; DNA; 18 BP.
 XX
 XX AC ABK11199;
 XX
 XX 05-JUN-2002 (first entry)
 XX
 XX Oligonucleotide #2 used to generate DNA with trinucleotide extensions.
 DE
 KW Inhibition of protein-protein interaction; Alzheimer's disease;
 KW polyglutamine-containing transcription factor; hexamerisation of p53;
 KW homodimerisation of jun; expanded trinucleotide repeat; CAG repeat;
 KW Huntington's disease; HD; Primal and bulbar muscular atrophy; SBMA;
 KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1;
 KW spinocerebellar ataxia type 2; spinocerebellar ataxia type 6;
 KW spinocerebellar ataxia type 7; Machado-Joseph disease; MJD/SCA3;
 KW neurotropic; anticonvulsant; cerebroprotective; neuroprotective; ss.
 XX
 OS Synthetic.

XX WO200216644-A1.
 XX
 XX
 XX PD 28-FEB-2002.
 XX
 XX
 XX PF 20-AUG-2001; 2001WO-US026097.
 XX
 XX PR 18-AUG-2000; 2000US-0226502P.
 XX
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 XX PI Kazantsev A, Thompson L, Housman DE;
 XX WPI; 2002-280948/32.
 XX
 XX PT Novel agent for inhibiting protein-protein interaction useful to treat
 XX Alzheimer's disease, has two domains which bind first, second proteins
 XX with seven consecutive glutamine residues and a domain separating two
 XX domains.
 XX
 XX PS Disclosure; Page 8; 40pp; English.
 XX
 XX CC The present invention relates to therapeutic agents comprising a first
 XX domain (D1) that binds a protein having at least seven consecutive
 XX glutamine (Glu) residues, a second domain (D2) that binds another protein
 XX having at least 7 consecutive Glu residues, and a third domain (D3) that
 XX separates D1 from D2. The therapeutic agents of the invention are useful
 XX for inhibiting protein-protein interactions (e.g. aggregation, and can
 XX dimerisation or other physiologically significant association), and can
 XX be used for treating Alzheimer's disease, and disorders in which
 XX polyglutamine-containing transcription factors or coactivators are
 XX desirably active (e.g. disorders associated with homodimerisation of jun
 XX or hexamerisation of p53. The therapeutic agents can also be used to
 XX treat various disorders, including those associated with expanded
 XX trinucleotide (CAG) repeats. For example such disorders can include
 XX Huntington's disease (HD), primal and bulbar muscular atrophy (SMA),
 XX dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1, type
 XX 2, type 6 or type 7, or Machado-Joseph disease (MJD/SCA3). The present
 XX sequence represents an oligonucleotide used to generate double stranded
 XX DNA with trinucleotide extensions
 XX
 XX SQ Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1451 CAGCAGCAACAGCA 1467
 |||||
 DB 18 CAGCAGCAACAGCA 2
 RESULT 149
 ABZ81759
 ID ABZ81759 standard; DNA; 18 BP.
 AC
 AC ABZ81759;
 XX
 XX DT 11-JUN-2003 (first entry)
 XX
 XX DE Huntington's disease exon 1 triplet repeat sequence.
 XX
 XX KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 XX gene therapy; ss.
 XX OS Homo sapiens.
 XX WO2003013437-A2.
 XX PN 20-FEB-2003.
 XX PD
 XX PF 07-AUG-2002; 2002WO-US025352.
 XX
 XX PT

PR 07-AUG-2001; 2001US-0310757P.
 PR 08-AUG-2001; 2001US-0310770P.
 PR 08-AUG-2001; 2001US-0310889P.
 PR 04-DEC-2001; 2001US-0337219P.
 XX
 XX PA (UYDE) UNIV DELAWARE.
 XX
 XX PI Kmiec EB, Parekh-Olmedo H;
 XX WPI; 2003-256478/25.
 XX
 XX DR New single stranded oligonucleotides comprising a DNA domain having at
 XX least one mismatch with respect to the genetic sequence of the
 XX PT Huntington's disease gene to be altered, useful for treating or
 XX PT preventing Huntington's disease.
 XX
 XX PS Example 5; Page 72; 133pp; English.
 XX
 XX CC The present sequence is an example of a poly-glutamine triplet repeat
 XX region found in exon 1 of the Huntington's disease (HD) gene. In an
 XX example from the invention, neuronal PC12 cells were engineered to
 XX include an HD gene exon 1 containing this sequence. These cells were used
 XX to demonstrate the ability of single-stranded chemically-modified
 XX oligonucleotides (see ABZ81747-51) to decrease the formation of
 XX CC Huntington's protein (huntingtin) aggregates in cell culture. The
 XX invention provides chemically modified oligonucleotides that target
 XX sequence alterations to the triplet repeat region of the HD gene exon 1
 XX and/or which reduce the formation of huntingtin protein-containing
 XX aggregates. These are useful for the treatment or prevention of HD
 XX
 XX SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1397 CACAGCAGCAACAGCA 1413
 |||||
 DB 1 CACAGCAGCAACAGCA 17
 RESULT 150
 ADK67650
 ID ADK67650 standard; DNA; 18 BP.
 XX
 XX AC ADK67650;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX
 XX DE Huntington's disease gene exon 1 DNA fragment.
 XX
 XX KW Huntington's disease; huntingtin; protein aggregation; gene therapy;
 XX human; ds.
 XX OS Homo sapiens.
 XX WO2004014306-A2.
 XX PN 19-FEB-2004.
 XX PD
 XX PF 07-AUG-2003; 2003WO-US024868.
 XX
 XX PR 07-AUG-2002; 2002US-0402198P.
 XX
 XX PA (UYDE) UNIV DELAWARE.
 XX
 XX PI Kmiec EB, Parekh-Olmedo H;
 XX WPI; 2004-180536/17.
 XX
 XX DR Identifying the oligonucleotide species that disrupts aggregation of a
 XX PT protein aggregant in a cell by introducing the oligonucleotide species or
 XX PT composition separately into cells that have or are likely to develop

```

PT aggregation.
XX
PS Example 1; Page 26; 59pp; English.
XX
CC The present sequence is that of a fragment of exon 1 of the Huntington's
CC disease (HD) gene comprising alternating repeating codons for Gln. A
CC fusion gene comprising HD gene exon 1 and an enhanced green fluorescent
CC protein gene was used in examples from an invention investigating the
CC ability of different oligonucleotides to reduce protein aggregation in
CC PC12 cells containing integrated copies of the fusion gene. The invention
CC is based on the discovery that oligonucleotides unrelated in sequence to
CC that of a nucleic acid which encodes a protein aggregant can be effective
CC in disrupting or preventing aggregation in disorders of protein assembly.
CC A claimed method for identifying, from a plurality of oligonucleotides
CC differing in sequence and/or composition, those oligonucleotide species
CC that disrupt aggregation of a protein aggregant in a cell, comprises
CC introducing the oligonucleotides separately into cells that have or are
CC likely to develop protein aggregates, and identifying those that are
CC effective at preventing, reducing or disrupting aggregation. The
CC oligonucleotides are useful for treating a disorder of protein assembly
CC such as HD, Alzheimer's disease, cystic fibrosis, amyotrophic lateral
CC sclerosis, Parkinson's disease, spinobulbar muscular atrophy,
CC spinocerebellar ataxia types 1, 2, 3, 6 and 7, dentatorubral-
CC pallidolysian atrophy, prion diseases, scrapie, bovine spongiform
CC encephalopathy, Creutzfeldt-Jacob disease, new variant CJD, Pick's
CC disease, diabetes type II, multiple myeloma-plasma cell dyscrasia,
CC medullary carcinoma of the thyroid, chronic renal failure, congestive
CC heart failure, chronic inflammation, atherosclerosis (apoA1) or familial
CC amyloidosis.
XX
SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 CAACAGCAGCAACACGCA 1413
Db 1 CAACAGCAGCAACACGCA 17

RESULT 151
ADSI16437/c
ID ADS16437 standard; DNA; 18 BP.
AC
AC ADS16437;
XX
XX 02-DEC-2004 (first entry)
XX
XX Allele A oligo #2, used in polynucleotide sequence detection.
XX
XX Single nucleotide polymorphism; SNP; genotyping; ss.
XX
XX Synthetic.
XX
XX US2004175704-A1.
XX
XX 09-SEP-2004.
XX
XX 12-MAY-2003; 2003US-00436231.
XX
XX 06-MAR-2003; 2003US-0452481P.
XX
XX (STRA-) STRATAGENE.
XX
XX Sorge JA, Firmin A;
XX
XX WPI; 2004-642120/62.
XX
XX Determining polynucleotide sequence differences by amplifying
XX polynucleotide in presence of labeled nucleotide and detecting variation
XX based on incorporation frequency of labeled nucleotide compared to known
XX reference frequency.

PT
XX
PS Example 1; Page 26; 59pp; English.
XX
CC The invention relates to compositions, kits and methods for detecting the
CC polynucleotide sequence differences. The method involves amplifying the
CC polynucleotide of interest in the presence of a labelled nucleotide and
CC detecting variation based on incorporation frequency of labelled
CC nucleotide compared to known reference frequency. The method is useful
CC for determining a sequence difference such as a single nucleotide
CC polymorphism (SNP) or a tandem repeat, between a region of interest in a
CC polynucleotide and a reference sequence. It is useful for determining the
CC presence of a mutation in a region of interest in a polynucleotide and is
CC also useful for genotyping. The present sequence is an allelic
CC oligonucleotide used in polynucleotide sequence detection.
XX
SQ Sequence 18 BP; 0 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAG 1423
Db 17 AACAGCAGCAGCAGCAG 1

RESULT 152
ADSI16436
ID ADS16436 standard; DNA; 18 BP.
XX
XX AC ADS16436;
XX
XX 02-DEC-2004 (first entry)
XX
XX Allele A oligo #1, used in polynucleotide sequence detection.
XX
XX Single nucleotide polymorphism ; SNP; genotyping; ss.
XX
XX Unidentified.
XX
XX US2004175704-A1.
XX
XX 09-SEP-2004.
XX
XX 12-MAY-2003; 2003US-00436231.
XX
XX 06-MAR-2003; 2003US-0452481P.
XX
XX (STRA-) STRATAGENE.
XX
XX Sorge JA, Firmin A;
XX
XX WPI; 2004-642120/62.
XX
XX Determining polynucleotide sequence differences by amplifying
XX polynucleotide in presence of labeled nucleotide and detecting variation
XX based on incorporation frequency of labeled nucleotide compared to known
XX reference frequency.

PT
XX
PS Disclosure; SEQ ID NO 2; 52pp; English.
XX
CC The invention relates to compositions, kits and methods for detecting the
CC polynucleotide sequence differences. The method involves amplifying the
CC polynucleotide of interest in the presence of a labelled nucleotide and
CC detecting variation based on incorporation frequency of labelled
CC nucleotide compared to known reference frequency. The method is useful
CC for determining a sequence difference such as a single nucleotide
CC polymorphism (SNP) or a tandem repeat, between a region of interest in a
CC polynucleotide and a reference sequence. It is useful for determining the
CC presence of a mutation in a region of interest in a polynucleotide and is
CC also useful for genotyping. The present sequence is an allelic
CC oligonucleotide used in polynucleotide sequence detection.
XX
SQ Sequence 18 BP; 0 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

```

SQ Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 AACGAGCAGCAGCAG 1423
DB 2 AACGAGCAGCAGCAG 18
|||||

RESULT 153
ABZ85595/c
ID ABZ85595 standard; DNA; 20 BP.
XX
AC ABZ85595;
XX
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
XX
KW Human; antiseize; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antiseize gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antiseize to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Claim 15; SEQ ID NO 837; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antiseize to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antiseize gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CACGAGCAGCAGCAGCA 1425
DB 20 CACGAGCAGCAGCAGCA 4
|||||

RESULT 154
ABD21825/c
ID ABD21825 standard; DNA; 20 BP.
XX
AC ABD21825;
XX
DT 29-JUL-2004 (first entry)
DE Human stanniocalcin-derived oligo SEQ ID 837.
XX
KW Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antiseize
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 837; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antisthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCA 1425
 Db 20 CAGCAGCAGCAGCAGCA 4

RESULT 155
 AAT72522/C
 ID AAT72522 standard; DNA; 21 BP.
 AC AAT72522;
 XX
 XX 17-OCT-1997 (first entry)
 DT
 DE
 XX
 XX 5-Cys-encoding oligonucleotide.
 XX Streptavidin; mutagenesis; stabilisation; Stv-43; ss.
 XX Synthetic.
 XX WO9711183-A1.
 XX 27-MAR-1997.
 XX
 XX 10-SEP-1996; 96WO-US005169.
 PF
 XX 11-APR-1995; 95US-00420010.
 PR
 XX (UYBO-) UNIV BOSTON.
 PA
 XX Sano T, Cantor CR, Vajda S, Reznik GO, Smith CL, Pandori MW;
 PI
 XX WPI; 1997-202890/18.
 DR
 XX New streptavidin mutants - have increased stability or altered affinity
 PT for biotin.
 PT
 XX Example 14; Page 33; 91pp; English.
 PS

XX Two 21-mer oligonucleotides (AAT72522 and AAT72523) were annealed and the
 CC resulting double-stranded DNA was ligated into the EcoRI and BamHI sites
 CC of the predigested DNA of a plasmid encoding residues 16 to 133 of
 CC streptavidin with Lys at position 127. The gene was cloned into a
 CC bacterial expression vector and the mutated streptavidin expressed and
 CC purified. The mutant streptavidin forms heterotetramers in solution and,
 CC with Phe at position 120, has a reduced biotin-binding affinity of less
 CC than about 10 power 8/M. It can be conjugated to other proteins and
 CC macromolecules, and also to solid supports through the sulphhydryl group
 CC on the cysteine residues
 XX

SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AGCAGCAGCAGCAGCA 1441
 Db 19 AGCAGCAGCAGCAGCA 3

RESULT 156
 AAV17227
 ID AAV17227 standard; DNA; 20 BP.
 XX
 XX AAV17227;
 AC
 XX 29-JUN-1998 (first entry)
 DT
 DE
 XX SCA2 gene CAG repeat unit fragment.
 XX
 XX SCA2 gene; spinocerebellar ataxia type II; CAG repeat; PCR primer; ss.
 KW
 XX Synthetic.
 OS
 XX WO9803679-A1.
 PN
 XX 29-JAN-1998.
 PD
 XX 18-JUL-1996; 96WO-JP001999.
 PF
 XX 18-JUL-1996; 96WO-JP001999.
 PR
 XX (SRLS-) SRL INC.
 PA
 XX Teuji S, Sanpei K;
 PI
 XX WPI; 1998-120796/11.
 DR
 XX Diagnosing spinocerebellar ataxia type II - by PCR and determining number
 PT of CAG repeat units.
 PT
 XX Example 1; Page 12; 23pp; Japanese.
 PS

XX This sequence represents a fragment of the SCA2 gene. It can be used in
 CC the method of the invention for diagnosing spinocerebellar ataxia type
 CC II, by performing PCR on the test DNA using two primers hybridising to
 CC parts of the SCA2 gene sequence, and determining the number of CAG
 CC repeats in the amplified products. The method provides an easy means for
 CC the diagnosis of spinocerebellar ataxia type II
 XX
 XX Sequence 20 BP; 9 A; 9 C; 2 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1448 CAGCAGCAGCAGCAACA 1467
 Db 1 CACCACCAGCAGCAGCA 20

RESULT 157
 AAV30272
 ID AAV30272 standard; DNA; 20 BP.
 XX
 AC AAV30272;
 XX
 XX C2-OCT-1998 (first entry)
 DT
 XX Spinocerebellar ataxia type 2 associated gene specific primer 1.
 DE
 XX Spinocerebellar ataxia type 2; SCA2; gene therapy; antisense therapy;
 KW CAG repeat; neurodegenerative disease; PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX Homo sapiens.
 OS
 XX WO9818920-A1.
 PN

XX 07-MAY-1998.
 XX 30-OCT-1997; 97WO-JP003946.
 XX 30-OCT-1996; 96JP-00304059.
 XX (SRLS-) SRL INC.
 XX Teuji S, Sanpei K;
 XX WPI; 1998-272215/24.
 XX Nucleic acid fragments associated with spinocerebellar ataxia type 2 -
 PT contain increased number of CAG repeat region compared to normal gene.
 XX Example 1; Page 7; 38pp; Japanese.
 XX This primer is used for the PCR amplification of a gene causative of
 CC spinocerebellar ataxia type 2 (SCA2), a neurodegenerative disease. The
 CC gene associated with SCA2, has a tri-nucleotide (CAG) repeat region which
 CC in the expression product produces a polyglutamine sequence from Gln-166
 CC to Gln-188. In the normal gene there are 15-25 CAG repeats but in SCA2
 CC patients this number is increased to 35-100. Peptides encoded by nucleic
 CC acid fragments (DNA or RNA) containing sequences from the SCA2 associated
 CC gene, antibodies recognising the peptides and antisense nucleic acids
 CC hybridising with the nucleic acid fragments can be used for the
 CC investigation and diagnosis of SCA2. They can also be used for the
 CC treatment of SCA2 by antisense therapy or gene therapy
 XX Sequence 20 BP; 9 A; 9 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX 1448 CAGCAGCAGCAACGCAACA 1467
 DB 1 CACCACCAGCAGCAACA 20
 |||||
 RESULT 158
 ADD68486
 ID ADD68486 standard; DNA; 20 BP.
 AC ADD68486;
 DT 15-JAN-2004 (first entry)
 DE SNP typing-related PCR primer - SEQ ID 43.
 XX single nucleotide polymorphism; SNP; typing; PCR; primer; ss.
 XX Unidentified.
 XX JP2002300894-A.
 XX 15-OCT-2002.
 XX 29-JAN-2002; 2002JP-00019752.
 XX 01-FEB-2001; 2001JP-00025700.
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX WPI; 2003-397221/38.
 XX A typing method for single nucleotide polymorphism (SNP) of several
 PT hundred thousands of SNP sites with comparatively a small amount of
 PT genome DNA.
 XX Example 2; SEQ ID NO 43; 45pp; Japanese.
 XX

CC The invention relates to a novel method for typing a single nucleotide
 CC polymorphism (SNP) using a small amount of genomic DNA comprising
 CC simultaneous amplification of plural base sequences containing one or
 CC more SNP sites and differentiation of the bases within the SNP sites. The
 CC method of the invention may be useful for typing several hundred thousand
 CC SNP sites using only a comparatively small amount of genomic DNA. The
 CC current sequence is that of the SNP typing-related PCR primer of the
 CC invention.
 XX Sequence 20 BP; 8 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX 1601 CAGCAGCAGCAACACATC 1620
 DB 1 CAGCAGCAGCAACACGTC 20
 |||||
 RESULT 159
 ABZ86069/c
 ID ABZ86069 standard; DNA; 20 BP.
 XX ABZ86069;
 AC ABZ86069;
 XX 17-OCT-2003 (first entry)
 DT Human oligonucleotide sequence.
 DE Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 OS WO200285308-A2.
 PN 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 PR (EPIG-) EPIGENESIS PHARM INC.
 XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 1311; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CAGCGCGCGCAGCAGCAGCA 1

RESULT 160

ABZ85597/c

ID ABZ85597 standard; DNA; 20 BP.

XX AC ABZ85597;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired

XX respiration, has oligo(s) antisense to specific gene(s) or its

XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX ubiquinone.

XX Claim 15; SEQ ID NO 839; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

XX first active agent comprising an oligonucleotide antisense to the

XX initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX junctions of genes encoding a polypeptide associated with lung and/or

XX nasal airway dysfunction and a second active agent comprising an

XX antiinflammatory steroid and ubiquinone. A composition of the invention

XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX immunosuppressive, and cytostatic activity. The composition may have a

XX use in antisense gene therapy. The composition is useful for treating or

XX preventing a respiratory, lung or malignant disease or condition, also

XX for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 977 CAGCAGCAGCAGCAGCAGCA 996
Db 20 CAGCAGCAGCAGCAGCAGCA 1

RESULT 161

ABZ92556/c

ID ABZ92556 standard; DNA; 20 BP.

XX AC ABZ92556;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired

XX respiration, has oligo(s) antisense to specific gene(s) or its

XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX ubiquinone.

XX Disclosure; SEQ ID NO 7798; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

XX first active agent comprising an oligonucleotide antisense to the

XX initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX junctions of genes encoding a polypeptide associated with lung and/or

XX nasal airway dysfunction and a second active agent comprising an

XX antiinflammatory steroid and ubiquinone. A composition of the invention

XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX immunosuppressive, and cytostatic activity. The composition may have a

XX use in antisense gene therapy. The composition is useful for treating or

XX preventing a respiratory, lung or malignant disease or condition, also

XX for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 83 GAGGAGACGGCGCTTCGA 102
 DB 20 GAGGAGACGGCGCTTCGA 1

RESULT 162
 ABZ86062/c
 ID ABZ86062 standard; DNA; 20 BP.

XX AC ABZ86062;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

XX PS Claim 15; SEQ ID NO 1304; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 1 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAACA 1443
 DB 20 CAGCAGCAGCAGCAGCAACA 1

RESULT 163

ABZ86061/c

ID ABZ86061 standard; DNA; 20 BP.

XX AC ABZ86061;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

XX PS Claim 15; SEQ ID NO 1303; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 1 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. NO. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1565 CAGCAGCAGCAACACACACA 1584
||| ||||| ||||| |||||
Db 20 CATCACCAGCAACACACACA 1

RESULT 164
ABZ98989/c
ID ABZ98989 standard; DNA; 20 BP.

XX AC ABZ98989;

XX 17-OCT-2003 (first entry)

XX Human PDE4A oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 14231; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. NO. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 602 GAACTGGAGAACATGATCAA 621
||||| ||||| ||||| |||||
Db 20 GAACTGGAGAACCTGAACAA 1

RESULT 165

ABZ86070/c

ID ABZ86070 standard; DNA; 20 BP.

XX AC ABZ86070;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Claim 15; SEQ ID NO 1312; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
 |||||
 DB 20 CAGCAGCAGCGCGCGCAGCA 1

RESULT 166
 ABZ86077/c

ID ABZ86077 standard; DNA; 20 BP.

XX AC ABZ86077;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI NYce JW, Li Y, Sandrasagra A, Katz' E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Claim 15; SEQ ID NO 1319; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1403 CAGCAACAGCAGCAGCAGCA 1422
 |||||
 DB 20 CAGCGACTGCAGCAGCAGCA 1

RESULT 167

ACC62133

ID ACC62133 standard; DNA; 20 BP.

XX AC ACC62133;

XX DT 20-JUN-2003 (first entry)

XX DE Human alipoprotein B antisense oligonucleotide SEQ ID NO: 22.

XX alipoprotein B; ApoB; antilipemic; antiarteriosclerotic; antidiabetic;
 KW anorectic; cardiovascular; gene therapy; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
 KW type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
 KW glucose; antisense oligonucleotide; ss.

XX OS Synthetic.

XX PN WO2003011887-A2.

XX PD 13-FEB-2003.

XX PF 30-JUL-2002; 2002WO-US024247.

XX PR 01-AUG-2001; 2001US-00920033.

XX PR 30-APR-2002; 2002US-00135985.

XX PR 15-MAY-2002; 2002US-00147196.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Crooke RM, Graham MJ;

XX DR WPI; 2003-268105/26.

XX New antisense oligonucleotides for modulating apolipoprotein B,
 PT especially for preventing or treating atherosclerosis, hyperlipidemia or
 PT diabetes, or for modulating glucose, cholesterol, lipoprotein or
 PT triglyceride levels.

XX Example 15; Page 96; 160pp; English.

XX The invention relates to a novel compound that is 8-50 nucleotides in
 CC length that is targeted to a nucleic acid molecule encoding
 CC apolipoprotein B (ApoB), and specifically hybridises with and inhibits
 CC the expression of a nucleic acid molecule encoding ApoB; or which
 CC specifically hybridises with at least an 8-nucleotide portion of an
 CC active site on a nucleic acid molecule encoding ApoB. A compound of the
 CC invention has antilipemic, antiarteriosclerotic, antidiabetic,
 CC anorectic, and cardiovascular activity. The compound may have a use in
 CC gene therapy. The antisense oligonucleotide is useful for treating an
 CC animal having a disease or conditions associated with ApoB, e.g. a
 CC condition involving abnormal lipid metabolism, a condition involving
 CC abnormal cholesterol metabolism, atherosclerosis, or a condition

CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
 CC (specifically Type 2 diabetes), obesity, atherosclerosis or
 CC cardiovascular disease). The new compound or the antisense
 CC oligonucleotide is also useful for modulating glucose levels
 CC (particularly plasma or serum glucose levels) in a human or diabetic
 CC animal, or for modulating serum cholesterol levels, lipoprotein levels
 CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,
 CC particularly in a human. The antisense compound is also useful for
 CC preventing or delaying the onset of a disease or condition associated
 CC with ApoB, or the onset of an increase in glucose levels in the animal or
 CC human. The present sequence is used in the exemplification of the
 CC invention

SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551

DB 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 168

ABZ84008/C

ID ABZ84008 standard; DNA; 20 BP.

XX AC ABZ84008;

XX DT 14-MAY-2003 (first entry)

XX DE Toxicologically relevant rat PCR primer #1167.

XX KW Toxicologically relevant gene; toxicological response; PCR primer; ss.

XX OS Rattus sp.

XX OS Synthetic.

XX PN WO2003016500-A2.

XX PD 27-FEB-2003.

XX PF 16-AUG-2002; 2002WO-US026514.

XX PR 16-AUG-2001; 2001US-0313080P.

XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;

XX PI Alen P;

XX DR WPI; 2003-268322/26.

XX PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

XX FS Claim 1; Page 327; 455pp; English.

XX CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in ABZ84008
 CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
 CC; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)

CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals

XX SQ Sequence 20 BP; 0 A; 6 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGCA 1419

DB 20 CAGCAGGACAGCAGCAAGCA 1

RESULT 169

ABD22299/C

ID ABD22299 standard; DNA; 20 BP.

XX AC ABD22299;

XX DT 29-JUL-2004 (first entry)

XX DE Human stanniocalcin-derived oligo SEQ ID 1311.

XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPIC-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-093058/08.

XX PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX FS Claim 15; SEQ ID NO 1311; 763pp; English.

XX CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428

Db 20 CAGCGCGCGCAGCAGCAGCA 1

RESULT 170

ABD22300/C

ID ABD22300 standard; DNA; 20 BP.

XX AC ABD22300;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannocalcin-derived oligo SEQ ID 1312.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (BPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-093058/08.

XX PT Pharmaceutical composition for treating asthma, has antisense
 FT oligonucleotide containing less percentage of adenosine, targeted to
 FT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1312; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating and
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428

Db 20 CAGCAGCAGCAGCAGCAGCA 1

RESULT 171

ABD22291/C

ID ABD22291 standard; DNA; 20 BP.

XX AC ABD22291;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannocalcin-derived oligo SEQ ID 1303.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.


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PR 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
FA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1303; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposcretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 1 A; 1 C; 8 G; 10 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1565 CAGCAGCAGCAACACCAACA 1584
DB 20 CATCACCAGCAACACCAACA 1
RESULT 172
ABD22307/c
ID ABD22307 standard; DNA; 20 BP.
XX
XX ABD22307;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human stannocalcin-derived oligo SEQ ID 1319.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW
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KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1319; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposcretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1403 CAGCAACAGCAGCAGCAGCA 1422
DB 20 CAGCAGCTGCAGCAGCAGCA 1
RESULT 173
ABD32020/c
ID ABD32020 standard; DNA; 20 BP.
```


XX AC ABD32020;
XX DT 29-JUL-2004 (first entry)
XX DE Human PDE4A-derived oligonucleotide SEQ ID 14231.
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.
XX PA (SPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 14231; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 602 GAACGAGACATGATCAA 621
Db 20 GAACGAGACATGATCAA 1
|||||
RESULT 174
ABD28786/C
ID ABD28786 standard; DNA; 20 BP.
XX AC ABD28786;
XX DT 29-JUL-2004 (first entry)
XX DE W81570-derived oligonucleotide SEQ ID 7798.
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.
XX PA (SPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 7798; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 XX Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 83 GAGGAGACGGCGCTTCGA 102
 Db 20 GAGGAGACGGCGCTTCGA 1
 |||||

RESULT 175
 ABD21827/c

ID ABD21827 standard; DNA; 20 BP.

XX AC ABD21827;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannioalcin-derived oligo SEQ ID 839.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPITG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmacological composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 839; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX

XX SQ Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 977 GAGGAGACCCAGCAGCAGCA 996

Db 20 GAGGAGACCCAGCAGCAGCA 1
 |||||

RESULT 176

ABD22282/c

ID ABD22282 standard; DNA; 20 BP.

XX AC ABD22282;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannioalcin-derived oligo SEQ ID 1304.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPITG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1304; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

XX comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

SQ Sequence 20 BP; 1 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCA 1443

DB 20 CAGCAGCAGCAGCAGCA 1

RESULT 177

ADH18033

ID ADH18033 standard; DNA; 20 BP.

XX

AC ADH18033;

XX

DT 11-MAR-2004 (first entry)

XX

DE 2'-MOE gapmer antisense oligo targeted to human ApoB DNA 1 - SEQ ID 22.

XX

KW apolipoprotein B; ApoB; antiarteriosclerotic; cardiant; antidiabetic;

KW anorectic; lipid; cholesterol metabolism; atherosclerosis;

KW diabetes Type 2; obesity; hyperlipidaemia; cardiovascular; gene therapy;

KW antisense; 2'-O-methoxyethyl gapmer; phosphorothioate backbone; 2'-MOE;

KW human; ss.

XX

OS Homo sapiens.

XX

PN WO2003097662-A1.

XX

PD 27-NOV-2003.

XX

PF 15-MAY-2003; 2003WO-US015493.

XX

PR 15-MAY-2002; 2002US-00147196.

XX

PR 13-NOV-2002; 2002US-0426324P.

XX

PA (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

XX WPI; 2004-022840/02.

XX

PT New antisense compound, useful for preparing a composition for treating

PT abnormal lipid or cholesterol metabolism, atherosclerosis, diabetes Type

XX 2, obesity, hyperlipidemia or cardiovascular disease.

XX

PS Example 15; SEQ ID NO 22; 405pp; English.

XX

CC The invention relates to a novel antisense compound targeted to a nucleic

CC acid molecule encoding human apolipoprotein B (ApoB) which specifically

CC hybridizes with and inhibits the expression of human apolipoprotein B.

CC The compound of the invention demonstrates antiarteriosclerotic,

CC cardiant, antidiabetic and anorectic activities and may be useful for

CC preparing a composition for treating abnormal lipid or cholesterol

CC metabolism, atherosclerosis, diabetes Type 2, obesity, hyperlipidemia or

CC cardiovascular disease. Furthermore, the compound has gene therapy

CC applications. The current sequence is that of the 2'-O-methoxyethyl (2'-

CC MOE) gapmer antisense oligo of the invention which has 2'-MOE 'wings', a

CC phosphorothioate backbone throughout and in which all cytidine residues

CC are 5-methylcytidines.

XX

SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551

DB 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 178

ADH65922/c

ID ADH65922 standard; DNA; 20 BP.

XX

AC ADH65922;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human glucocorticoid receptor-specific antisense oligonucleotide #2756.

XX

KW antisense oligonucleotide; glucocorticoid receptor; infection;

KW inflammation; tumour formation; diabetes; obesity;

KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX

OS Homo sapiens.

XX

PN WO2003099215-A2.

XX

PD 04-DEC-2003.

XX

PF 20-MAY-2003; 2003WO-US016084.

XX

PR 20-MAY-2002; 2002US-0381857P.

XX

PA (PHAA) PHARMACIA CORP.

XX

PI Crosby SD, Nalseth AB;

XX

DR WPI; 2004-035034/03.

XX

PT New antisense compound targeted to a nucleic acid molecule encoding

PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,

PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.

XX

PS Claim 4; SEQ ID NO 2756; 985pp; English.

XX

CC The invention comprises an antisense oligonucleotides that are targeted

CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 465 TGGATGGCCAAATGACCCAA 484
Db 20 TGGATGACCAATGACCCCTA 1

RESULT 179
ADH64974/c
ID ADH64974 standard; DNA; 20 BP.
AC ADH64974;
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #1808.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 1808; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 465 TGGATGGCCAAATGACCCAA 484
Db 20 TGGATGACCAATGACCCCTA 1

RESULT 181
ADH66562/c
ID ADH66562 standard; DNA; 20 BP.
AC ADH66562;
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #3396.
XX

Qy 463 CATGGATGGCCAAATGACCC 482
Db 20 CCTGGATGACCAATGACCC 1

RESULT 180
ADH66495/c
ID ADH66495 standard; DNA; 20 BP.
XX
AC ADH66495;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #3329.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 3329; 985pp; English.
XX
CC The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 462 ACATGGATGGCCAAATGACCC 481
Db 20 ACCTGGATGACCAATGACCC 1

RESULT 181
ADH66562/c
ID ADH66562 standard; DNA; 20 BP.
AC ADH66562;
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #3396.
XX

KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 OS Homo sapiens.
 XX
 XX W02003099215-A2.
 XX
 XX 04-DEC-2003.
 XX
 XX 20-MAY-2003; 2003WO-US016084.
 XX
 XX 20-MAY-2002; 2002US-0381857P.
 XX
 XX (PHAA) PHARMACIA CORP.
 XX
 XX Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX
 XX Claim 4; SEQ ID NO 3396; 985pp; English.
 XX
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX
 XX Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 461 CACATGGATGCCAAATGAC 480
 DB 20 CACCTGGATGACCAATGAC 1
 RESULT 182
 ADH64132/c
 ID ADH64132 standard; DNA; 20 BP.
 XX
 XX ADH64132;
 AC
 XX 25-MAR-2004 (first entry)
 DT
 XX Human glucocorticoid receptor-specific antisense oligonucleotide #966.
 DE
 XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 XX Homo sapiens.
 OS
 XX W02003099215-A2.
 PN
 XX 04-DEC-2003.
 PD
 XX 20-MAY-2003; 2003WO-US016084.
 PF
 XX 20-MAY-2002; 2002US-0381857P.
 XX

PA (PHAA) PHARMACIA CORP.
 XX
 XX Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.
 DR
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX
 XX Claim 4; SEQ ID NO 966; 985pp; English.
 XX
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX
 XX Sequence 20 BP; 0 A; 3 C; 7 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1580 CAACAGCAACACAGCAGCA 1599
 DB 20 CAACAGCAACACAGCAGCA 1
 RESULT 183
 ADJ60872/c
 ID ADJ60872 standard; DNA; 20 BP.
 XX
 XX ADJ60872;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Oligonucleotide associated to PDE4A #155.
 DE
 XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
 KW airway inflammation; allergy; asthma; impeded respiration;
 KW cystic fibrosis; acute respiratory distress syndrome;
 KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX W02004011613-A2.
 PN
 XX 05-FEB-2004.
 PD
 XX 25-JUL-2003; 2003WO-US023509.
 PF
 XX 29-JUL-2002; 2002US-0399076P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 PI WPI; 2004-203534/19.
 DR
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codons and introns of respiratory disease-relevant genes e.g.,
 PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
 PT disease e.g., asthma.
 XX
 XX Claim 2; SEQ ID NO 1728; 85pp; English.
 PS
 XX

CC The present invention relates to an oligonucleotide anti-sense to e.g.,
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
 CC end of nucleic acid target comprising gene(s) chosen from e.g.
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
 CC oligonucleotide and optionally surfactant operatively linked to a
 CC oligonucleotide. The method is useful for preventing or treating a
 CC respiratory or lung disease, which involves administering to the airways
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is
 CC useful for production of a medicament for the prevention and/or treatment
 CC of a respiratory or lung disease. The respiratory or lung disease is
 CC chosen from airway inflammation, allergy(ies), asthma, impeded
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
 CC obstruction. The present sequence represents an oligonucleotide of the
 CC invention.

XX
 SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 GAACCTGGAGAACATGATCAA 621
 |||||
 DB 20 GAACCTGGAGAACCTGAACAA 1

RESULT 184
 ADJ53419/c
 ID ADJ53419 standard; DNA; 20 BP.
 AC ADJ53419;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human G protein-coupled receptor 6 DNA antisense oligonucleotide #68.
 XX Human; G protein-coupled receptor 6; GPCR-6; ss;
 KW antisense oligonucleotide; phosphorothioate linkage;
 KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; metabolic disorder;
 KW aberrant signal transduction; brain tissue; neuronal disorder;
 KW motor disorder; sensory disorder; psychiatric disorder;
 KW behavioural disorder; drug addiction; chemical addiction; neuroleptic.
 XX
 OS Homo sapiens.
 XX
 PN US2004023380-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 31-JUL-2002; 2002US-00210479.
 XX
 PR 31-JUL-2002; 2002US-00210479.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Dobie KW;
 XX
 DR WPI; 2004-142661/14.
 XX
 XX Novel antisense compound targeted to nucleic acids encoding G protein-
 PT coupled receptor 6 (GPCR-6), useful for treating animal having disease
 PT associated with GPCR-6 e.g. metabolic, neuronal, motor, sensory or
 PT behavioural disorders.
 XX
 XX Example 15; SEQ ID NO 79; 54pp; English.
 XX
 XX The invention relates to an antisense oligonucleotide targeted to a
 CC nucleic acid encoding the human G protein-coupled receptor 6 (GPCR-6),
 CC which specifically hybridises with the nucleic acid encoding the GPCR-6
 CC and inhibits expression of the GPCR-6. The antisense oligonucleotide
 CC comprises at least one modified internucleoside linkage, i.e. a

CC phosphorothioate linkage, at least one modified sugar moiety, preferably
 CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
 CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful
 CC for inhibiting expression of the GPCR-6 and in preparation of a GPCR-6,
 CC composition for treating a disease or condition associated with GPCR-6,
 CC e.g., a metabolic disorder, aberrant signal transduction in brain tissue,
 CC a neuronal, motor, sensory, psychiatric or behavioural disorder or drug
 CC or chemical addiction. This sequence represents an antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1645 AGCCAGCCTTTCCTAAGGT 1664
 |||||
 DB 20 AGCCAGCCTTTCCTAAGCT 1

RESULT 185
 ADO46361/c
 ID ADO46361 standard; DNA; 20 BP.
 XX
 AC ADO46361;
 XX
 DT 15-JUL-2004 (first entry)
 DE Human oligonucleotide #1727.
 XX
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease; cystic fibrosis; CF;
 KW airway inflammation; allergy; impeded respiration; allergic rhinitis;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 OS Homo sapiens.
 XX
 PN US2004049022-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 XX WPI; 2004-293804/27.
 XX
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 1728; 174pp; English.
 XX

CC The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
 CC -5 receptor, CCR1, CCR3, Botaxin-1, RANVES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Botaxin-1, RANVES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.

XX
 SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 602 GAACGGAGAACATGATCAA 621
 |||||
 Db 20 GAACGGAGAACCTGACAA 1

RESULT 186
 ADO32574
 ID ADO32574 standard; DNA; 20 BP.
 AC ADO32574;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Antisense 2'-MOE gapmer oligo targeted to human ApoB RNA - SEQ 22.
 XX
 KW apolipoprotein B; ApoB; cardiovascular; antiarteriosclerotic;
 KW antilipaeamic; antidiabetic; anorectic; cardiant; vasotropic; hypotensive;
 KW anabolic; eating disorder; cytostatic; endocrine; vasotropic;
 KW neuroprotective; nootropic; lipid; cholesterol metabolism;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW Von Gierke's disease; lipodystrophy; Cushing's syndrome;
 KW sexual ateliotic dwarfism; hyperthyroidism; hypertension;
 KW anorexia nervosa; Werner's syndrome; hepatoma; multiple myeloma; uraemia;
 KW impotence; obstructive liver disease; Alzheimer's; dementia; diabetes;
 KW obesity; atherosclerosis; antisense; 2'-MOE gapmer; 2'-methoxyethyl wing;
 KW phosphorothioate backbone; human; chromosome 2p23-2p24; ss.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER = Phosphorothioate backbone, bases 1-5 and
 16-20, 2'-MOE wing bases, all cytidine residues are 5-
 FT methylcytidines"
 XX
 FN WO200404181-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036411.

XX
 PR 13-NOV-2003; 2002US-0426234P.
 PR 15-MAY-2003; 2003WO-US015493.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PA Crooke R, Graham M, Lemonidis-Tarbet K, Dobie KW;
 WIPI; 2004-420321/39.
 XX
 PT Antisense oligonucleotide compound that inhibits expression of mRNA
 encoding human apolipoprotein B, useful for treating hyperlipidemia,
 PT diabetes, obesity, von Gierke's disease, lipodystrophies, Cushing's
 PT syndrome.
 XX
 PS Example 15; SEQ ID NO 22; 483pp; English.
 XX
 CC The invention relates to a novel antisense compound where the compound
 CC hybridises to and inhibits expression of mRNA encoding human
 CC apolipoprotein B (ApoB) after 16-24 hours by at least 30% in 80%
 CC confluent HepG2 cells in culture at a concentration of 150 nM. The
 CC compound of the invention demonstrates cardiovascular,
 CC antiarteriosclerotic, antilipaeamic, antidiabetic, anorectic, cardiant,
 CC vasotropic, hypotensive, anabolic, eating disorder-related, cytostatic,
 CC endocrine, vasotropic, neuroprotective and nootropic activities and may
 CC be useful for inhibiting the expression of apolipoprotein B in cells or
 CC tissues in vivo in order to address a condition associated with abnormal
 CC lipid or cholesterol metabolism. The compound may be useful for
 CC decreasing circulating lipoprotein levels, triglyceride levels,
 CC cholesterol levels, lipid levels, fatty acid levels, acute phase
 CC reactants and chylomicrons and thus may be utilised during treatment of
 CC hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia,
 CC cardiovascular disorders, Von Gierke's disease, lipodystrophy, Cushing's
 CC syndrome, sexual ateliotic dwarfism, hyperthyroidism, hypertension,
 CC anorexia nervosa, Werner's syndrome, hepatoma, multiple myeloma, uraemia,
 CC impotence, obstructive liver disease, Alzheimer's disease, dementia,
 CC diabetes, obesity and atherosclerosis. The current sequence is that of an
 CC antisense 2'-MOE (2'-methoxyethyl) gapmer oligo of the invention which is
 CC targeted to human ApoB RNA.
 XX
 SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1532 GCCACAGCAGCAGCAGCA 1551
 |||||
 Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 187
 ADO26559/C
 ID ADO26559 standard; DNA; 20 BP.
 XX
 AC ADO26559;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE HOXB1 RT-PCR primer, SEQ ID 45.
 XX
 KW Cytostatic; Pre-B-cell transformation related gene; PBX; HOX; cancer;
 KW HOX heptapeptide region; RT-PCR; primer; ss; HOXB1.
 XX
 OS Homo sapiens.
 XX
 FN WO2004055049-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 12-DEC-2003; 2003WO-GB005425.
 XX
 PR 13-DEC-2002; 2002GB-00029151.


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XX PA (SGEO-) ST GEORGES ENTERPRISES LTD.
XX PI Morgan RGL, Pettengell R, Forraz NPB, Meguckin CP;
XX DR WPI; 2004-533662/51.
XX PS Use of peptide that impairs Pre-B-cell transformation related gene-
XX PT dependent regulation of gene transcription by affecting binding to Hox,
XX PT for treating or preventing disorders involving aberrant cell division,
XX PT especially cancer.
XX PS Example 4; SEQ ID NO 45; 113pp; English.
XX CC The present invention relates to peptides which impair Pre-B-cell
XX CC transformation related gene (PBX)-dependent regulation of gene
XX CC transcription, since they mimic the region of HOX to which PBX binds and
XX CC act as antagonists of that binding. The peptides are based on the
XX CC hexapeptide region of HOXB-4 but have been found to have cross-reactivity
XX CC and reduce the binding of PBX to all HOX proteins. The peptides are
XX CC useful for manufacturing a medicament for the treatment or prevention of
XX CC a disorder in which aberrant cell division occurs e.g. cancer. The
XX CC peptides also further comprise a cell penetration moiety that is linked
XX CC directly to the carboxy-terminal of the peptide. The peptides are also
XX CC useful for reducing the side effects of a cytotoxic or chemotherapeutic
XX CC agent, or for maintaining or expanding a stem cell population in vivo.
XX CC The stem cells, which are originally derived from the recipient
XX CC individual, may be used in manufacturing a medicament for the treatment
XX CC or prevention of a condition resulting in a decreased level of stem
XX CC cells, such as a condition resulting from chemotherapy or radiotherapy.
XX CC The present sequence is a RT-PCR which was used in an example from the
XX CC invention.
XX SQ Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 67 CAATCAGAAGCGGCGGAGG 86
DB 20 CAATCAGAAGCGGCGGAGG 1

RESULT 188
AAV40968
ID AAV40968 standard; DNA; 21 BP.
XX AC AAV40968;
XX DT 25-SEP-1998 (first entry)
XX DE Primer HOX11:857121 for abnormality detection.
XX KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
XX KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
XX KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9824928-A2.
XX PD 11-JUN-1998.
XX PF 08-DEC-1997; 97WO-DK000556.
XX PR 06-DEC-1996; 96DK-00001401.
XX PA (PALL/) PALLISGAARD N.
XX PI Pallsgaard N, Hokland P;

WPI; 1998-333344/29.
Detection of chromosomal abnormalities - by subjecting patient sample
nucleic acids to a multiplex molecular amplification procedure using
primers specific for characteristic nucleic acid sequence.
Claim 73; Page 79; 126pp; English.
This sequence represents a primer used in the method of the invention for
the detection of the presence or absence of chromosomal abnormalities,
each abnormality being associated with a condition in a subject and each
being defined by at least one characteristic nucleic acid sequence. The
method comprises: (a) obtaining a sample of nucleic acids derived from a
subject which may harbour one of the chromosomal abnormalities; (b)
subjecting the sample to a multiplex molecular amplification (MMA)
procedure, where a number of the characteristic sequences, if present in
a sufficient amount, will be amplified; (c) retrieving the product(s)
from step (b), and detecting the presence and/or absence of an amplicon
characteristic of the abnormal sequences to detect the presence or
absence of corresponding chromosomal abnormalities; where the MMA
procedure comprises the use of at least 7 mutually distinct primers (MDP)
in one single reaction mixture, each of the primers defining an end of at
least one characteristic nucleic acid sequence, and where at least one of
the primers defines the first end of at least two characteristic nucleic
acid sequences, the characteristic nucleic acid sequences each being
determined in their opposite ends by MDP selected from the remainder of
the MDP. The methods can be used for detecting chromosomal abnormalities
associated with diseases including numerous leukaemia's, lymphoma's,
carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
medullablastoma, malignant melanoma, and malignant neoplastic conditions
Sequence 21 BP; 1 A; 8 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 815 TCTGCCCTCTCCACTTCGTC 834
DB 2 TCTGCCCTCTCCACTTCGTC 21

RESULT 189
AAF95430/C
ID AAF95430 standard; DNA; 21 BP.
XX AC AAF95430;
XX DT 18-NOV-2004 (revised)
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #191.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT variation 11
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX PW WO200118250-A2.
XX XX 15-MAR-2001.
XX PD
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR
XX PF 10-SEP-1999; 99US-0153357P.
XX PR

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PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX Example; Page 61; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX Revised record issued on 18-NOV-2004 : The variation feature was
XX incorrectly given a capital V
XX Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1554 AACACAGCAGCAGCAGCAG 1573
DB 20 AACACAGCAGCAGCAGCAG 1
RESULT 190
AAH89072
ID AAH89072 standard; DNA; 21 BP.
XX AAH89072;
AC AAH89072;
XX 09-SEP-2004 (revised)
DT 27-FEB-2002 (first entry)
XX Human polymorphic oligonucleotide L21952 fragment.
XX Human; single nucleotide polymorphic; SNP; forensic science;
XX paternity testing; phenotypic trait; genetic mapping; animal breeding;
XX plant breeding; ds.
XX Homo sapiens.
XX Unidentified.
XX Key Location/Qualifiers
XX variation 11 /*tag= a
XX /standard_name= "single nucleotide polymorphism"
XX WO200134840-A2.
XX 17-MAY-2001.
XX 10-NOV-2000; 2000WO-US030766.
XX 10-NOV-1999; 99US-0164596P.
PR
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XX (GLAX ) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
XX determine sites correlating with phenotypic traits, particularly disease,
XX and also in forensics and paternity testing.
XX Claim 82; Page 13; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
XX single nucleotide polymorphic site (SNP: AAH89797-AAH89219). The present
XX sequence is one such oligonucleotide. The oligonucleotides can be used in
XX forensics, paternity testing, correlation of polymorphisms with
XX phenotypic traits, genetic mapping of phenotypic traits and marker
XX assisted breeding of animals and crop plants
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1440 AACAGCAGCAGCAGCAGCAA 1459
DB 2 AACAGCAGCAGCAGCAGCCA 21
RESULT 191
ABK70314
ID ABK70314 standard; DNA; 21 BP.
XX ABK70314;
AC ABK70314;
XX 15-JUL-2002 (first entry)
XX Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #2.
XX Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
XX insulin-like growth factor binding protein-2; hormone-regulated tumour;
XX breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
XX hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;
XX ODN; endocrine tumour therapy; ss.
XX Synthetic.
XX WO200222642-A1.
XX 21-MAR-2002.
XX 13-SEP-2001; 2001WO-US028748.
XX 14-SEP-2000; 2000US-0232641P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Satoshi K, Nelson C, Rennie PS;
XX WPI; 2002-339861/37.
XX Composition for treating hormone-regulated cancer, particularly of
XX prostate or breast, comprises oligonucleotide antisense to insulin-like
XX growth factor binding protein-2.
XX Claim 3; Page 12; 36pp; English.
XX The present invention relates to a new composition for treating hormone-
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CC regulated cancer. The composition comprises an antisense oligonucleotide
CC that inhibits expression of IGFBP-2 (insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense
CC IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy
XX
SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 2 GCCCAGTAGCAGCAGCAGCA 21
||||| |||||||

RESULT 192
ABK70358
ID ABK70358 standard; DNA; 21 BP.
XX
AC ABK70358;
XX
DT 15-JUL-2002 (first entry)
XX
DE Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #46.
XX
KW Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KW insulin-like growth factor binding protein-2; hormone-regulated tumour;
KW breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KW hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;
KW ODN; endocrine tumour therapy; ss.
XX
OS Synthetic.
XX
FN WO200222642-A1.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028748.
XX
PR 14-SEP-2000; 2000US-0232641P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Satoshi K, Nelson C, Rennie PS;
XX
XX WPI; 2002-339861/37.
XX
PT Composition for treating hormone-regulated cancer, particularly of
PT prostate or breast, comprises oligonucleotide antisense to insulin-like
PT growth factor binding protein-2.
XX
PS Claim 3; Page 13; 36pp; English.
XX
CC The present invention relates to a new composition for treating hormone-
CC regulated cancer. The composition comprises an antisense oligonucleotide
CC that inhibits expression of IGFBP-2 (insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense
CC IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy
XX
SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 2 GCCCAGTAGCAGCAGCAGCA 21
||||| |||||||

RESULT 193
ADL723446
ID PDL23446 standard; DNA; 21 BP.
XX
AC ADL23446;
XX
DT 20-MAY-2004 (first entry)
XX
DE Plant AMP-binding protein PCR primer #7.
XX
KW plant; acyl-coenzyme A synthetase; acyl-CoA synthetase; enzyme;
KW transgenic plant; PCR; ss; primer; AMP-binding protein.
XX
OS Unidentified.
XX
FN WO200209295-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US022774.
XX
PR 21-JUL-2000; 2000US-0220474P.
XX
PR 16-JUL-2001; 2001US-00906419.
XX
PA (SHOC/) SHOCKEY J M.
PA (SCHW/) SCHNURR J.
PA (BROW/) BROWSE J A.
XX
XX Shockey JM, Schnurr J, Browse JA;
XX WPI; 2002-241594/29.
XX
PT Novel acyl coenzyme A synthetases gene useful for altering a phenotype of
PT a plant, making a transgenic plant and for producing variants of acyl-CoA
PT synthetases.
XX
PS Example 3; SEQ ID NO 91; 155pp; English.
XX
CC The invention comprises the amino acid and coding sequences of plant acyl
CC -coenzyme A synthetase (acyl-CoA synthetase) enzymes. The DNA and protein
CC sequences of the invention are useful for altering a phenotype of a plant
CC (transgenic plant). The DNA and protein sequences of the invention are
CC also useful for producing variants of acyl-CoA synthetases. The present
CC DNA sequence represents a PCR primer that was used in an example of the
CC invention.
XX
SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGCTTTTCAAGGAATG 2921
Db 2 CAGGCTTTTCAAGGAATG 21
||||| |||||||

RESULT 194
ADL72332
ID ADL72332 standard; DNA; 21 BP.
XX
AC ADL72332;
XX

DT 20-MAY-2004 (first entry)
 DE Arabidopsis thaliana acyl-CoA synthetase gene primer #40.
 KW plant; acyl-CoA synthetase; soybean; sunflower; cotton; maize; castor;
 KW transgenic plant; triacylglycerol biosynthesis; fatty acid; seedling;
 KW beta-oxidation cycle substrate; jasmonic acid; plant defence; primer; ss.
 OS Arabidopsis thaliana.
 XX WO2003087321-A2.
 XX PD 23-OCT-2003.
 XX 09-APR-2003; 2003WO-US010754.
 XX 09-APR-2002; 2002US-00119136.
 PR 08-APR-2003; 2003US-00119136.
 XX (UYWA-) UNIV WASHINGTON STATE RES FOUND.
 PA Shockey JM, Schnurr J, Browae JA;
 PI WPI; 2003-853948/79.
 DR New plant acyl-CoA synthetase protein derived from soybean, sunflower,
 PT cotton, maize, and castor, useful in cuticle was synthesis, and in the
 PT synthesis of jasmonic acid which is involved in reproduction and plant
 PT defense.
 XX Disclosure; SEQ ID NO 91; 226pp; English.
 PS The invention relates to a new purified plant acyl-CoA synthetase protein
 CC comprising at least one of the motifs selected from 9 fully defined
 CC motifs given in the specification, and derived from a crop plant selected
 CC from soybean, sunflower, cotton, maize, and castor. The purified plant
 CC acyl-CoA synthetase protein comprises at least one motif selected from: V
 CC -P/T-L-I-Y-D/A/S-L-G; I-M/C-Y/F/K-T-S-T/S-G-XI-P-K-G-V; S/A-
 CC -Y/M/F-L-P-L/S-A/W-H; L/Q-K/R-P-T/P/S; S/G/V/-G-A/G/S-A/L/S-P-L/I/M; G-Y-G
 CC -L/M-E-T/S; P/S-A-R-K-G/A-E-I-V-C/K/V-I/V/L-R/G-G; IIRKK; and L-
 CC L/V/M/L-P/A-T/S-F/L/M/Y-X-K-XI-K/R-R. The nucleic acid is useful in
 CC producing a transgenic plant (claimed). The plant acyl-CoA synthetase is
 CC useful in TAG biosynthesis, for activating fatty acids released from oil
 CC bodies in newly germinated seedlings, as substrates for the beta-
 CC oxidation cycle which supplies the plant with cellular energy until it
 CC becomes photosynthetically competent. In cuticle was synthesis, and in
 CC the synthesis of jasmonic acid, a fatty acid-derived signaling compound
 CC involved in reproduction, plant defence, and other response reactions.
 CC This sequence corresponds to a PCR primer to amplify the ACS genes of the
 CC invention.
 SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2502 CAGGGCTTTTCAAGGAACTG 2921
 Db 2 CAGGGCTTCTCAGGAATG 21
 RESULT 195
 ADP75370
 ID ADP75370 standard; DNA; 21 BP.
 AC ADP75370;
 XX 12-AUG-2004 (first entry)
 DT Human ADAM19 gene exon K reverse sequencing primer.
 DE Human; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
 KW

KW a disintegrin and metalloprotease; neuroregulin 2; SNP;
 KW single nucleotide polymorphism;
 KW a disintegrin and metalloprotease with thrombospondin type motif 2;
 KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
 OS Homo sapiens.
 XX WO2003031594-A2.
 XX PD 17-APR-2003.
 XX 11-OCT-2002; 2002WO-US032700.
 XX 11-OCT-2001; 2001US-0328424P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
 PI Allen K;
 XX WPI; 2003-381712/36.
 DR New isolated nucleic acid or alternate splice variant, useful for
 PT diagnosing and treating a disintegrin and metalloprotease (ADAM) or
 PT interactor gene-associated disorder, e.g. asthma, atopy, obesity or
 PT inflammatory bowel disease.
 XX Claim 2; Page 128; 338pp; English.
 PS The invention relates to an isolated nucleic acid or alternate splice
 CC variant comprising a nucleotide sequence containing at least one of the
 CC single nucleotide polymorphisms given in the specification, a nucleotide
 CC sequence having at least 15 contiguous nucleotides of them, or
 CC complements of them. The genes are ADAM19 (a disintegrin and
 CC metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
 CC known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
 CC (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
 CC with thrombospondin type motif 2, also known as gene 962). Also included
 CC are a vector comprising the isolated nucleic acid (or alternate splice
 CC variant), a host cell containing the vector, an isolated polypeptide
 CC encoded by the novel nucleic acid (or alternate splice variant), an
 CC antibody or antibody fragment that binds to the polypeptide,
 CC pharmaceutical compositions (comprising the nucleic acid or alternate
 CC splice variant, vector, polypeptide or antibody, and a carrier,
 CC excipient or diluent), a kit for detecting a disintegrin and
 CC metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
 CC nucleic acid or alternate splice variant, antibody or antibody fragment,
 CC and at least one component to detect the hybridisation of the variant or
 CC the binding of the antibody to an ADAM gene amino acid sequence), a kit
 CC for detecting an interactor gene amino acid sequence (comprising the
 CC antibody or antibody fragment, and at least one component to detect the
 CC binding of the antibody to the interactor gene amino acid sequence),
 CC diagnosing an ADAM or interactor gene-associated disorder or a
 CC respiratory disorder in a human subject, determining an ADAM or
 CC interactor gene pharmacogenetic profile in a human subject, identifying
 CC an orthologue of a human ADAM or interactor gene, treating an ADAM or
 CC interactor gene-associated disorder (or a respiratory disorder) by
 CC administering the pharmaceutical composition, a transgenic mouse (whose
 CC genome comprises an introduced null mutation in an endogenous gene that
 CC is orthologous to a human ADAM gene), making a homozygous transgenic
 CC knockout mouse, forming a crystal of the isolated polypeptide, a cell
 CC line comprising the isolated nucleic acid or alternate splice variant, a
 CC biochip comprising the isolated nucleic acid or alternate splice variant,
 CC an isolated nucleic acid probe or primer comprising at least 8 contiguous
 CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,
 CC identifying an ADAM or interactor gene ligand and an isolated nucleic
 CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or
 CC alternate splice variants, methods, kits and antibody/antibody fragment
 CC are useful for diagnosing and treating an ADAM or interactor gene-
 CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel
 CC disease. The present sequence is a primer used to sequence the regions
 CC surrounding polymorphisms in the above genes.
 XX

```
SQ Sequence 21 BP; 6 A; 0 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2210 GTTCAGATATGGGGATGTA 2229
    ||| ||||| ||||| |||||
DB 2 GTTCAGATATGGGGATGGA 21

RESULT 196
ADP45615/C
ID ADP45615 standard; DNA; 21 BP.
XX
AC ADP45615;
XX
XX
DT 26-AUG-2004 (first entry)
XX
DE PCR primer 2 used to genotype human MAP kinase MAPK10 polymorphism.
XX
KW breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
KW single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;
KW p54BSAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
KW c-Jun N-terminal kinase 3; stress activated protein kinase beta;
KW chromosome 4q22.1-q23.
XX
XX Homo sapiens.
OS
XX WO2004047623-A2.
PN
XX 10-JUN-2004.
PD
XX
XX 25-NOV-2003; 2003WO-US037948.
PF
XX 25-NOV-2002; 2002US-0429136P.
PR
XX 24-JUL-2003; 2003US-0490234P.
PR
XX (SEQU-) SEQUENOM INC.
PA
XX
XX
PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX WPI; 2004-441051/41.
DR
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUWA1 or GALE
PT regions which are associated with breast cancer in a nucleic acid sample
PT from a subject.
XX
XX Example 2; Page 74; 289pp; English.
PS
XX The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of one or
CC more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a subject at risk of
CC breast cancer, for early diagnosis, prevention and treatment of breast
CC cancer, possibly via gene therapy, as well as to analyse and predict a
CC response to a breast cancer treatment and in clinical drug trials. The
CC current sequence is that of a PCR primer of the invention which was used
CC to genotype human MAP kinase MAPK10 (JNK3;JNK3A;p493F12;p54BSAPK MAP
CC kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-Jun N-terminal kinase 3
CC ;stress activated protein kinase beta) gDNA which has been mapped to
CC chromosomal position 4q22.1-q23.
XX
XX Sequence 21 BP; 4 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2958 AACAAATGATACATGGGC 2977
    ||| ||||| ||||| |||||
```

```
DB 20 AAGAAAAATGTTAACATGGGC 1

RESULT 197
AAC73261
ID AAC73261 standard; DNA; 18 BP.
XX
AC AAC73261;
XX
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #48 used in multiplexing PCR/SBE assay.
XX
XX Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
XX Unidentified.
OS
XX WO200058516-A2.
PN
XX 05-OCT-2000.
PD
XX 27-MAR-2000; 2000WO-US008069.
XX
XX 26-MAR-1999; 99US-0126473P.
PR
XX 23-JUN-1999; 99US-0140359P.
PR
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
XX Pan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
XX Example 7; Page 52; 70pp; English.
PS
XX The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
XX Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1395 AGCAACAGCAGCAACAGC 1412
    ||| ||||| ||||| |||||
DB 1 AGCAACAGCAGCAACAGC 18

RESULT 198
AAF26668
ID AAF26668 standard; DNA; 18 BP.
XX
AC AAF26668;
XX
XX 09-SEP-2004 (revised)
DT 02-APR-2001 (first entry)
XX
XX Human Smad7 phosphorothioate antisense oligonucleotide SEQ ID NO:11.
DE
```

```

XX Human; Smad7; antisense oligonucleotide; phosphorothioate; inhibition;
KW antiinflammatory; cytostatic; infection; inflammation; tumour formation;
KW ss.
XX
XX Homo sapiens.
OS Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /mod_base
FT /note= "phosphorothioate linkages"
FT
XX
XX US6159697-A.
PN
XX
XX 12-DEC-2000.
PD
XX
XX 09-JAN-2000; 2000US-00487444.
PF
XX
XX 09-JAN-2000; 2000US-00487444.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Cowsett LM;
PI
XX WPI; 2001-070108/08.
XX
XX
XX Antisense compound capable of inhibiting the expression of human Smad7,
PT useful for preventing or delaying infection, inflammation or tumor
PT formation.
XX
XX Claim 1; Col 40; 33pp; English.
PS
XX
XX The present invention describes an antisense compound (I) of up to 30
CC nucleobases in length capable of inhibiting the expression of human
CC Smad7. (I) has antiinflammatory and cytostatic, and is a modulator of
CC Smad7 expression. (I) can be useful for inhibiting the expression of
CC human Smad7 in human cells or tissues, in vitro. (I) is commonly used as
CC a research reagent and in diagnostics for example, to elucidate the
CC function of particular genes. (I) is also useful for distinguishing
CC between functions of various members of a biological pathway and for
CC research use. (I) is also utilised for diagnostics, therapeutics,
CC prophylaxis and in kits. (I) is also useful prophylactically, e.g. to
CC prevent or delay infection, inflammation or tumour formation. AAF26667 to
CC AAF26706 represent human Smad7 antisense oligonucleotides from the
CC present invention
CC
CC Revised record issued on 09-SEP-2004 : Correction to feature table key
CC
XX
XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.4%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1406 CACAGCAGCAGCAGCAG 1423
QY | | | | | | | | | | | | | | | |
DB 1 CGACAGCAGCAGCAGCAG 18

RESULT 199
AAS13708
ID AAS13708 standard; DNA; 18 BP.
XX
XX AAS13708;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX Simple sequence repeat, SSR, #5.
DE
XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW gamma-amino-butyric acid B receptor; epileps; pain syndrome;
KW cereal profiling; grass profiling; seed batch purity testing.

```

```

XX Poae.
OS
XX NZ509193-A.
PN
XX
XX 25-MAY-2001.
PD
XX
XX 03-JAN-2001; 2001NZ-00509193.
PF
XX
XX 24-DEC-1999; 99AU-00004906.
PR
XX 04-MAY-2000; 2000AU-00007310.
XX
XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
PA (UYSC-) UNIV SOUTHERN CROSS.
PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
PA (UYAD-) UNIV ADELAIDE.
PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX
XX Forster JW, Jones ES;
PI
XX WPI; 2001-512563/56.
DR
XX
XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
PT core elements isolated from ryegrass and fescue, useful for selecting of
PT genes in grass or cereal breeding or profiling grass or cereal species
PT varieties.
XX
XX Claim 6; Page 51; 72pp; English.
PS
XX
XX The invention relates to a substantially purified or isolated nucleic
CC acid (I) from ryegrass or fescue species including a simple sequence
CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
CC 2-6 nucleotides in length. Also included are a nucleic acid primer
CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
CC library of ryegrass or fescue genomic DNA enriched for SSRs and
CC identifying clones in the library containing SSRs, a library of ryegrass
CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
CC a gene in grass or cereal breeding by identifying an SSR that is closely
CC associated with the gene such that the SSR and the gene are
CC preferentially co-inherited, and selecting for the SSR in the breeding, a
CC method for DNA profiling grass or cereal species varieties by assessing
CC variation between SSR varieties and testing the purity of grass or cereal
CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a ryegrass or fescue SSR
XX
XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.4%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1574 CAACAACAACAGCAGCAAA 1591
QY | | | | | | | | | | | | | | | |
DB 1 CAACAACAACAGCAGCAAA 18

RESULT 200.
ABA93493
ID ABA93493 standard; DNA; 18 BP.
XX
XX ABA93493;
AC
XX
XX 25-APR-2002 (first entry)
DT
XX
XX GAGA-B receptor 1a (gbl a) antisense oligonucleotide.
DE
XX Identification; gamma-amino-butyric acid; GABA; GABA-B receptor;
KW gamma-amino-butyric acid B receptor; epileps; pain syndrome;
KW antisense oligonucleotide; ss.

```

XX Homo sapiens.
OS Synthetic.
XX WO200198779-A2.
XX 27-DEC-2001.
XX 19-JUN-2001; 2001WO-CA000909.
XX 19-JUN-2000; 2000US-0212426P.
XX 24-APR-2001; 2001US-0285969P.
XX (MERI) MERCK FROSST CANADA & CO.
XX Ng G;
XX WPI; 2002-062650/08.
XX Identifying agonists of GABA(B) receptors, useful for treating epilepsy
XX and certain pain syndromes, comprises determining that the substance is
XX not an agonist of GABA(B) receptors with gb-1b or gb-1c subunits.
XX Example 7; Page 79; 142pp; English.
XX The present invention describes a method for identifying gb-1a subtype-
XX specific agonists of the gamma-amino-butyric acid B (GABA-B) receptor,
XX comprising determining the substance is an agonist of GABA-B receptors
XX with a gb-1a subunit, and is not an agonist of GABA-B receptors
XX comprising gb-1b or gb-1c subunits. The method can be used for
XX identifying agonists of GABA-B receptors which are heteromers of gb-1a
XX and gb2 subunits. The substances are useful for treating conditions such
XX as epilepsy, and pain syndromes. The method identifies substances that
XX are not agonists of GABA-A receptors, which exhibit more selectivity for
XX effector pathways and distinct mechanisms of action compared to other
XX compounds such as baclofen. The present sequence represents a GABA-B
XX receptor 1a (gb1a) antisense oligonucleotide, which is used in an example
XX from the present invention
XX Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 983 CACCAGCAGCAGCAGCAG 1000
DB 1 CACCAGCAGCAGCAGCAG 18
RESULT 201
ABZ81757
ID ABZ81757 standard; DNA; 18 BP.
XX
XX AC ABZ81757;
XX
XX 11-JUN-2003 (first entry)
XX
XX Huntington's disease exon 1 triplet repeat sequence.
XX
XX Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
XX gene therapy; ss.
XX Homo sapiens.
XX WO2003013437-A2.
XX
XX 20-FEB-2003.
XX
XX 07-AUG-2002; 2002WO-US025352.
XX
XX 07-AUG-2001; 2001US-0310757P.
XX 08-AUG-2001; 2001US-0310770P.
XX

PR 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX (UYDE) UNIV DELAWARE.
XX Kmiec EB, Parekh-Olmedo H;
XX WPI; 2003-256478/25.
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
XX least one mismatch with respect to the genetic sequence of the
XX Huntington's disease gene to be altered, useful for treating or
XX preventing Huntington's disease.
XX Example 1; Page 57; 133pp; English.
XX The present sequence is an example of a poly-glutamine triplet repeat
XX region found in exon 1 of the Huntington's disease (HD) gene. The
XX invention is based on the discovery that oligonucleotides can be designed
XX to target sequence alterations to the triplet repeat region of the HD
XX gene. Preferred oligonucleotides are single-stranded, have at least one
XX mismatch with respect to the HD gene region to be altered, and have
XX chemical modifications, or are chimeric RNA/DNA oligonucleotides. They
XX can be used for the treatment or prevention of HD
XX Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1394 CAGCAACAGCAGCAACAG 1411
DB 1 CAACACAGCAGCAGCAACAG 18
RESULT 202
ABZ81780
ID ABZ81780 standard; DNA; 18 BP.
XX
XX AC ABZ81780;
XX
XX 11-JUN-2003 (first entry)
XX
XX Huntington's disease gene mutated exon 1 region.
XX Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
XX gene therapy; mutant; ds.
XX Homo sapiens.
XX Synthetic.
XX Key mutation Location/Qualifiers
XX replace(5,A) /*tag= a
XX WO2003013437-A2.
XX
XX 20-FEB-2003.
XX
XX 07-AUG-2002; 2002WO-US025352.
XX
XX 07-AUG-2001; 2001US-0310757P.
XX 08-AUG-2001; 2001US-0310770P.
XX 08-AUG-2001; 2001US-0310889P.
XX 04-DEC-2001; 2001US-0337219P.
XX (UYDE) UNIV DELAWARE.
XX Kmiec EB, Parekh-Olmedo H;
XX WPI; 2003-256478/25.
XX

PT New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.
 XX
 PS Example 7; Fig 20; 133pp; English.
 XX
 CC The present sequence is that of a portion of a mutated glutamine (CAG)
 CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
 CC gene (see also AB281760). The triplet repeat region is mutated following
 CC treatment with single-stranded phosphorothioate-containing HD gene-
 CC targeted oligonucleotide HD35/52 (see AB281756). The second glutamine
 CC (CAG) repeat triplet is converted to CTG, creating a restriction fragment
 CC length polymorphism site that enables cleavage by PvuII. HD35/25 is an
 CC example of oligonucleotides of the invention for targeted alteration of
 CC the HD gene. Such oligonucleotides can be used for the treatment or
 CC prevention of HD
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CAGCTGCAGCAGCAGCAG 18

QY 1409 CAGCAGCAGCAGCAGCAG 1426
 Db ||||| ||||| ||||| ||||| |||||
 1 CAGCTGCAGCAGCAGCAG 18

RESULT 203
 AB281779
 ID AB281779 standard; DNA; 18 BP.
 AC AB281779;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE Huntington's disease gene mutated exon 1 region.
 XX
 KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 KW gene therapy; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mutation replace(5,A)
 FT /*tag= a
 XX
 PN WO2003013437-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 07-AUG-2002; 2002WO-US025352.
 XX
 PR 07-AUG-2001; 2001US-0310757P.
 PR 08-AUG-2001; 2001US-0310770P.
 PR 08-AUG-2001; 2001US-0310889P.
 PR 04-DEC-2001; 2001US-0337219P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Parekh-Olmedo H;
 XX
 DR WPI; 2003-256478/25.
 XX
 PT New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.
 XX
 PS Example 7; Fig 20; 133pp; English.
 XX

CC The present sequence is that of a portion of a mutated glutamine (CAG)
 CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
 CC gene (see also AB281760). The triplet repeat region is mutated following
 CC treatment with single-stranded phosphorothioate-containing HD gene-
 CC targeted oligonucleotide HD35/25 (see AB281755). The second glutamine
 CC (CAG) repeat triplet is converted to CTG, creating a restriction fragment
 CC length polymorphism site that enables cleavage by PvuII. HD35/25 is an
 CC example of oligonucleotides of the invention for targeted alteration of
 CC the HD gene. Such oligonucleotides can be used for the treatment or
 CC prevention of HD
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 CAGCTGCAGCAGCAGCAG 18

QY 1409 CAGCAGCAGCAGCAGCAG 1426
 Db ||||| ||||| ||||| ||||| |||||
 1 CAGCTGCAGCAGCAGCAG 18

RESULT 204
 ADP75262
 ID ADP75262 standard; DNA; 18 BP.
 XX
 AC ADP75262;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human ADAM19 gene exon X SSCP reverse primer.
 XX
 KW Human; SSCP; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2;
 KW ADAMTS2; a disintegrin and metalloprotease; neuroregulin 2; SNP;
 KW single nucleotide polymorphism;
 KW a disintegrin and metalloprotease with thrombospondin type 1 motif 2;
 KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder;
 KW single-strand conformation polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031594-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032700.
 XX
 PR 11-OCT-2001; 2001US-0328424P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
 PI Allen K;
 XX
 DR WPI; 2003-381712/36.
 XX
 PT New isolated nucleic acid or alternate splice variant, useful for
 PT diagnosing and treating a disintegrin and metalloprotease (ADAM) or
 PT interactor gene-associated disorder, e.g. asthma, atopy, obesity or
 PT inflammatory bowel disease.
 XX
 PS Claim 2; Page 124; 338pp; English.
 XX
 CC The invention relates to an isolated nucleic acid or alternate splice
 CC variant comprising a nucleotide sequence containing at least one of the
 CC single nucleotide polymorphisms given in the specification, a nucleotide
 CC sequence having at least 15 contiguous nucleotides of them, or
 CC complements of them. The genes are ADAM19 (a disintegrin and
 CC metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
 CC known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
 CC (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
 CC with thrombospondin type 1 motif 2, also known as gene 962). Also included
 CC are a vector comprising the isolated nucleic acid (or alternate splice

variant), a host cell containing the vector, an isolated polypeptide encoded by the novel nucleic acid (or alternate splice variant), an antibody or antibody fragment that binds to the polypeptide, an pharmaceutical compositions (comprising the nucleic acid or alternate splice variant, vector, polypeptide or antibody, and a carrier, excipient or diluent), a kit for detecting a disintegrin and metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated nucleic acid or alternate splice variant, antibody or antibody fragment, and at least one component to detect the hybridisation of the variant or the binding of the antibody to an ADAM gene amino acid sequence), a kit for detecting an interactor gene amino acid sequence (comprising the antibody or antibody fragment, and at least one component to detect the binding of the antibody to the interactor gene amino acid sequence), diagnosing an ADAM or interactor gene-associated disorder or a respiratory disorder in a human subject, determining an ADAM or interactor gene pharmacogenetic profile in a human subject, identifying an orthologue of a human ADAM or interactor gene, treating an ADAM or interactor gene-associated disorder (or a respiratory disorder) by administering the pharmaceutical composition, a transgenic mouse (whose genome comprises an introduced null mutation in an endogenous gene that is orthologous to a human ADAM gene), making a homozygous transgenic knockout mouse, forming a crystal of the isolated polypeptide, a cell line comprising the isolated nucleic acid or alternate splice variant, a biochip comprising the isolated nucleic acid or alternate splice variant, an isolated nucleic acid probe or primer comprising at least 8 contiguous nucleotides of the nucleic acid, an isolated antisense nucleic acid, identifying an ADAM or interactor gene ligand and an isolated nucleic acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or alternate splice variants, methods, kits and antibody/antibody fragment are useful for diagnosing and treating an ADAM or interactor gene-associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel disease. The present sequence is an SSCP (single-strand conformation polymorphism) primer used to analyse the above genes for the presence of polymorphisms.

Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1541 CAGCAGCAGCAGCAACAA 1558
||| ||||| ||||| |||||
Db 1 CAGGAGCAGCAGCAACAA 18

RESULT 205

ADN97298
ID ADN97298 standard; DNA; 18 BP.

AC ADN97298;

DT 01-JUL-2004 (first entry)

DE Primer of the invention #88.

KW DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
KW forensic identification; marijuana; primer; ss.

OS Synthetic.

FN WO2004008841-A2.

PD 29-JAN-2004.

PF 21-JUL-2003; 2003WO-US022887.

PR 19-JUL-2002; 2002US-0397179P.

PA (UVAR-) UNIV ARIZONA.

PA (KEIM/) KEIM P S.

PA (ZINN/) ZINNAMON K.

PI Keim PS, Zinnamon K;
XX WPI; 2004-143139/14.
XX New isolated nucleic acid for amplification of a short tandem repeat
PT located in DNA isolated from Cannabis sativa L species, useful for
PT forensic identification of marijuana or for linking a marijuana sample to
PT its plant source.
XX Disclosure; SEQ ID NO 165; 79pp; English.
XX The present invention relates to DNA fingerprinting for Cannabis Sativa
CC using short tandem repeat markers. The nucleic acid is useful for
CC forensic identification of marijuana or for linking a marijuana sample to
CC its plant source. The present sequence represents a primer of the
CC invention.
XX Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 984 ACCAGCAGCAGCACCAGC 1001
||| ||||| ||||| |||||
Db 1 AGCAGCAGCAGCACCAGC 18

RESULT 206

ADO26670/c
ID ADO26670 standard; DNA; 18 BP.

AC ADO26670;

DT 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:63.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

OS Synthetic.

FN WO2004042059-A1.

PD 21-MAY-2004.

PF 10-NOV-2003; 2003WO-AU001487.

PR 08-NOV-2002; 2002US-0425163P.

PA (UYQU) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-411519/38.

DR P-PSDB; ADO26671.

XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 63; 86pp; English.

XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism

of interest and organisms that are related to the organisms of interest;
 and (b) replacing the first codon with the synonymous codon to construct
 the synthetic polynucleotide. Also described: (1) a method for
 determining the phenotypic preference of a first codon in an organism of
 interest or its parts; (2) a synthetic polynucleotide constructed from
 the method above; (3) an organism of interest or part containing a
 synthetic polynucleotide constructed from the method above; (4) an
 organism of interest or part containing a synthetic construct that
 comprises a regulatory polynucleotide operably linked to a tandem repeat
 of a first codon fused in frame with a reporter polynucleotide that
 encodes a reporter protein, which produces, or is predicted to produce a
 selected phenotype or a phenotype of the same class as the selected
 phenotype in the organism or part; (5) a method of modulating the quality
 of a selected phenotype that is displayed by an organism of interest or
 part and that results from the expression of a parent polynucleotide that
 encodes the polypeptide; (6) a method of enhancing the quality of a
 selected phenotype that is displayed by an organism of interest or part
 and that results from the expression of a parent polynucleotide that
 encodes the polypeptide; and (7) a method of reducing the quality of a
 selected phenotype that is displayed by an organism of interest or part
 and that results from the expression of a parent polynucleotide that
 encodes the polypeptide. The method is useful for constructing a
 synthetic polynucleotide from which a polypeptide is producible to confer
 a selected phenotype to an organism of interest or part in a different
 quality than that conferred by a parent polynucleotide that encodes the
 same polypeptide. It is useful for modulating the quality of a selected
 phenotype displayed by an organism or part. The present sequence encodes
 a synthetic leader sequence, which is used in an example from the present
 invention.

XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACACAGCAACAA 1591
 Db 18 CAACAACACACAAACAA 1

RESULT 207

AD026722/c
 ID AD026722 standard; DNA; 18 BP.

XX AD026722;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic leader sequence encoding DNA SEQ ID NO:115.
 XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
 XX Synthetic.
 XX WO2004042059-A1.
 XX
 XX 21-MAY-2004.
 XX
 XX 10-NOV-2003; 2003WO-AU001487.
 XX
 XX 08-NOV-2002; 2002US-0425163P.
 XX (UQU) UNIV QUEENSLAND.
 XX
 XX Frazer IH;
 XX
 XX WPI; 2004-411519/38.
 XX P-PSDB; AD026723.
 XX
 XX Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 115; 86pp; English.
 XX

The present invention describes a method for constructing a synthetic
 polynucleotide from which a polypeptide is producible to confer a
 selected phenotype to an organism of interest or part in a different
 quality than that conferred by a parent polynucleotide that encodes the
 same polypeptide. The method comprises: (a) selecting a first codon of
 the parent polynucleotide for replacement with a synonymous codon, where
 the synonymous codon is selected on the basis that it exhibits a
 different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct;
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism of interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism of interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1575 AACAAACACAGCAACAA 1592
 Db 18 AACAAACACAAACAAACAA 1

RESULT 208

AD026640/c
 ID AD026640 standard; DNA; 18 BP.

XX AD026640;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic leader sequence encoding DNA SEQ ID NO:33.
 XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
 XX Synthetic.
 XX WO2004042059-A1.
 XX
 XX 21-MAY-2004.
 XX
 XX 10-NOV-2003; 2003WO-AU001487.

```
XX 08-NOV-2002; 2002US-0425163P.
PR (UYQU ) UNIV QUEENSLAND.
XX
XX Frazer IH;
XX
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26641.
XX
XX Constructing synthetic polynucleotide for modulating the quality of a
XX selected phenotype displayed by an organism comprises replacing a first
XX codon with a synonymous codon to construct the synthetic polynucleotide.
XX
XX Example 1; SEQ ID NO 33; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
XX polynucleotide from which a polypeptide is producible to confer a
XX selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. The method comprises: (a) selecting a first codon of
XX the parent polynucleotide for replacement with a synonymous codon, where
XX the synonymous codon is selected on the basis that it exhibits a
XX different phenotypic preference than the first codon in a comparison of
XX phenotypic preferences in test organisms or parts, where the test
XX organism are selected from organisms of the same species as the organism
XX of interest and organisms that are related to the organisms of interest;
XX and (b) replacing the first codon with the synonymous codon to construct
XX the synthetic polynucleotide. Also described: (1) a method for
XX determining the phenotypic preference of a first codon in an organism of
XX interest or its parts; (2) a synthetic polynucleotide constructed from
XX the method above; (3) an organism or interest or part containing a
XX synthetic polynucleotide constructed from the method above; (4) an
XX organism or interest or part containing a synthetic construct that
XX comprises a regulatory polynucleotide operably linked to a tandem repeat
XX of a first codon fused in frame with a reporter polynucleotide that
XX encodes a reporter protein, which produces, or is predicted to produce a
XX selected phenotype or a phenotype of the same class as the selected
XX phenotype in the organism or part; (5) a method of modulating the quality
XX of a selected phenotype that is displayed by an organism of interest or
XX part and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; (6) a method of enhancing the quality of a
XX synthetic polynucleotide from which a polypeptide is producible to confer
XX a selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. It is useful for modulating the quality of a selected
XX phenotype displayed by an organism or part. The present sequence encodes
XX a synthetic leader sequence, which is used in an example from the present
XX invention.
XX
XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1576 ACAACACAGCAACACACA 1593
XX ||||||| |||||||
XX Db 18 ACAACACACACACACACA 1
XX
XX RESULT 209
XX ADO26708
XX ID ADO26708 standard; DNA; 18 BP.
XX
XX AC ADO26708;
XX
```

12-AUG-2004 (first entry)

Synthetic leader sequence encoding DNA SEQ ID NO:101.

phenotype; phenotypic preference; phenotype modulation; leader; ds.

Synthetic.

WO2004042059-A1.

21-MAY-2004.

10-NOV-2003; 2003WO-AU001487.

08-NOV-2002; 2002US-0425163P.

(UYQU) UNIV QUEENSLAND.

Frazer IH;

WPI; 2004-411519/38.

F-PSDB; ADO26709.

Constructing synthetic polynucleotide for modulating the quality of a selected phenotype displayed by an organism comprises replacing a first codon with a synonymous codon to construct the synthetic polynucleotide.

Example 1; SEQ ID NO 101; 86pp; English.

The present invention describes a method for constructing a synthetic polynucleotide from which a polypeptide is producible to confer a selected phenotype to an organism of interest or part in a different quality than that conferred by a parent polynucleotide that encodes the same polypeptide. The method comprises: (a) selecting a first codon of the parent polynucleotide for replacement with a synonymous codon, where the synonymous codon is selected on the basis that it exhibits a different phenotypic preference than the first codon in a comparison of phenotypic preferences in test organisms or parts, where the test organism are selected from organisms of the same species as the organism of interest and organisms that are related to the organisms of interest; and (b) replacing the first codon with the synonymous codon to construct the synthetic polynucleotide. Also described: (1) a method for determining the phenotypic preference of a first codon in an organism of interest or its parts; (2) a synthetic polynucleotide constructed from the method above; (3) an organism or interest or part containing a synthetic polynucleotide constructed from the method above; (4) an organism or interest or part containing a synthetic construct that comprises a regulatory polynucleotide operably linked to a tandem repeat of a first codon fused in frame with a reporter polynucleotide that encodes a reporter protein, which produces, or is predicted to produce a selected phenotype or a phenotype of the same class as the selected phenotype in the organism or part; (5) a method of modulating the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide; (6) a method of enhancing the quality of a synthetic polynucleotide from which a polypeptide is producible to confer a selected phenotype to an organism of interest or part in a different quality than that conferred by a parent polynucleotide that encodes the same polypeptide. It is useful for modulating the quality of a selected phenotype displayed by an organism or part. The present sequence encodes a synthetic leader sequence, which is used in an example from the present invention.

Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.2e+02;

Query Match 0.4%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ACAACACAGCAACAA 1593
|||||
Db 1 ACAACACACACAA 18

RESULT 210
ADO26630
ID ADO26630 standard; DNA; 18 BP.
XX
AC ADO26630;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:23.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
XX 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26631.
XX
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
PS Example 1; SEQ ID NO 23; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that

CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 AACACACAGCAACAA 1592
|||||
Db 1 AACACACACACAA 18

RESULT 211
ADO26642
ID ADO26642 standard; DNA; 18 BP.
XX
AC ADO26642;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic leader sequence encoding DNA SEQ ID NO:35.
XX
KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
OS Synthetic.
XX
PN WO2004042059-A1.
XX
PD 21-MAY-2004.
XX
PF 10-NOV-2003; 2003WO-AU001487.
XX
PR 08-NOV-2002; 2002US-0425163P.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Frazer IH;
XX
DR WPI; 2004-411519/38.
DR P-PSDB; ADO26643.
XX
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
PS Example 1; SEQ ID NO 35; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that

comprises a regulatory polynucleotide operably linked to a tandem repeat of a first codon fused in frame with a reporter polynucleotide that encodes a reporter protein, which produces, or is predicted to produce a selected phenotype or a phenotype of the same class as the selected phenotype in the organism or part; (5) a method of modulating the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide; (6) a method of enhancing the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide; and (7) a method of reducing the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide. The method is useful for constructing a synthetic polynucleotide from which a polypeptide is producible to confer a selected phenotype to an organism of interest or part in a different quality than that conferred by a parent polynucleotide that encodes the same polypeptide. It is useful for modulating the quality of a selected phenotype displayed by an organism or part. The present sequence encodes a synthetic leader sequence, which is used in an example from the present invention.

Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACACACACACACACAA 1591
DB 1 CAACACACACACACACAA 18
|||||

RESULT 212
AAAX77030/c

ID AAAX77030 standard; DNA; 20 BP.

AC AAAX77030;

DT 10-AUG-1999 (first entry)

XX PCR primer for the Rad23 (HHR23B) gene.

XX PCR primer; proto-oncogene; oncogene; nucleic acid synthesis; ultrasound;
XX stress protein; repair protein; phenylketonuria; p53 tumour suppressor;
XX phenylalanine hydroxylase; IL-2 production; cancer; AIDS; haemophilia;
XX autoimmune disease; chronic viral infection; cystic fibrosis; therapy;
XX ss.

XX Synthetic.

OS Homo sapiens.

XX WO925385-A1.

PN 27-MAY-1999.

XX 11-NOV-1998; 98WO-US023843.

XX 17-NOV-1997; 97US-00971540.

XX (IMAR-) IMARX PHARM CORP.

XX Unger EC, McCreery T, Sadewasser D;

XX WPI; 1999-370731/31.

XX Increasing nucleic acid synthesis by ultrasonic treatment of cells.

XX Example 1; Page 108; 124pp; English.

XX This sequence represents a PCR primer for a proto-oncogene/oncogene, and
XX was used to test the method of the invention. The method is for
XX increasing synthesis of nucleic acid (I) in a cell by exposing it to

CC ultrasound, where (I) is: (a) an endogenous sequence (Ia) encoding a
CC stress or repair protein; or (b) an introduced exogenous sequence (Ib).
CC The method is specifically used therapeutically: (i) to treat
CC phenylketonuria (following introduction of (Ib) for phenylalanine
CC hydroxylase); (ii) to increase expression of the p53 tumour suppressor;
CC (iii) to increase production of IL-2, particularly associated with
CC natural killer cells; and (iv) for treating cancer by administering a
CC sequence antisense to initiation factor 3 and/or tRNA synthase. More
CC generally, (Ib) may include one or more genes or fragments, or even
CC complete chromosomes, for delivery (in vivo, in vitro or ex vivo) to
CC animal or plant cells for treating a very wide range of conditions, e.g.
CC acquired immune deficiency syndrome, autoimmune diseases, chronic viral
CC infections, haemophilia, cystic fibrosis, and cancer. Ultrasonic
CC treatment increases expression of (I) and increases uptake of (Ib),
XX particularly of 4-6 kb

SQ Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2000 TTGTCAAGGCCACCTCCA 2017
DB 18 TTGTCAAGGCCACCTCCA 1
|||||

RESULT 213

AAA66287

ID AAA66287 standard; DNA; 20 BP.

XX AAA66287;

DT 09-OCT-2000 (first entry)

XX Dog genomic marker oligonucleotide sequence SEQ ID NO:149.

XX Dog; genome; genomic marker; radiation hybrid map; identification;
XX chromosome location; gene marker; polymorphic microsatellite marker;
XX phenotype; behaviour; pedigree; ss.

XX Canis familiaris.

XX WO200029615-A2.

XX 25-MAY-2000.

XX 15-NOV-1999; 99WO-IB001907.

XX 13-NOV-1998; 98US-0108193P.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Galibert F, Andre C;

XX WPI; 2000-387821/33.

XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX or in genetic diseases and for studying dog pedigrees.

XX Claim 1; Page 59; 87pp; English.

XX The present invention describes a radiation hybrid map of the dog (Canine
XX familiaris) genome comprising the genome location of a marker selected
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX identifying and localising dog genes, since it covers approximately 80 %
XX of the dog genome and provides a dense map integrating different types
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX (or complementary sequences) are especially useful to identify genes
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX morbid genes, to analyse diseases and identify implicated genes in such
XX diseases and their alleles, and to study dog pedigrees. They may also be

CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases
 CC
 SQ Sequence 20 BP; 7 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1426
 |||||
 Db 1 CAGCAGCAGCAGCAGCAG 18

RESULT 214
 AAH56692/c
 ID AAH56692 standard; DNA; 20 BP.
 XX
 AC AAH56692;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:340.
 XX
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 XX
 OS Streptococcus pyogenes.
 XX
 XX WO200136625-A2.
 XX
 XX 25-MAY-2001.
 XX
 PF 20-NOV-2000; 2000WO-CA001347.
 XX
 XX 18-NOV-1999; 99US-0166249P.
 XX
 XX (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 XX Wright JA, Young AH, Dugourd D;
 PI WPI; 2001-355633/37.
 XX
 XX
 XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
 PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 XX
 PS Claim 3; Page 50; 110pp; English.
 XX
 XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to

CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1466 CAGCAGCAGCAGCAGCAG 1483
 |||||
 Db 20 CAGCAGCAGCAGCAGCAG 3

RESULT 215
 ABK30537/c
 ID ABK30537 standard; DNA; 20 BP.
 XX
 AC ABK30537;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human glioma-associated oncogene-1 antisense oligonucleotide ISIS 124869.
 XX
 KW Human; glioma-associated oncogene-1 associated disease; infection;
 KW inflammation; tumour formation; cytostatic; antiinflammatory; antisense;
 KW phosphorothioate; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6329203-B1.
 XX
 XX 11-DEC-2001.
 XX
 PF 08-SEP-2000; 2000US-00657042.
 XX
 XX 08-SEP-2000; 2000US-00657042.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Wyatt J;
 PI WPI; 2002-138363/18.
 XX
 XX Novel antisense compounds targeted to nucleic acids encoding glioma-
 PT associated oncogene-1, for modulating the gene expression and treating
 PT diseases associated with expression of the oncogene in humans.
 XX
 PS Example 15; Col 45-46; 43pp; English.
 XX
 XX The present invention relates to antisense compounds and methods for
 CC modulating the expression of human glioma-associated oncogene-1. The
 CC antisense compounds, particularly antisense oligonucleotides, target and
 CC inhibit the expression of human glioma-associated oncogene-1. The
 CC antisense compounds are useful for inhibiting the expression of human
 CC glioma-associated oncogene-1 in human cells or tissues and for treating
 CC an animal, particularly a human suspected of having or being prone to a
 CC disease or condition associated with expression of glioma-associated
 CC oncogene-1. The compounds are useful for diagnostics, therapeutics and as
 CC research reagent, e.g. prophylactically to prevent or delay infection,
 CC inflammation or tumour formation. The antisense compounds are safely and
 CC effectively administered to humans. ABK30509-ABK30586 represent the
 CC antisense oligonucleotides of the invention which comprise a
 CC phosphorothioate backbone
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 GCAGCAGCACCAGCAGCA 993
DB 19 GCAGCAGCTCCAGCAGCA 2

RESULT 216
ACC46964

ID ACC46964 standard; DNA; 20 BP.
XX
AC ACC46964;
XX
DT 05-JUN-2003 (first entry)
XX
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:61.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"

XX WO200297133-A1.
PN
XX
XX 05-DEC-2002.
PD
XX
XX 21-MAY-2002; 2002WO-US016135.
PF
XX
XX 25-MAY-2001; 2001US-00865866.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Bennett CF, Wyatt JR;
PI
XX
XX WPI; 2003-140495/13.
DR
XX
XX

XX New compound that hybridizes with and inhibits the expression of
PT Phospholipase A2, group IIA, useful for preparing a composition for
PT treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX
PS Example 15; Page 87; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridises with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with phospholipase A2, group IIA
CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
CC antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents a human phospholipase A2 group IIA (synovial)
CC chimeric phosphorothioate antisense oligonucleotide, which is used in an

CC example from the present invention
XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2556 TGACGTCTGCAGGAGTCC 2573
DB 3 TGACTTCTGCAGGAGTCC 20

RESULT 217
AAD56488/C

ID AAD56488 standard; DNA; 20 BP.
XX
AC AAD56488;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 11.
XX
KW EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;
KW epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;
KW Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;
KW memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;
KW amyotrophic lateral sclerosis; attention deficit disorder; depression;
KW injury; human; RT; reverse transcription; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO2003040304-A2.
FN
XX
PD 15-MAY-2003.
XX
XX 11-NOV-2002; 2002WO-IB004930.
PF
XX
XX C9-NOV-2001; 2001US-0345206P.
PR
XX
XX 02-JUL-2002; 2002US-0393272P.
PR
XX
XX (NEUR-) NEURONOVA AB.
PA
XX
XX Holmberg J, Frisen J;
PI
XX
XX WPI; 2003-441543/41.
DR
XX
XX

XX Alleviating a symptom of a disease or disorder of the nervous system by
PT administering a modulator of neural stem or neural progenitor cell
PT activity in vivo to a patient.
XX
XX
PS Example 6; Page 54; 93pp; English.

XX The invention relates to a method for alleviating a symptom of a disease
CC or disorder of nervous system which involves administering a modulator to
CC modulate an activity of a neural stem cell or a neural progenitor cell in
CC vivo to a patient suffering from the disease or disorder of the nervous
CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5
CC or an interaction between EphA7 and ephrin-A2). The method is useful for
CC alleviating a symptom of a disease or disorder of the nervous system,
CC e.g., drug and alcohol abuse, neurological traumas, or neurodegenerative,
CC neural stem cell, neural progenitor, ischaemic, affective,
CC neuropsychiatric or learning and memory disorders, such as Parkinson's
CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,
CC cancer-related lateral sclerosis, ischaemic stroke, spinal cord injury or
CC cancer-related brain/spinal cord injury, schizophrenia, psychoses,
CC depression, bipolar depression/disorder, anxiety syndromes/ disorders,
CC phobias, stress and related syndromes, cognitive function disorders,
CC aggression, obsessive compulsive behaviour syndromes, multi-infarct
CC dementia, seasonal mood disorder, Lewy body dementia, borderline
CC personality disorder, cerebral palsy, age related/geriatric dementia,
CC epilepsy and injury related to epilepsy, spinal cord injury, brain
CC injury, trauma related brain/spinal cord injury, anticancer treatment

CC related brain/spinal cord tissue injury, infection and inflammation
 CC related brain/spinal cord injury, environmental toxin related brain/
 CC spinal cord injury, multiple sclerosis, autism, attention deficit
 CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
 CC to the retina or sleep disorders. The invention is also used in gene
 CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
 CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
 CC illustrate the method of the invention
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1407 AACAGCAGCAGCAGCAGC 1424
 DB 19 AACAGCAGGAGCAGCAGC 2
 RESULT 218
 AAD56486/C
 ID AAD56486 standard; DNA; 20 BP.
 AC AAD56486;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 9.
 XX
 KW EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;
 KW epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;
 KW Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;
 KW memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;
 KW amyotrophic lateral sclerosis; attention deficit disorder; depression;
 KW injury; human; RT; reverse transcription; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040304-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 11-NOV-2002; 2002WO-IB004930.
 XX
 PR 09-NOV-2001; 2001US-0345206P.
 PR 02-JUL-2002; 2002US-0393272P.
 XX
 PA (NEUR-) NEURNOVA AB.
 XX
 PI Holmberg J, Friese J;
 XX
 DR WPI; 2003-441543/41.
 XX
 PT Alleviating a symptom of a disease or disorder of the nervous system by
 PT administering a modulator of neural stem or neural progenitor cell
 PT activity in vivo to a patient.
 XX
 PS Example 6; Page 54; 93pp; English.
 XX
 CC The invention relates to a method for alleviating a symptom of a disease
 CC or disorder of nervous system which involves administering a modulator to
 CC modulate an activity of a neural stem cell or a neural progenitor cell in
 CC vivo to a patient suffering from the disease or disorder of the nervous
 CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5
 CC or an interaction between EphA7 and ephrin-A2). The method is useful for
 CC alleviating a symptom of a disease or disorder of the nervous system,
 CC e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,
 CC neural stem cell, neural progenitor, ischaemic, affective,
 CC neuropsychiatric or learning and memory disorders, such as Parkinson's
 CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,
 CC amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or
 CC cancer-related brain/spinal cord injury, schizophrenia, psychoses,

CC depression, bipolar depression/disorder, anxiety syndromes/ disorders,
 CC phobias, stress and related syndromes, cognitive function disorders,
 CC aggression, obsessive compulsive behaviour syndromes, multi-infarct
 CC dementia, seasonal mood disorder, Lewy body dementia, borderline
 CC personality disorder, cerebral palsy, age related/geriatric dementia,
 CC epilepsy and injury related to epilepsy, spinal cord injury, brain
 CC injury, trauma related brain/spinal cord injury, anticancer treatment
 CC related brain/spinal cord tissue injury, infection and inflammation
 CC related brain/spinal cord injury, environmental toxin related brain/
 CC spinal cord injury, multiple sclerosis, autism, attention deficit
 CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
 CC to the retina or sleep disorders. The invention is also used in gene
 CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
 CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
 CC illustrate the method of the invention
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1407 AACAGCAGCAGCAGCAGC 1424
 DB 19 AACAGCAGGAGCAGCAGC 2
 RESULT 219
 ADP75418
 ID ADP75418 standard; DNA; 20 BP.
 XX
 AC ADP75418;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human NRG2 gene exon 1 reverse sequencing primer #4.
 XX
 KW Human; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
 KW a disintegrin and metalloprotease; neuroregulin 2; SNP;
 KW single nucleotide polymorphism;
 KW a disintegrin and metalloprotease with thrombospondin type motif 2;
 KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031594-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032700.
 XX
 PR 11-OCT-2001; 2001US-0328424P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
 PI Allen K;
 XX
 DR WPI; 2003-381712/36.
 XX
 CC New isolated nucleic acid or alternate splice variant, useful for
 CC diagnosing and treating a disintegrin and metalloprotease (ADAM) or
 CC interactor gene-associated disorder, e.g. asthma, atopy, obesity or
 CC inflammatory bowel disease.
 XX
 PS Claim 2; Page 129; 339pp; English.
 XX
 CC The invention relates to an isolated nucleic acid or alternate splice
 CC variant comprising a nucleotide sequence containing at least one of the
 CC single nucleotide polymorphisms given in the specification, a nucleotide
 CC sequence having at least 15 contiguous nucleotides of them, or
 CC complements of them. The genes are ADAM19 (a disintegrin and
 CC metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also

CC known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
 CC (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
 CC with thrombospondin type1 motif 2, also known as gene 962). Also included
 CC are a vector comprising the isolated nucleic acid (or alternate splice
 CC variant), a host cell containing the vector, an isolated polypeptide
 CC encoded by the novel nucleic acid (or alternate splice variant), an
 CC antibody or antibody fragment that binds to the polypeptide,
 CC pharmaceutical compositions (comprising the nucleic acid or alternate
 CC splice variant, vector, polypeptide or antibody, and a carrier,
 CC excipient or diluent), a kit for detecting a disintegrin and
 CC metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
 CC nucleic acid or alternate splice variant, antibody or antibody fragment,
 CC and at least one component to detect the hybridisation of the variant or
 CC the binding of the antibody to an ADAM gene amino acid sequence), a kit
 CC for detecting an interactor gene amino acid sequence (comprising the
 CC antibody or antibody fragment, and at least one component to detect the
 CC binding of the antibody to the interactor gene amino acid sequence),
 CC diagnosing an ADAM or interactor gene-associated disorder or a
 CC respiratory disorder in a human subject, determining an ADAM or
 CC interactor gene pharmacogenetic profile in a human subject, identifying
 CC an orthologue of a human ADAM or interactor gene, treating an ADAM or
 CC interactor gene-associated disorder (or a respiratory disorder) by
 CC administering the pharmaceutical composition, a transgenic mouse (whose
 CC genome comprises an introduced null mutation in an endogenous gene that
 CC is orthologous to a human ADAM gene), making a homozygous transgenic
 CC knockout mouse, forming a crystal of the isolated polypeptide, a cell
 CC line comprising the isolated nucleic acid or alternate splice variant, a
 CC biochip comprising the isolated nucleic acid or alternate splice variant,
 CC an isolated nucleic acid probe or primer comprising at least 8 contiguous
 CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,
 CC identifying an ADAM or interactor gene ligand and an isolated nucleic
 CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or
 CC alternate splice variants, methods, kits and antibody/antibody fragment
 CC are useful for diagnosing and treating an ADAM or interactor gene-
 CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel
 CC disease. The present sequence is a primer used to sequence the regions
 CC surrounding polymorphisms in the above genes.

XX SQ Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 844 TTCAGTCCCTCAGAGCCA 861
 Db 1 TTCAGACCTCAGAGCCA 18

RESULT 220
 ADH65705/C
 ID ADH65705 standard; DNA; 20 BP.

XX AC ADH65705;

XX DT 25-MAR-2004 (first entry)

XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #2539.

XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX OS Homo sapiens.

XX PN WO2003099215-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016084.

XX PF 20-MAY-2002; 2002US-0381857P.

XX PA (PHAA) PHARMACIA CORP.
 XX PI Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.

XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.

XX Claim 4; SEQ ID NO 2539; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity, The
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 465 TGGATGCCCAATGACCC 482

Db 19 TGGATGCCCAATGACCC 2

RESULT 221

ADN06173/C

ID ADN06173 standard; DNA; 20 BP.

XX AC ADN06173;

XX DT 17-JUN-2004 (first entry)

XX DE Human SPS2 specific antisense oligonucleotide, ISIS 138242.

XX KW Selenophosphate synthetase 2; SPS2; rheumatoid arthritis; infection;
 KW inflammation; tumour; antisense therapy; human; antisense;
 KW phosphorothioate backbone; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..20

XX /*tag= b

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone in which all cytidines
 are 5-methylcytidines"

XX modified_base 1..5

XX /*tag= a

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotides"

XX modified_base 16..20

XX /*tag= c

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotides"

XX US2004002151-A1.

XX 01-JAN-2004.

XX PF 28-JUN-2002; 2002US-00186157.

XX PF 28-JUN-2002; 2002US-00186157.

XX PA (ISIS-) ISIS PHARM INC.
 XX PI Watt AT, Freier SM;
 XX XX WPI; 2004-070740/07.
 XX DR
 XX XX New antisense oligonucleotides for modulating selenophosphate synthetase
 PT 2 (SPS2) expression, useful for diagnosing, preventing or treating
 PT conditions associated with SPS2, e.g. rheumatoid arthritis, inflammation
 PT or tumors.
 XX XX
 XX PS Example 15; SEQ ID NO 17; 47pp; English.
 XX XX The invention relates to antisense compounds, compositions and methods
 CC for modulating the expression of selenophosphate synthetase 2 (SPS2). The
 CC composition comprises antisense oligonucleotides targeted to SPS2 gene.
 CC The antisense oligonucleotide is useful for modulating the expression of
 CC SPS2 in cells or tissues to treat diseases associated with their
 CC expression, e.g. rheumatoid arthritis, infections, inflammation or
 CC tumours. It is also used for diagnostics, prophylaxis, or as research
 CC reagents or kits. The antisense oligonucleotide is useful in antisense
 CC therapy. The present sequence is an antisense oligonucleotide targeted to
 CC human SPS2 DNA. This sequence is used in the exemplification of the
 CC invention.
 XX XX
 XX SQ Sequence 20 BP; 4 A; 9 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 738 CGGCTTGACTCAGGCCC 755
 DB 18 CGGCTTGACTCTGGCC 1
 RESULT 222
 ABL46975
 ID ABL46975 standard; RNA; 17 BP.
 AC ABL46975;
 XX 27-JUN-2003 (first entry)
 DT
 XX Human GRID zinzyme substrate oligonucleotide #59.
 DE
 XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX Homo sapiens.
 OS
 XX WO200162911-A2.
 FN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-US005957.
 PF
 XX 24-FEB-2000; 2000US-0184594P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 PA
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550089/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 72; 108pp; English.

XX CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX XX
 XX SQ Sequence 17 BP; 5 A; 7 C; 4 G; 0 T; 1 U; 0 Other;
 Query Match 0.4%; Score 16; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 975 TGCAGCAGCAGCAGCA 990
 DB 2 UGCAGCAGCAGCAGCA 17
 RESULT 223
 ABZ81758
 ID ABZ81758 standard; DNA; 17 BP.
 XX
 XX AC ABZ81758;
 XX 11-JUN-2003 (first entry)
 DT
 XX Huntington's disease exon 1 triplet repeat sequence.
 DE
 XX Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 KW Gene therapy; ss.
 KW Homo sapiens.
 OS
 XX WO2003013437-A2.
 FN
 XX 20-FEB-2003.
 PD
 XX 07-AUG-2002; 2002WO-US025352.
 PF
 XX 07-AUG-2001; 2001US-0310757P.
 PR
 XX 08-AUG-2001; 2001US-0310770P.
 PR
 XX 08-AUG-2001; 2001US-0310889P.
 PR
 XX 04-DEC-2001; 2001US-0337219P.
 PR
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmiec EB, Parekh-Olmedo H;
 PI WPI; 2003-256478/25.
 XX
 XX New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.
 XX
 XX Example 2; Page 61; 133pp; English.
 PS
 XX The present sequence is an example of a poly-glutamine triplet repeat
 CC region found in exon 1 of the Huntington's disease (HD) gene. In an
 CC example from the invention, neuronal PC12 cells were engineered to
 CC include an HD gene exon 1 containing this sequence. These cells were used
 CC to demonstrate the ability of a single-stranded, phosphorothioate-
 CC modified oligonucleotide, HDA37/53 (see ABZ81736) having a mismatch with
 CC respect to the HD gene, to convert a CAG triplet to CTG in HD gene exon
 CC 1, and to reduce the formation of Huntington's protein (huntingtin)
 CC aggregates. HDA37/53 is an example of oligonucleotides of the invention
 CC that target sequence alterations to the triplet repeat region of the HD
 CC gene, and which can be used for the treatment or prevention of HD
 XX
 XX SQ Sequence 17 BP; 9 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

```

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1398 AACGACGACGACGACG 1413
Db 1 AACGACGACGACGACG 16

RESULT 224
ADC37824
ID ADC37824 standard; DNA; 17 BP.
AC ADC37824;
XX
XX 18-DEC-2003 (first entry)
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:173.
XX human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 173; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
XX Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1402 GCAGCAACGACGACG 1417
Db 1 GCAGCAACGACGACG 16

RESULT 225
ADC37817
ID ADC37817 standard; DNA; 17 BP.
AC ADC37817;
XX
XX 18-DEC-2003 (first entry)
DE
```

```

XX
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:166.
XX human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 166; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
XX Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAG 1444
Db 2 GCAGCAGCAGCAACAG 17

RESULT 226
ADM54298
ID ADM54298 standard; mRNA; 17 BP.
XX
XX ADM54298;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Human GRID mRNA substrate sequence #608.
DE
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; ambarzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
XX Homo sapiens.
OS
XX US2003134806-A1.
XX
XX 17-JUL-2003.
PD
XX 23-FEB-2001; 2001US-00792818.
XX
XX 10-FEB-2000; 2000US-0181594P.
XX
```


CC polynucleotide and a reference sequence. It is useful for determining the
CC presence of a mutation in a region of interest in a polynucleotide and is
CC also useful for genotyping. The present sequence is an allelic
CC oligonucleotide used in polynucleotide sequence detection.

XX Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGC 1424
| | | | | | | | | | | | | | | | | |
Db 1 CAGCAGCAGCAGCAGC 16

RESULT 229
AAH57033/C

ID AAH57033 standard; DNA; 20 BP.

XX AC AAH57033;

DT 10-SEP-2001 (first entry)

XX Human oestrogen receptor alpha search PCR primer 58.

XX Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; PCR primer; probe; ss.

XX Homo sapiens.

XX WO2000142307-A1.

XX 14-JUN-2001.

XX 01-DEC-2000; 2000WO-JP008553.

XX 07-DEC-1999; 99JP-00348022.

XX 27-DEC-1999; 99JP-00370667.

XX 07-JUL-2000; 2000JP-00207011.

XX 21-JUL-2000; 2000JP-00320508.

XX 02-AUG-2000; 2000JP-00234053.

XX 03-AUG-2000; 2000JP-00235460.

XX 03-AUG-2000; 2000JP-00235461.

XX 03-AUG-2000; 2000JP-00235463.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX Saito K, Ohe N, Satoh H;

XX WPI; 2001-367866/38.

XX Ligand dependent transcriptional factors, nucleic acids encoding them and
XX cells comprising them and a specified reporter gene, useful for screening
XX agents for the treatment of breast cancer.
XX Example 9; Page 226; 276pp; English.
XX The present invention relates to ligand dependent transcriptional factors
XX including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
XX receptor protein (GR), mineralocorticoid receptor protein (MR),
XX peroxisome proliferator-activated receptor protein (PPAR), progesterone
XX receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
XX receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
XX acids encoding them and cells comprising them and a specified reporter
XX gene for the ligand dependent transcriptional factor. These proteins are
XX useful in the modulation of ligand dependent transcriptional factor
XX activity. The cells, mutant ERalpha and the polynucleotide encoding it
XX may be used in assays for qualitatively analysing an activity for

CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer

XX Sequence 20 BP; 1 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 986 CAGCAGCAGCAGCAGC 1001
| | | | | | | | | | | | | | | | | |
Db 18 CAGCAGCAGCAGCAGC 3

RESULT 230
ABS73433/C

ID ABS73433 standard; DNA; 20 BP.

XX AC ABS73433;

XX 03-DEC-2002 (first entry)

XX Chimeric phosphorotioate oligonucleotide #14.

XX Human; glioma-associated oncogene-2; antisense compound; infection;
KW inflammation; tumour formation; antiinflammatory; antitumour;
KW inhibitor of human glioma-associated oncogene-2 expression;
KW antisense gene therapy; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

OS Chimeric.

XX US6440739-B1.

XX 27-AUG-2002.

XX 17-JUL-2001; 2001US-00907843.

XX 17-JUL-2001; 2001US-00907843.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Freier SM;

XX WPI; 2002-697096/75.

XX Novel antisense compound that hybridizes and inhibits nucleic acid
XX encoding human glioma-associated oncogene-2, useful for treatment of
XX diseases associated with human glioma-associated oncogene-2.

XX Example 15; Col 45; 43pp; English.

XX The present invention relates to a new antisense compound targeted to
XX human glioma-associated oncogene-2. The invention is useful for
XX inhibiting the expression of human glioma-associated oncogene-2 in cells
XX or tissues. The invention is also useful for treatment of diseases
XX associated with human glioma-associated oncogene-2. The invention is
XX further useful for diagnostics, therapeutics, prophylaxis, as research
XX reagents and kits, for distinguishing functions of various members of a
XX biological pathway, and in antisense gene therapy. The invention is also
XX useful prophylactically, e.g. to prevent or delay infection,
XX inflammation or tumour formation. The present nucleic acid sequence
XX represents an oligonucleotide that was used in the methods of the
XX invention to inhibit human glioma-associated oncogene-2

XX Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAAC 1442
 Db 17 CAGCAGCAGCAGCAAC 2

RESULT 231
 AA82617/c
 ID AA82617 standard; DNA; 19 BP.
 XX AC AA82617;
 XX 04-DEC-2000 (first entry)
 XX cdk2 ribozyme binding site #54.
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; reestenosis; ss.
 XX Mammalia.
 XX WO200032765-A2.
 XX 08-JUN-2000.
 XX 06-DEC-1999; 99WO-US028772.
 XX 04-DEC-1998; 98US-0110954P.
 XX (IMMU-) IMMUSOL INC.
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX Disclosure; Page 49; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATAGC 948
 Db 19 AGCAGCTGGAACAGATAGC 1

RESULT 232
 AAH57779/c
 ID AAH57779 standard; DNA; 19 BP.
 XX AC AAH57779;
 XX 10-SEP-2001 (first entry)
 XX Cell-cycle dependent kinase cdk2 ribozyme binding site SEQ ID NO:203.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200130362-A2.
 XX 03-MAY-2001.
 XX 26-OCT-2000; 2000WO-US029500.
 XX 26-OCT-1999; 99US-0161532P.
 XX (IMMU-) IMMUSOL INC.
 XX Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX Example 1; Page 86; 408pp; English.
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATAGC 948
 Db 19 AGCAGCTGGAACAGATAGC 1

RESULT 233
 ADQ62508
 ID ADQ62508 standard; RNA; 19 BP.
 XX AC ADQ62508;
 XX 09-SEP-2004 (first entry)
 XX Anti-TOP2A siRNA SEQ ID NO:2211.
 DE
 XX

KW	ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW	RNA interference.
XX	
OS	Synthetic.
XX	
PN	WO2004045543-A2.
XX	
PD	03-JUN-2004.
XX	
XX	14-NOV-2003; 2003WO-US036787.
PF	
XX	
XX	14-NOV-2002; 2002US-0426137P.
PR	
PR	10-SEP-2003; 2003US-0502050P.
XX	
PA	(DHAR-) DHARMACON INC.
XX	
XX	Anastasia K, Angela R, Devin L, William M, Stephen S;
PI	
XX	WPI; 2004-420527/39.
DR	
XX	
PT	Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT	by selecting a target gene and measuring the functionality of the
PT	nucleotide sequences that are complementary to a stretch of nucleotides
PT	of the target sequence.
XX	
XX	Example 12; SEQ ID NO 2211; 199pp; English.
PS	
XX	
CC	The invention relates to a novel method for selecting siRNA (short
CC	interfering RNA) comprising selecting an siRNA molecule of 19-25
CC	nucleoside bases by selecting a target gene and measuring the
CC	functionality of sequences of 19-25 nucleotides in length that are
CC	substantially complementary to a stretch of nucleotides of the target
CC	sequence, where the functionality is dependent upon non-target specific
CC	criteria. Also claimed are methods for gene-silencing, developing an
CC	siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC	functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC	effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC	siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC	sequence consisting of GGGAGAUAGUGAAGAU; GAAGUACUCCAUUAUAG;
CC	GUACGACACCGGAGUA; AGAUAGUGAUGAUGACAU; UGAAGACUCUGCAGUUAU;
CC	CAUGCGGUCUGUUUAU; UGGCGCCUCUUGUUAUU; GAGAUGUGAUGAAGUACA;
CC	GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCAGUUAU. The siRNA molecule
CC	comprises a sense strand and an anti-sense strand. The siRNA molecule
CC	comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC	pairs. The kit comprises at least two siRNA, comprising a first optimised
CC	siRNA and a second optimised siRNA. The method is useful in selecting
CC	siRNA for generating a gene silencing reagent. The present sequence is
CC	used in the exemplification of the invention.
XX	
SQ	Sequence 19 BP; 8 A; 2 C; 5 G; 0 T; 4 U; 0 Other;
	Query Match 0.4%; Score 15.8; DB 1; Length 19;
	Best Local Similarity 73.7%; Pred. No. 1.7e+02;
	Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0
Qy	1149 CGAAGTAATGGCTAACTA 1167
	: :
Db	1 CGAAGGAUGGUUACUA 19
RESULT 234	
ABZ81777/c	
ID	ABZ81777 standard; DNA; 30 BP.
XX	
AC	ABZ81777;
XX	
XX	
DT	11-JUN-2003 (first entry)
XX	
DE	Huntington's disease gene mutated exon 1 region.
XX	
KW	Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
XX	gene therapy; mutant; ds.
XX	

XX PD 29-OCT-2002.
 XX PF 31-DEC-1999; 99US-00475947.
 XX PR 31-DEC-1999; 99US-00475947.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX DR WPI; 2003-208818/20.
 XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
 XX PT understanding or treating genetic disease, comprises detecting tandem
 XX PT repeats in a target coding sequence and scoring the repeats for
 XX PT polymorphic probability.
 XX PS Example; Col 1089; 588pp; English.
 XX CC The invention discloses a method for identifying a candidate polymorphic
 XX CC repeat within a coding sequence (expressed sequence tag, EST), which
 XX CC comprises detecting tandem repeats in a target coding sequence, scoring
 XX CC the repeats for polymorphic probability and generating a dataset
 XX CC correlating the repeats with polymorphic probability to identify a
 XX CC candidate polymorphic repeat. The computational methods (polymorphic
 XX CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 XX CC useful for identifying and detecting candidate polymorphic repeats in
 XX CC human genes, which can be used to understand, treat or eliminate genetic
 XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
 XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 XX CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 XX CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 XX CC the polymorphic repeats identified for a search of human ESTs
 XX SQ Sequence 33 BP; 11 A; 10 C; 11 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.6; DB 1; Length 33;
 Best Local Similarity 70.0%; Pred. No. 5.2e+02;
 Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1925 CAGCAACTTCTTCTCCAGCAGATGCTG 1954
 Db 30 CTGCTACTGCTGCTGCTGCTGCTGCTG 1
 RESULT 236
 AAX72851/c
 ID AAX72851 standard; RNA; 17 BP.
 XX AC AAX72851;
 XX DT 28-JUL-1999 (first entry)
 XX DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #284.
 XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 XX KW foetal liver kinase 1; ss.
 XX OS Mus sp.
 XX PN WO9715662-A2.
 XX PD 01-MAY-1997.
 XX PF 25-OCT-1996; 96WO-US017480.
 XX PR 26-OCT-1995; 95US-0005974P.
 XX PR 11-JAN-1996; 96US-00584040.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (CHIR) CHIRON CORP.
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX XX WPI; 1997-259017/23.
 XX DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 XX PT rheumatoid arthritis, etc., in a human patient.
 XX PS Claim 4; Page 131; 218pp; English.
 XX CC The present invention describes nucleic acid molecules which modulate the
 XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 XX CC receptors of vascular endothelial growth factor (VEGF). A patient
 XX CC (preferably human) having a condition associated with the level of the
 XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 XX CC treated by administering the nucleic acid molecule or the expression
 XX CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 XX CC of nucleic acid molecules from the present invention
 XX SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 326 TTGCTATGAGCCCAAGC 342
 Db 17 TTGCTGTGAGCCAAGC 1
 RESULT 237
 AAV97395
 ID AAV97395 standard; RNA; 17 BP.
 XX AC AAV97395;
 XX DT 17-MAR-1999 (first entry)
 XX DE Human EGF-R target sequence nucleotide position 1455.
 XX KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 XX KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 XX KW cancer; genetic drift; detection; mutation; ss.
 XX OS Homo sapiens.
 XX PN WO9833893-A2.
 XX PD 06-AUG-1998.
 XX PF 14-JAN-1998; 98WO-US000730.
 XX PR 31-JAN-1997; 97US-0036476P.
 XX PR 04-DEC-1997; 97US-00985162.
 XX XX (RIBO-) RIBOZYME PHARM INC.
 XX PA (UYAS-) UNIV ASTON.
 XX PI Akhtar S, Fell P, Mcswiggen JA;
 XX XX WPI; 1998-437449/37.
 XX DR Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 XX PT growth factor receptor, useful for inhibiting cell proliferation and for
 XX PT treating cancers.
 XX PS Claim 5; Page 71; 109pp; English.

XX The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX
 SQ Sequence 17 BP; 8 A; 3 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3633 GAGAACCTAGAAACAT 3649
 |||||:|||||
 Db 1 GAGACCUGAAAUCAU 17
 RESULT 238
 ABL46976
 ID ABL46976 standard; RNA; 17 BP.
 XX
 AC ABL46976;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID zinzyme substrate oligonucleotide #60.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 72; 108pp; English.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 72; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3633 GAGAACCTAGAAACAT 3649
 |||||:|||||
 Db 1 GAGACCUGAAAUCAU 17
 RESULT 238
 ABL46976
 ID ABL46976 standard; RNA; 17 BP.
 XX
 AC ABL46976;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID zinzyme substrate oligonucleotide #60.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 72; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 986 CAGCAGCAGCAGCCAGCC 1002
 |||||:|||||
 Db 1 CAGCACCAGCAGCCAGCC 17
 RESULT 239
 ABL46729
 ID ABL46729 standard; RNA; 17 BP.
 XX
 AC ABL46729;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID NCH ribozyme substrate oligonucleotide #183.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antisense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 66; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 6 A; 7 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 978 AGCAGCAGCAGCAGCCAG 994
 |||||:|||||
 Db 1 AGCAGCAGCAGCAGCCAG 17
 RESULT 240
 ABL46727
 ID ABL46727 standard; RNA; 17 BP.
 XX
 AC ABL46727;
 XX
 DT 27-JUN-2003 (first entry)
 XX

DE Human GRID NCH ribozyme substrate oligonucleotide #181.
XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytosstatic; ss.
XX Homo sapiens.
XX WO200162911-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-US005957.
XX 24-FEB-2000; 2000US-0184594P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX Claim 4; Page 66; 108pp; English.
XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
SQ Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 985 CCAGCAGCAGCAGCAGC 1001
DB 1 CCUGCAGCAGCAGCAGC 17
RESULT 241
ABL46728
ID ABL46728 standard; RNA; 17 BP.
XX ABL46728;
AC ABL46728;
XX 27-JUN-2003 (first entry)
DT Human GRID NCH ribozyme substrate oligonucleotide #182.
DE Human; Grb2-related with Insert Domain; GRID; T-cell;
XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytosstatic; ss.
XX Homo sapiens.
XX WO200162911-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-US005957.
XX 24-FEB-2000; 2000US-0184594P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX Claim 4; Page 66; 108pp; English.
XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
SQ Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 985 CCAGCAGCAGCAGCAGC 1001
DB 1 CCUGCAGCAGCAGCAGC 17

PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX Claim 4; Page 66; 108pp; English.
XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 976 GCAGCAGCAGCAGCAGC 992
DB 1 GCAGCAGCAGCAGCAGC 17
RESULT 242
ABL46730
ID ABL46730 standard; RNA; 17 BP.
XX ABL46730;
AC ABL46730;
XX 27-JUN-2003 (first entry)
DT Human GRID NCH ribozyme substrate oligonucleotide #184.
DE Human; Grb2-related with Insert Domain; GRID; T-cell;
XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytosstatic; ss.
XX Homo sapiens.
XX WO200162911-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-US005957.
XX 24-FEB-2000; 2000US-0184594P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX Claim 4; Page 66; 108pp; English.
XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides are useful
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful

CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 979 GCAGCACCAGCAGCAGC 995
Db 1 GCAGCACCAGCAGCAGC 17

RESULT 243
ABT38591
ID ABT38591 standard; DNA; 17 BP.
XX AC
XX ABT38591;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4228.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.

XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 528; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1909 GATCATGAGCAGCAAC 1925
Db 1 GATCATGTAGCAAAAC 17

RESULT 244
ACC67653/c
ID ACC67653 standard; DNA; 17 BP.
XX AC
XX ACC67653;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4900.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.

XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumours and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 603; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 4 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 705 TGGAGAAAATAGTGATC 721
Db 17 TAGAGAAAATAGTGATC 1

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RESULT 245
ADB40670/c
ID ADB40670 standard; DNA; 17 BP.
XX
XX
AC ADB40670;
XX
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX
DE Tumour suppression/reversion associated nucleotide #993.
XX
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003040369-A2.
XX
XX
PD 15-MAY-2003.
XX
XX
PP 17-SEP-2002; 2002WO-IB004219.
XX
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Anson R, Tuijnder M;
XX
XX
DR WPI; 2003-441574/41.
XX
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
PS Disclosure; Page 148; 771pp; French.
XX
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 8% identity, after optimal alignment, with the
CC the nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX
SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1222 GCAAAGCCTCAGGATC 1238
Db 17 GCCAAGCCTCAGGATC 1
RESULT 246
ADC37825
ID ADC37825 standard; DNA; 17 BP.
XX
XX
AC ADC37825;
XX
XX
DT 18-DEC-2003 (first entry)
DT 04-DEC-2003 (first entry)
XX
XX
DE Human AMLPla scanning 17-mer oligonucleotide SEQ ID NO:174.
XX
XX
KW human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLPla; ss.
XX
XX
OS Synthetic.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003037931-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PP 01-NOV-2002; 2002WO-US035129.
XX
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX
PI Shannon M, Phan T;
XX
XX
DR WPI; 2003-430501/40.
XX
XX
PT New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX
PS Example 2; SEQ ID NO 174; 172pp; English.
XX
XX
CC The present invention describes the human angiomotin-like protein 1
CC (AMLPL). human AMLPL has cytostatic activity, and can be used in gene
CC therapy. The AMLPL protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLPL. The present sequence represents a scanning
CC oligonucleotide for human AMLPLa, which is used in an example from the
CC present invention.
XX
XX
SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1505 CAGCAACAGCAGCAGAG 1521
Db 1 CAGCAACAGCAGCAGAG 17
RESULT 247
ADB44769
ID ADB44769 standard; DNA; 17 BP.
XX
XX
AC ADB44769;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Tumour suppression/reversion associated nucleotide #5092.
XX
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003040369-A2.
XX
XX

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PA (MCSW//) MCSWIGGEN J.
PA (HAMB//) HAMBLIN P A.
PA (ELLI//) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
XX WPI; 2003-829646/77.
XX
XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
XX WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
XX Claim 4; SEQ ID NO 360; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
XX expression of Grb2-related with insert domain (GRID) gene, e.g. a
XX hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
XX amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
XX including the novel nucleic acid molecule, reducing GRID activity in a
XX cell by contacting the cell with the novel nucleic acid molecule,
XX treating a patient having a condition associated with the level of GRID
XX (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
XX the novel nucleic acid molecule, cleaving RNA of a GRID gene by
XX contacting the cell with the novel nucleic acid molecule, an expression
XX vector comprising a nucleic acid sequences (encoding at least the novel
XX mammalian cell including the expression vector and an enzymatic nucleic
XX acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
XX molecule is useful for treating a condition associated with the level of
XX GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
XX a target region for the enzymatic nucleic acids of the invention.
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 985 CCAGCAGCAGCAGCAGC 1001
DB 1 CCUGCAGCAGCAGCAGC 17

RESULT 250
ADM54086
ID ADM54086 standard; mRNA; 17 BP.
XX
XX ADM54086;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human GRID mRNA substrate sequence #361.
XX
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
XX NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberzyme; Inozyme;
XX hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
XX Homo sapiens.
XX
XX US2003134806-A1.
XX
XX 17-JUL-2003.
XX
XX 23-FEB-2001; 2001US-00792818.
XX
XX 10-FEB-2000; 2000US-0181594P.
XX
XX (JARV//) JARVIS T.
XX (CARL//) CARLOWITZ I V.
XX (MCSW//) MCSWIGGEN J.
XX (HAMB//) HAMBLIN P A.
XX (ELLI//) ELLIS J H.
XX
XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
XX WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
XX Claim 4; SEQ ID NO 360; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
XX expression of Grb2-related with insert domain (GRID) gene, e.g. a
XX hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
XX amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
XX including the novel nucleic acid molecule, reducing GRID activity in a
XX cell by contacting the cell with the novel nucleic acid molecule,
XX treating a patient having a condition associated with the level of GRID
XX (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
XX the novel nucleic acid molecule, cleaving RNA of a GRID gene by
XX contacting the cell with the novel nucleic acid molecule, an expression
XX vector comprising a nucleic acid sequences (encoding at least the novel
XX mammalian cell including the expression vector and an enzymatic nucleic
XX acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
XX molecule is useful for treating a condition associated with the level of
XX GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
XX a target region for the enzymatic nucleic acids of the invention.
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 GCAGCAGCAGCAGCAGC 992
DB 1 GCAGCAGCAGCAGCAGC 17

RESULT 251
ADM54299
ID ADM54299 standard; mRNA; 17 BP.
XX
XX ADM54299;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human GRID mRNA substrate sequence #609.
XX
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
XX NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberzyme; Inozyme;
XX hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
XX Homo sapiens.
XX
XX US2003134806-A1.
XX
XX 17-JUL-2003.
XX
XX 23-FEB-2001; 2001US-00792818.
XX
XX 10-FEB-2000; 2000US-0181594P.
XX
XX (JARV//) JARVIS T.
XX (CARL//) CARLOWITZ I V.
XX (MCSW//) MCSWIGGEN J.
XX (HAMB//) HAMBLIN P A.
XX (ELLI//) ELLIS J H.
XX
XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
XX WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
XX Claim 4; SEQ ID NO 361; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
XX expression of Grb2-related with insert domain (GRID) gene, e.g. a
XX hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
XX amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
XX including the novel nucleic acid molecule, reducing GRID activity in a
XX cell by contacting the cell with the novel nucleic acid molecule,
XX treating a patient having a condition associated with the level of GRID
XX (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
XX the novel nucleic acid molecule, cleaving RNA of a GRID gene by
XX contacting the cell with the novel nucleic acid molecule, an expression
XX vector comprising a nucleic acid sequences (encoding at least the novel
XX mammalian cell including the expression vector and an enzymatic nucleic
XX acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
XX molecule is useful for treating a condition associated with the level of
XX GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
XX a target region for the enzymatic nucleic acids of the invention.
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;

```

DR WPI; 2003-829646/77.
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition and
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
PS Claim 4; SEQ ID NO 609; 74pp; English.
XX
CC The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
CC amberyzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule, and
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequence (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 CAGCAGCAGCAGCC 1002
DB 1 CAGCAGCAGCAGCC 17

RESULT 252
AAQ91051/C
ID AAQ91051 standard; DNA; 18 BP.
XX
XX AAQ91051;
AC
XX 30-JAN-1996 (first entry)
DT
XX HHV-6 associated MS genetic marker 38E external primer 38E8.
DE
XX Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; 38E;
KW external primer 38E8; diagnosis; ss.
KW
XX Synthetic.
OS
XX W09512313-A1.
PN
XX 11-MAY-1995.
PD
XX 04-NOV-1994; 94WO-US012655.
PF
XX 05-NOV-1993; 93US-00149176.
PR 24-MAR-1994; 94US-00218029.
PR 05-AUG-1994; 94US-00287942.
PR 04-NOV-1994; 94US-00334482.
XX
XX (PATH-) PATHOGENESIS CORP.
PA
XX Burmer GC, Challoner PB, Smith KT, Brown JP, Parker JD;
PI Nowinski RC;
PI
XX WPI; 1995-215032/28.
DR
XX Treatment of human herpes-virus-6-associated multiple sclerosis - using
PT an antiviral agent, e.g. a nucleoside analogue, administered to the

PT cerebrospinal fluid.
XX
PS Disclosure; Page 35; 116pp; English.
XX
CC AAQ91050 and AAQ91051 are an external primer pair for the human herpes
CC virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, 38E
CC (AAQ91054). The primers can be used in the diagnosis of MS
XX
SQ Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1972 TGCTCCCAAGATCAGA 1988
DB 17 TGCTCCCAAGATCAGA 1

RESULT 253
AAV94830
ID AAV94830 standard; RNA; 18 BP.
XX
XX AAV94830;
AC
XX 24-FEB-1999 (first entry)
DT
XX Human IL-2 receptor g-chain substrate position 256.
DE
XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX
XX Homo sapiens.
OS
XX W09824913-A2.
PN
XX 1-JUN-1998.
PD
XX 02-DEC-1997; 97WO-US021748.
PF
XX 03-DEC-1996; 96US-00758306.
PR (RIBO-) RIBOZYME PHARM INC.
PA
XX Stinchcomb DT, Mcswiggen JA;
PI
XX WPI; 1998-333332/29.
DR
XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
PT
XX Claim 4; Page 38; 61pp; English.
PS
XX The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 18 BP; 5 A; 10 C; 2 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 993 AGCACCAGCCTACCAAC 1009
DB 1 AGCCCCAGCCUACCAAC 17

RESULT 254
 AAL10553/c
 ID AAL10553 standard; DNA; 18 BP.
 XX
 AC AAL10553;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Smad2 antisense oligonucleotide sequence #6 (ISIS# 27783).
 XX
 KW Smad2; MADH2; MADR2; hMAD2; JV18-1; transcription factor; inflammation;
 KW chromosome 18q21; antisense compound; treat; infection; tumour;
 KW diagnostic reagent; research reagent; ss; cancer.
 XX
 OS Synthetic.
 XX
 PN US6037142-A.
 XX
 PD 14-MAR-2000.
 XX
 PF 23-FEB-1999; 99US-00255912.
 XX
 PR 23-FEB-1999; 99US-00255912.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowbert LM;
 XX
 DR WPI; 2000-269886/23.
 XX
 KW New antisense compound that inhibits human Smad2, useful e.g. for
 PT treating or preventing infection, inflammation and tumors.
 XX
 PS Claim 11; Col 39; 31pp; English.
 XX
 CC This sequence represents an antisense nucleotide sequence targeting human
 CC Smad2. Smad2 is also known as MADH2, MADR2, hMAD2 and JV18-1, and is a
 CC member of a subgroup of Smad family transcription factors which are
 CC cytosolic proteins regulated by transforming growth factor-beta (TGF-
 CC beta) and activins. Smads exist as monomers in unstimulated cells as homo
 CC - or heterodimerise and translocate to the nucleus and activate target
 CC gene transcription upon ligand binding. The Smad2 gene is located on
 CC chromosome 18q21. The invention relates to antisense compounds (see
 CC AAL10548-A10587) targeted to the Smad2 nucleotide sequence. The antisense
 CC oligonucleotide sequences inhibit Smad2 expression by hybridising to DNA
 CC or RNA. The antisense nucleotides are used to treat or prevent diseases
 CC associated with expression of Smad2, e.g. infection, inflammation and
 CC tumours. The oligonucleotides can also be used as diagnostic or research
 CC reagents.
 XX
 SQ Sequence 18 BP; 0 A; 11 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 73 GAAGCAGCGGAGGAGA 89
 Db 18 GGAGCAGCGGAGGAGA 2
 RESULT 255
 AAS07309/c
 ID AAS07309 standard; DNA; 18 BP.
 XX
 AC AAS07309;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE CPS1/TES1 genomic DNA sequencing primer FP11.
 XX

KW CPS1; peptide synthetase; peptide toxin; fungal pathogen;
 KW corn crop infection; ss; sequencing primer; FP11.
 XX
 OS Cochliobolus heterostrophus.
 XX
 PN WO200138489-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032227.
 XX
 PR 23-NOV-1999; 99US-00448215.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Yoder OC, Turgeon BC, Lu S;
 XX
 DR WPI; 2001-367672/38.
 XX
 KW New isolated nucleic acid molecule from a plant pathogen useful in
 PT preventing plant pathogenic infections.
 XX
 PS Example 1; Page 54; 132pp; English.
 XX
 CC The sequence represents a sequencing primer used to sequence a genomic
 CC clone from Cochliobolus heterostrophus which contains the CPS1 and TES1
 CC peptide synthetase genes. CPS1 is an enzyme thought to be involved in the
 CC production of peptide toxins, which are involved in the pathogenic
 CC infection of corn crops. The nucleic acids and proteins can be used as
 CC targets for anti-fungal compounds to prevent fungal corn infection and
 CC the nucleic acids can be used in gene therapy to alter the biosynthetic
 CC pathway for the peptide toxins to lower the pathogenicity of the fungi
 XX
 SQ Sequence 18 BP; 0 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 978 AGCAGCACCAGCAGCAG 994
 Db 18 AGAGCAGCACCAGCAGCAG 2
 RESULT 256
 ABL40838
 ID ABL40838 standard; DNA; 18 BP.
 XX
 AC ABL40838;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE P. putida exbB and exbD genes amplifying RT-PCR primer.
 XX
 KW exbB; exbD; tonB; antibiotic; toluene; PHBA; aromatic compound; parabene;
 KW para-hydroxybenzoic acid; RT-PCR; primer; ss.
 XX
 OS Pseudomonas putida.
 XX
 PN WO200229034-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 28-SEP-2001; 2001WO-US031180.
 XX
 PR 30-SEP-2000; 2000US-0236879P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Ramos JL, Ben-Bassat A, Godoy P, Ramos-Gonzales MI, Duque E;
 XX
 DR WPI; 2002-340103/37.
 XX

PT Novel isolated nucleic acid of the tonB operon from *Pseudomonas*, useful
 PT for producing transformed bacterial strains which are more sensitive to
 PT antibiotics, and toluene.

XX Disclosure; Page 80; 81pp; English.

XX The invention relates to a novel gene cluster comprising the exbB, exbD
 CC and tonB genes from *P. putida*. These genes are useful for producing
 CC bacterial cells more sensitive to antibiotics, toluene, pHBA (para-
 CC hydroxybenzoic acid), aromatic compounds, parabenes, and aromatic amino
 CC acids. Methods are also provided to identify pHBA tolerant genes, and
 CC pHBA tolerant strains, useful for producing pHBA. The present sequence
 CC represents a primer for RT-PCR amplification of *P. putida* exbB and exbD
 CC mRNA

SQ Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 977 CAGCAGCACCAGCAGCA 993
 DB 1 CAGCAGCACCAGCATCA 17
 |||||

RESULT 257

ABS68433/C
 ID ABS68433 standard; DNA; 18 BP.

AC ABS68433;

XX 19-NOV-2002 (first entry)

XX Sequencing primer #24 for fungal DNA flanking REMI insertion site.

XX Fungal pathogen; peptide synthetase gene cluster; iron reductase;
 KW permease; major facilitator superfamily transporter; MFS transporter;
 KW anti-fungal agent; fungicide; pathogenic fungi; plant pathogen; CPS1;
 KW animal pathogen; fungal infection; wild grass; cereal; corn; mycocide;
 KW leaf spot maize; immunocompromised vertebrate; pneumonia; arthritis;
 KW military disease; bone infection; joint infection; skin disease;
 KW aseptophagitis; vaginitis; onychomycosis; inflammation; urinary tract;
 KW kidney; liver; brain; gastrointestinal tract; lung; fungicidal;
 KW mycoid; antiarthritic; antiinflammatory; dermatological; CoA ligase;
 KW sequencing; primer; ss.

XX Cochliobolus heterostrophus.
 OS Synthetic.

XX WO200242444-A2.

XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-US043381.

XX 22-NOV-2000; 2000US-0252645P.

XX 22-NOV-2000; 2000US-0252732P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

FA (CORR) CORNELL RES FOUND INC.

FA (YODE/) YODER O.

FA (TURG/) TURGEON B G.

FA (LUSS/) LU S.

XX Yoder O, Turgeon BG, Lu S;

XX WPI; 2002-666824/71.

XX Nucleic acid molecules comprising fungal, e.g. *Cochliobolus*
 PT heterostrophus, genes from a peptide synthetase gene cluster, useful for
 PT identifying anti-fungal agents for treating fungal infections such as
 PT pneumonia and arthritis.

XX Example 1; Page 189; 315pp; English.

XX The present invention relates to nucleic acid molecules comprising
 CC fungal, e.g. *Cochliobolus heterostrophus*, genes from a peptide synthetase
 CC gene cluster, encoding e.g. an iron reductase and/or a permease, or a
 CC major facilitator superfamily (MFS) transporter protein. The
 CC polynucleotides and polypeptides are useful for identifying a novel
 CC fungicidal or mycocidal mode of action which permits rapid discovery of
 CC novel inhibitors of gene products that are useful as fungicides or
 CC mycocides. Anti-fungal agents identified using the polynucleotide and
 CC polypeptide sequences of the invention, and antisense DNA are useful as
 CC fungicides to suppress the growth of pathogenic fungi. The fungal
 CC pathogens include plant pathogens such as *Septoria tritici*, or *Cochliobolus*
 CC heterostrophus, or animal pathogens such as *Candida albicans*. The anti-
 CC fungal agents are useful for treating fungal infections in plants such as
 CC wild grasses or cereals (e.g. corn). For example they can be used to
 CC treat a disease called leaf spot maize caused by the pathogen *C.*
 CC heterostrophus. The anti-fungal agents are particularly useful for
 CC treating fungal infections of vertebrates, including immunocompromised
 CC vertebrates, for e.g. pneumonia, arthritis, military disease, bone and
 CC joint infection, skin disease, aseptophagitis, vaginitis, onychomycosis,
 CC and inflammation of the urinary tract, kidney, liver, brain,
 CC gastrointestinal tract and lung. ABS68410-ABS68443 represent sequencing
 CC primers used to sequence *C. heterostrophus* DNA flanking the REMI vector
 CC insertion site in the examples of the present invention

SQ Sequence 18 BP; 0 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 978 AGCAGCACCAGCAGCAG 994

DB 18 AGAAGCACCAGCAGCAG 2
 |||||

RESULT 258

ADG88997

ID AGG88997 standard; DNA; 18 BP.

XX AGG88997;

XX 11-MAR-2004 (first entry)

XX *Pseudomonas putida* exbB and exbD gene amplifying RT-PCR primer #2.

XX Antibiotic; tonB operon; *Pseudomonas*; bactericidal agent; RT-PCR;
 XX reverse transcription; primer; ss.

XX *Pseudomonas putida*.

XX US2003158397-A1.

XX 21-AUG-2003.

XX 01-OCT-2001; 2001US-00968122.

XX 01-OCT-2001; 2001US-00968122.

XX (RAMO/) RAMOS J L.

XX (BENB/) BEN-BASSAT A.

XX (DUQU/) DUQUE E.

XX (GODO/) GODOY P.

XX (RAMO/) RAMOS-GONZALEZ M I.

XX Ramos JL, Ben-Bassat A, Duque E, Godoy P, Ramos-Gonzalez MI;

XX WPI; 2003-801890/75.

XX New nucleic acid fragment of the tonB operon from *Pseudomonas*, useful for
 PT designing antibiotics, for generating microbes with enhanced biocatalytic

PT potential or for controlling microbial tolerance to pHBA or aromatic compounds.

XX

PS Disclosure; SEQ ID NO 9; 34pp; English.

XX

CC The present invention relates to new isolated nucleic acid fragment of the tona operon from Pseudomonas. The invention is useful for designing antibiotics or bacteriostatic agents, for generating microbes with enhanced biocatalytic potential and controlling microbial tolerance to pHBA, aromatic compounds or amino acids, antibiotics or bactericidal agents. The present sequence is Pseudomonas putida exbB and exbD gene amplifying RT-PCR primer.

XX

SQ Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 1.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 977 CAGCAGCAGCAGCAGCA 993

DB 1 CAGCAGCAGCAGCATCA 17

RESULT 259

AAA82737

ID AAA82737 standard; DNA; 19 BP.

XX

AC AAA82737;

XX

DT 04-DEC-2000 (first entry)

XX

DE cdk3 ribozyme binding site #22.

XX

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

XX

PN WO200032765-A2.

XX

PD 08-JUN-2000.

XX

PF 06-DEC-1999; 99WO-US028772.

XX

PR 06-DEC-1999; 99WO-US028772.

XX

PR 04-DEC-1998; 98US-0110954P.

XX

PA (IMMU-) IMMUSOL INC.

XX

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

XX

DR WPI; 2000-412314/35.

XX

PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

XX

PS Disclosure; Page 51; 109pp; English.

XX

CC The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX

SQ Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2942 TTGACTTCTCTCAGCCA 2958

DB 2 TTGAGTTCTCTCAGCCA 18

RESULT 261

AAH57900

ID AAH57900 standard; DNA; 19 BP.

XX

AC AAH57900;

XX

DT 10-SEP-2001 (first entry)

XX

DE Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:324.

XX

KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

KW Antiinflammatory; rat periodontium; cell strain; bioactivity;
 KW tooth disease; periodontitis; periodontosis; mouse; murine; PCR; primer;
 KW ss.
 XX
 OS Mus sp.
 XX
 PN JP2002262862-A.
 XX
 PD 17-SEP-2002.
 XX
 XX 12-MAR-2001; 2001JP-00069249.
 PF
 XX 12-MAR-2001; 2001JP-00069249.
 PR
 XX (TOHO-) TOHOKU TECHNOARCH KK.
 PA
 XX WPI; 2003-132121/13.
 DR
 XX A new cell strain derived from rat periodontium useful for treating or
 PT preventing tooth diseases such as periodontitis.
 XX
 PS Example 1; Page 9; 28pp; Japanese.
 XX
 CC The invention relates to a cell strain which is derived from rat
 CC periodontium and can be maintained in passage. The methods of the
 CC invention are useful for acquiring a cell strain, establishing a cell
 CC strain, and measuring the bioactivity against the cell of a rat-derived
 CC periodontium. The cell strain can be used for treating and preventing
 CC tooth diseases such as periodontitis and periodontosis. This
 CC polynucleotide sequence represents a PCR primer used in the
 CC exemplification of the invention
 XX
 SQ Sequence 19 BP; 0 A; 2 C; 5 G; 12 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1575 AACAAACACAGCAACAA 1591
 DB 19 AACACACACACACACAA 3
 |||||
 RESULT 264
 ID ADN34019/C
 ID ADN34019 standard; RNA; 19 BP.
 XX
 AC ADN34019;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Upper strand of cyclin D1 targeted double stranded siNA #39.
 XX
 DE short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
 KW cancer; cell-proliferation disorder; restenosis; drug screening;
 KW genetic engineering; pharmacogenomics; gene mapping;
 KW single nucleotide polymorphisms; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072705-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 06-FEB-2003; 2003WO-US0003662.
 XX
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 17-SEP-2002; 2002US-0411275P.
 PR 17-SEP-2002; 2002US-0411275P.

PR 15-JAN-2003; 2003US-0440129P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Thompson J, Mcswiggen J, Beigelman L;
 PI
 XX WPI; 2003-689983/65.
 DR
 XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer and restenosis, down regulates expression of at least
 PT one cyclin gene.
 XX
 PS Example 3; SEQ ID NO 39; 144pp; English.
 XX
 CC The present invention relates to a short interfering nucleic acid (siNA)
 CC that down regulates expression of at least one cyclin gene by RNA
 CC interference. siNA are used to modulate expression of cyclin genes, in
 CC cells, tissue explants or organisms, e.g. for treating a wide range of
 CC cancers and other cell-proliferation disorders such as restenosis, but
 CC also for drug screening, diagnosis, target identification and validation;
 CC genetic engineering, pharmacogenomics, studying gene function and gene
 CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
 CC represents the upper strand of cyclin D1 targeted double stranded siNA
 CC which is identical to the cyclin D1 transcript target sequence.
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 1 G; 0 T; 8 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 549 AGGAAGTGTTCATGAA 565
 DB 17 AGGAAGTGTTCATGAA 1
 |||||
 RESULT 265
 ID ADN34258
 ID ADN34258 standard; RNA; 19 BP.
 XX
 AC ADN34258;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Lower strand of cyclin D1 targeted double stranded siNA #39.
 XX
 DE short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
 KW cancer; cell-proliferation disorder; restenosis; drug screening;
 KW genetic engineering; pharmacogenomics; gene mapping;
 KW single nucleotide polymorphisms; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072705-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 06-FEB-2003; 2003WO-US0003662.
 XX
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 17-SEP-2002; 2002US-0411275P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Thompson J, Mcswiggen J, Beigelman L;
 PI
 XX WPI; 2003-689983/65.
 DR

XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, down regulates expression of at least
PT one cyclin gene.
XX
XX Example 3; SEQ ID NO 278; 144pp; English.
XX
XX The present invention relates to a short interfering nucleic acid (siRNA)
CC that down regulates expression of at least one cyclin gene by RNA
CC interference. siRNA are used to modulate expression of cyclin genes, in
CC cells, tissue explants or organisms, e.g. for treating a wide range of
CC cancers and other cell-proliferation disorders such as restenosis, but
CC also for drug screening, diagnosis, target identification and validation;
CC genetic engineering, pharmacogenomics, studying gene function and gene
CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
CC represents the lower strand of cyclin D1 targeted double stranded siRNA.
XX
XX Sequence 19 BP; 8 A; 1 C; 6 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 549 AGGAAGUGUCAAUGAA 565
DB 3 AGGAAGUGUCAAUGAA 19
|||||:|:|:|:|:|:|
RESULT 266
ADH01571
ID ADH01571 standard; RNA; 19 BP.
AC ADH01571;
XX
DT 11-MAR-2004 (first entry)
XX
DE Protein tyrosine phosphatase siRNA sequence, SEQ ID No 183.
XX
XX small interfering RNA; siRNA; protein tyrosine phosphatase; PTP; PTP1B;
KW insulin receptor protein phosphorylation; Jak2; antidiabetic; anorectic;
KW antiinflammatory; neuroprotective; cytotatic; immunosuppressive;
KW antimicrobial; gene therapy; ss; siRNA.
XX
OS Unidentified.
XX
PN WO2003099227-A2.
XX
PD 04-DEC-2003.
XX
PF 23-MAY-2003; 2003WO-US016651.
XX
PR 23-MAY-2002; 2002US-0383249P.
PR 14-APR-2003; 2003US-0462942P.
XX
PA (CEPT-) CEPTYR INC.
XX
PI Lewis SP, Klinghoffer R, Wilson LK;
XX
XX WPI; 2004-035036/03.
DR
XX
PT New small interfering polynucleotide that modulates protein tyrosine
PT phosphatase (PTP)1B polypeptide signal transduction, useful for treating
PT disorders associated with altered PTP1B signal transduction, e.g.
PT diabetes or cancer.
XX
PS Example 3; SEQ ID NO 183; 234pp; English.
XX
XX The invention relates to a novel isolated small interfering RNA (siRNA)
CC polynucleotide, comprising at least one nucleotide sequence from any of
CC the 20 fully defined sequences given in the specification. The invention
CC further relates to a pharmaceutical composition comprising a new siRNA
CC polynucleotide and a physiological carrier; a recombinant nucleic acid
CC construct, comprising a polynucleotide that is capable of directing

CC transcription of an siRNA; a host cell transformed or transfected with
CC the above recombinant nucleic acid construct; a method for interfering
CC with expression of a protein tyrosine phosphatase (PTP)1B polypeptide, or
CC its variant; a method for identifying a component of a PTP1B signal
CC transduction pathway; a method for modulating an insulin receptor protein
CC phosphorylation state in a cell; a method for altering a Jak2 protein
CC phosphorylation state in a cell; and a method for treating a Jak2-
CC associated disorder. The siRNA has the following activities:
CC antidiabetic, anorectic, antiinflammatory, neuroprotective, cytotatic,
CC immunosuppressive, and antimicrobial. The novel siRNA polynucleotides can
CC be used in gene therapy to treat disorders. The composition and methods
CC are useful in treating disorders associated with PTP1B-mediated signal
CC transduction, such as diabetes, obesity, hyperglycaemia-induced
CC apoptosis, inflammation, neurodegenerative disorders, cancer, autoimmune
CC diseases or infection. This polynucleotide sequence represents an siRNA
CC used for modulating the signal transduction of a protein tyrosine
CC phosphatase of the invention.
XX
XX Sequence 19 BP; 5 A; 8 C; 2 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3674 CCATATTCACCTCTCCTCAC 3690
DB 2 CCAUAUUCACACCTCCTCAC 18
|||||:|:|:|:|:|:|
RESULT 267
ADR80899/C
ID ADR80899 standard; DNA; 19 BP.
XX
AC ADR80899;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human glucose-6-phosphatase oligonucleotide seqid 5398.
XX
XX antilipemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytotatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; siRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase; ss.
XX
OS Homo sapiens.
XX
XX WO2004080406-A2.
XX
XX 23-SEP-2004.
XX
XX 08-MAR-2004; 2004WO-US007070.
XX
XX 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX

PA (ALNY-) ALNYLAM PHARM.
 XX Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 5398; 378pp; English.
 XX
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human glucose-6-phosphatase antisense oligonucleotide that
 CC can be used to control glucose-6-phosphatase gene expression.
 XX
 XX Sequence 19 BP; 6 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3352 TGTGGTGTCAATGTGTA 3368
 Db 18 TGTGGTGTCAATGTGGA 2
 RESULT 268
 ADR80898/c
 ID ADR80898 standard; DNA; 19 BP.
 XX
 XX ADR80898;
 AC
 DT 16-DEC-2004 (first entry)
 XX
 XX Human glucose-6-phosphatase oligonucleotide seqid 5397.
 KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease; ss.
 KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase;
 XX
 OS Homo sapiens.

XX PN WO2004080406-A2.
 XX PD 23-SEP-2004.
 XX
 XX 08-MAR-2004; 2004WO-US007070.
 XX
 XX 07-MAR-2003; 2003US-0452682P.
 PR 12-MAR-2003; 2003US-0454265P.
 PR 13-MAR-2003; 2003US-0454962P.
 PR 13-MAR-2003; 2003US-0455050P.
 PR 14-APR-2003; 2003US-0462894P.
 PR 17-APR-2003; 2003US-0463772P.
 PR 23-APR-2003; 2003US-0465665P.
 PR 25-APR-2003; 2003US-0465802P.
 PR 09-MAY-2003; 2003US-0469612P.
 PR 08-AUG-2003; 2003US-0493986P.
 PR 11-AUG-2003; 2003US-0494597P.
 PR 26-SEP-2003; 2003US-0506341P.
 PR 09-OCT-2003; 2003US-0510246P.
 PR 10-OCT-2003; 2003US-0510318P.
 PR 07-NOV-2003; 2003US-0518453P.
 XX
 PA (ALNY-) ALNYLAM PHARM.
 XX Manoharan M, Bumcrot D;
 XX WPI; 2004-677362/66.
 XX
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 5397; 378pp; English.
 XX
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human glucose-6-phosphatase antisense oligonucleotide that
 CC can be used to control glucose-6-phosphatase gene expression.
 XX
 XX Sequence 19 BP; 6 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3352 TGTGGTGTCAATGTGTA 3368
 Db 18 TGTGGTGTCAATGTGGA 2
 RESULT 268
 ADR80898/c
 ID ADR80898 standard; DNA; 19 BP.
 XX
 XX ADR80898;
 AC
 DT 16-DEC-2004 (first entry)
 XX
 XX Human glucose-6-phosphatase oligonucleotide seqid 5397.
 KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease; ss.
 KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase;
 XX
 OS Homo sapiens.

Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3352 TGTGGTGTCAATGTGTA 3368
 Db 17 TGTGGTGTCAATGTGGA 1

```
RESULT 269
ACD82527
ID ACD82527 standard; DNA; 17 BP.
XX
AC ACD82527;
XX
DT 19-SEP-2003 (first entry)
XX
DE Nucleic acid cloning associated adaptor molecule #228.
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
XX internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
OS Synthetic.
XX
PN US2003044791-A1.
XX
PD 06-MAR-2003.
XX
PF 13-JUN-2001; 2001US-00880313.
XX
PR 13-JUN-2001; 2001US-00880313.
XX
PA (FLEM/) FLEMINGTON E K.
XX
PI Flemington EK;
XX
WPI; 2003-521745/49.
XX
New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.
XX
PS Claim 12; Fig 5; 100pp; English.
XX
The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2586 GTACACCTGCAGCCT 2600
Db 1 GTACACCTGCAGCCT 15
XX
RESULT 270
ADC37816
ID ADC37816 standard; DNA; 17 BP.
XX
AC ADC37816;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:165.
XX
WPI human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
```

```
KW AMLP1a; ss.
XX
OS Synthetic.
OS Homo sapiens.
PN KO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
WPI; 2003-430501/40.
XX
New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 165; 172pp; English.
XX
The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACA 1443
Db 3 GCAGCAGCAGCAACA 17
XX
RESULT 271
ADI50157/c
ID ADI50157 standard; DNA; 17 BP.
XX
AC ADI50157;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2660.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
```

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.

XX Disclosure; SEQ ID NO 2660; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytostatic, virucide, neuroprotective,

CC neotropic or neuroleptic activity. The DNA sequences may be useful as

CC probes and primers for detecting, identifying, quantifying and/or

CC amplifying nucleic acid, for example as one component of a gene chip, in

CC vitro as antisense reagents and for production of recombinant

CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration,

CC specifically cancer but also Alzheimer's disease and schizophrenia. The

CC present sequence is that of a nucleic acid sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishedpct_sequences

XX

XX Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 GGTTCCTTGAAGA 163

Db 17 GGTTCCTTGAAGA 3

RESULT 272

AD40522

ID ADC40522 standard; DNA; 18 BP.

XX

XX

AC ADC40522;

XX

XX 18-DEC-2003 (first entry)

XX

XX Human G-protein coupled receptor (GPCR) related reverse primer.

XX

XX gene expression analysis; collective quantitative analysis;

KW G protein coupled receptor; tyrosine oxidase receptor family;

KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

KW myocardial infarction; infarct; ischaemic disease; GPCR; primer; PCR; ss.

XX

XX Unidentified.

XX

XX WO2003052096-A1.

XX

XX

XX 26-JUN-2003.

XX

XX 13-DEC-2002; 2002WO-JP013097.

XX

XX 14-DEC-2001; 2001JP-00382053.

XX

XX 21-FEB-2002; 2002JP-00045104.

XX

XX 15-MAY-2002; 2002JP-00140111.

XX

XX 18-NOV-2002; 2002JP-00333769.

XX

XX (TAKE) TAKEDA CHEM IND LTD.

XX

XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsumura F, Kawamata Y, Ogi K;

XX

XX WPI; 2003-533023/50.

XX

XX Method for gene expression analysis for treatment of cancers.

XX Example 2; SEQ ID NO 6; 261pp; Japanese.

XX

XX The invention relates to a novel method for gene expression analysis by

CC collective quantitative analysis of the expression of a number of genes

CC to identify those that are promoted or inhibited in a given cell or

CC tissue. The genes are preferably gene families such as the G protein

CC coupled receptor family, tyrosine oxidase receptor family, or ion channel

CC gene family. The methods may be used in treatment of cancers, including

CC prostate, ovarian, stomach, bladder, breast, and cancer of the

CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used

CC in the treatment and prevention of atherosclerosis, myocardial

CC infarction, infarct or ischaemic disease of the brain. This

CC polynucleotide sequence represents a PCR primer used in the

CC exemplification of the invention.

XX

XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3447 AAACCCCATGTCATG 3461

Db 4 AAACCCCATGTCATG 18

RESULT 273

ADN08161/C

ID ADN08161 standard; DNA; 18 BP.

XX

XX

AC ADN08161;

XX

XX 17-JUN-2004 (first entry)

XX

XX Human S9-RNA RT-PCR primer #2.

XX

XX Human; ss; PCR; endocrine gland vascular endothelial growth factor;

KW EG-VEGF; EG-VEGF receptor; endometrial disease; uterine receptivity;

KW endometriosis; endometrial carcinoma; dysfunctional bleeding;

KW gene therapy; primer; RT-PCR; reverse transcriptase PCR; S9-RNA.

XX

XX Homo sapiens.

XX

XX DE10229379-A1.

XX

XX 29-JAN-2004.

XX

XX 26-JUN-2002; 2002DE-01029379.

XX

XX 26-JUN-2002; 2002DE-01029379.

XX

XX (SCHD) SCHERING AG.

XX

XX Haendler B, Hess-Stumpp H, Schmidt A;

XX

XX WPI; 2004-134408/14.

XX

XX Treatment and prevention of endometrial disease, e.g. endometriosis or

PT carcinoma, by inhibiting endocrine gland vascular endothelial growth

PT factor, also diagnosis.

XX

XX Example 1; Page 5; 13pp; German.

XX

XX The invention relates to a composition that contains, as active agent, an

CC endocrine gland vascular endothelial growth factor (EG-VEGF) nucleic

CC acid, polypeptide or antisense nucleic acid, antibody against EG-VEGF or

CC its receptor (EG-VEGF-R), or EG-VEGF-R antisense nucleic acid, is useful

CC for the treatment or prevention of endometrial diseases. Also included

CC are a method for detecting uterine receptivity (by determining the amount

CC of EG-VEGF polypeptide and/or nucleic acid, using the new composition) or

CC a test system for identifying antagonists of EG-VEGF-R. Also disclosed as

CC new is a splice variant of the human GPR73a receptor. It contains an

CC additional exon which includes a stop codon, so produces a truncated
 CC protein that can not mediate signal transduction, i.e. it functions as a
 CC dominant-negative inhibitor. The composition is used to treat
 CC endometriosis, endometrial carcinoma or dysfunctional bleeding, e.g. by
 CC gene therapy, to diagnose endometriosis or endometrial carcinoma and to
 CC detect uterine receptivity (especially to determine the best time for
 CC implantation of eggs fertilised in vitro). Also the test system that
 CC comprises cells that express the EG-VEGF receptor is used to screen for
 CC receptor antagonists, potentially useful for treating endometriosis. The
 CC present sequence is a human S9-RNA control RT-PCR (reverse transcriptase
 CC PCR) primer used in the isolation of the EG-VEGF cDNA.
 CC
 SQ Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 CCTCTCTGCTGGA 1036
 Db 16 CCTCTCTGCTGGA 2

RESULT 274
 AAQ98457/c
 ID AAQ98457 standard; cDNA; 31 BP.

AC AAQ98457;

DT 23-APR-1996 (first entry)

DE Sense probe CAG-30.

KW Probe; trinucleotide repeat; myotonic dystrophy; DM; Mt-PK gene;
 KW fluorescent label; fluorescein isothiocyanate; fragile X syndrome;
 KW muscular dystrophy; Huntington's disease; ss.

OS Synthetic.

PN WO9525179-A1.

PD 21-SEP-1995.

PF 08-MAR-1995; 95WO-US002861.

PR 17-MAR-1994; 94US-00214823.

PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

PI Singer RH, Taneja KL;

PS WPI; 1995-336982/43.

PT Detecting trinucleotide repeat expansion by in situ hybridisation - with
 PT detection sensitive enough to distinguish between probe bound to expanded
 PT and normal repeat regions, esp. for myotonic dystrophy diagnosis.

PS Disclosure; Page 38; 51pp; English.

CC The sequences represented by AAQ98457 and AAQ98458 are synthetic probes
 CC for the trinucleotide repeat CTG. These probes can be used in a method of
 CC in situ hybridisation for the detection of a trinucleotide repeat
 CC expansion. These probes were used specifically to identify myotonic
 CC dystrophy (DM). DM is associated with an expanded CTG repeat in the 3',
 CC untranslated region of the Mt-PK gene. These probes are labelled with a
 CC fluorescent label (e.g. fluorescein isothiocyanate) and then used to
 CC treat nucleated cells. The hybridisation of the probe to the expanded
 CC trinucleotide repeat can then be detected by fluorescence microscopy. Due
 CC to the large variation between expanded repeat size, and normal repeat
 CC size in DM (5-27 repeats in non-expanded, 50-2000 repeats in expanded),
 CC the expanded repeat will bind more probes. Only the expanded repeat will
 CC bind enough of the probes to give a detectable fluorescent signal. By
 CC detecting the number of transcripts in a cell of a diagnosed individual,

CC progress of treatment, and severity of the disease can be monitored. This
 CC method can also be used to diagnose other diseases associated with
 CC trinucleotide repeat expansions, such as fragile X syndrome, muscular
 CC dystrophy and Huntington's disease. For some of these diseases a greater
 CC detection specificity would be required due to the smaller difference in
 CC repeat number between normal and infected individuals
 CC
 SQ Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 31;
 Best Local Similarity 67.7%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTTCCAGCAGCAGATGCTG 1954
 Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 275
 AAZ24996/c
 ID AAZ24996 standard; DNA; 31 BP.

XX AAZ24996;

DT 24-DEC-1999 (first entry)

DE Oligonucleotide CAG30 targeted to myotonic-protein kinase gene.

KW Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
 KW in situ hybridisation; detection; expansion; fragile X syndrome; ss.

OS Synthetic.

OS Homo sapiens.

PN US95962332-A.

PD 05-OCT-1999.

PF 11-DEC-1995; 95US-00570155.

PR 17-MAR-1994; 94US-00214823.

PR 07-MAR-1995; 95US-00399499.

XX (UYMA-) UNIV MASSACHUSETTS.

PI Taneja KL, Singer RH;

DR WPI; 1999-579615/49.

XX Detection of trinucleotide repeats.

XX Disclosure; Col 25; 18pp; English.

XX Oligonucleotides AAZ24983-224995 are targeted to the CTG trinucleotide
 CC repeats found in the myotonic-protein kinase (Mt-PK) gene. Excessive
 CC numbers of the trinucleotide repeats in the Mt-PK gene leads to the
 CC disease myotonic dystrophy. The oligonucleotides are used to probe the 5',
 CC -most 7 exons of 14 in the Mt-PK gene. This sequence is used as an
 CC antisense control oligonucleotide for the hybridisation reaction. The
 CC invention relates to a method for the detection of trinucleotide repeat
 CC expansion, e.g. in the Mt-PK gene or FMR1 gene (leading to fragile X
 CC syndrome) by in situ hybridization

Query Match 0.4%; Score 15; DB 1; Length 31;
 Best Local Similarity 67.7%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTTCCAGCAGCAGATGCTG 1954
 Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1


```

RESULT 276
AAQ90869
ID AAQ90869 standard; DNA; 18 BP.
XX
XX AC AAQ90869;
XX
XX DT 04-MAR-1996 (first entry)
XX
XX DE hMLH1 gene exon 9 first stage amplification primer N-18765.
XX
XX hMLH1; MutL homologue; cancer diagnosis; mismatch repair; tumour;
KW susceptibility; mutation detection; exon 9; primer N-18765;
XX first stage amplification; ss.
XX
XX OS Synthetic.
XX
XX PN W09516793-A1.
XX
XX PD 22-JUN-1995.
XX
XX PF 16-DEC-1994; 94WO-US014746.
XX
XX PR 17-DEC-1993; 93US-00168877.
XX
XX PR 08-MAR-1994; 94US-00209521.
XX
XX PR 09-DEC-1994; 94US-00352902.
XX
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX PA (DAND ) DNA FARRER CANCER INST INC.
XX
XX PI Baker SM, Bollag RJ, Koelodner RD, Bronner CE, Liskay RM;
XX
XX WPI; 1995-231583/30.
XX
XX PT Determn. of a mutation in a mutL homologue or gene prod. in a tissue -
XX used to diagnose cancer susceptibility, and to identify and classify a
XX DNA mismatch-repair-defective tumour.
XX
XX PS Claim 13; Fig 4B-2; 168pp; English.
XX
XX CC AAQ90869 and AAQ90870 are a primer pair for the 1st stage amplification
XX of the hMLH1 (a MutL homologue) gene exon 9. A mutation in an analogous
XX segment of a hMLH1 or hPMS1 nucleic acid isolated from a subject, can be
XX detected by comparing it with the above gene fragment. This method can be
XX used to diagnose cancer susceptibility, or to identify and classify a DNA
XX mismatch-repair defective tumour
XX
XX SQ Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCCTCAGATCTC 1240
Db 1 CAAAAGCCTCAGATCTC 18

RESULT 277
AAAX71721
ID AAAX71721 standard; RNA; 18 BP.
XX
XX AC AAAX71721;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Human KDR VEGF receptor hairpin ribozyme substrate #19.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

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XX Homo sapiens.
XX OS
XX PN W09715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US017480.
XX
XX PR 26-OCT-1995; 95US-0005974P.
XX
XX PR 11-JAN-1996; 96US-00584040.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PA (CHIR ) CHIRON CORP.
XX
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX PS Claim 4; Page 119; 218pp; English.
XX
XX CC The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX SQ Sequence 18 BP; 5 A; 7 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTCAGCCACAGAC 1111
Db 1 ACAUGCAGCCACUGAGC 18

RESULT 278
AAZ59187/C
ID AAZ59187 standard; DNA; 18 BP.
XX
XX AC AAZ59187;
XX
XX DT 15-SEP-2003 (revised)
XX
XX DT 20-APR-2000 (first entry)
XX
XX DE Reverse primer for construct MWpSp-MwPmp5 DNA.
XX
XX KW Fusion protein; Bacillus; cell wall protein; promoter; cleavage site;
XX TEV protease; PCR primer; ss.
XX
XX OS Brevibacillus brevis.
XX
XX PN JP11341991-A.
XX
XX PD 14-DEC-1999.
XX
XX PF 30-MAR-1999; 99JP-00089488.
XX
XX PR 31-MAR-1998; 98JP-00087339.
XX
XX PA (ITOHI-) ITOHAM FOODS INC.
XX
XX PA (UDAK/) UDAKA S.

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ID AA286831 standard; DNA; 18 BP.
XX
AC AA286831;
XX
DT 26-APR-2000 (first entry)
XX
DE Human Smad1 antisense inhibitor ISIS #28190.
XX
KW Antisense inhibitor; human; Smad1; disease therapy; ss.
XX
XX Homo sapiens.
OS
XX USG013522-A.
PN
XX 11-JAN-2000.
PD
XX 23-FEB-1999; 99US-00255911.
PF
XX 23-FEB-1999; 99US-00255911.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Cowseert LM;
PI
XX WPI; 2000-136324/12.
XX
XX Antisense oligonucleotides useful for inhibiting expression of human
PT Smad1 in vitro or in vivo.
PT
XX Claim 11; Col 38; 3lpp; English.
PS
XX This sequence represents an antisense inhibitor of human Smad1 of the
CC invention. The antisense compounds are useful for inhibiting Smad1
CC expression in human cells or tissues in vitro or in vivo for the
CC treatment of diseases associated with Smad1 expression
XX
XX Sequence 18 BP; 1 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
SQ
    Query Match      0.4%; Score 14.8; DB 1; Length 18;
    Best Local Similarity 88.9%; Pred. No. 2.1e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAAC 1442
DB 18 AGCAGCAGCAGCAGCTAC 1

RESULT 282
AAZ89196/c
ID AAZ89196 standard; DNA; 18 BP.
XX
AC AAZ89196;
XX
DT 09-JUN-2000 (first entry)
XX
XX Human riboprotein L21 reverse PCR primer.
DE
XX Human; expression profile; Three Prime End Amplification; TPEA;
KW riboprotein L21; RFL21; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200008208-A2.
PN
XX 17-FEB-2000.
PD
XX 05-AUG-1999; 99WO-GB002579.
PF
XX 05-AUG-1998; 98GB-00017055.
PR
XX (MEDI-) MEDICAL RES COUNCIL.
PA
XX Freeman TC, Richardson PJ, Dixon AK;
PI
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XX WPI; 2000-224033/19.
XX
XX Reverse transcription of mRNA species used for expression profiling of
PT single cells by employing a first heeled primer to provide first strand
PT cDNA species and then a second heeled primer population to generate
PT second strand cDNAs.
XX
XX Example 1; Page 29; 50pp; English.
XX
XX This invention describes a novel process (M1) of reverse transcribing
CC mRNA species present in a sample from an organism by: (a) reverse
CC transcribing the mRNA species using a first heeled primer, to provide a
CC first strand cDNA species; and (b) synthesizing second cDNA species using
CC a second heeled primer population, the nucleotide sequences of the non-
CC heel portions of the second heeled primers being such that the reverse
CC transcribed first strand cDNA species are capable of hybridizing to at
CC least one second primer. The processes can be used for expression
CC profiling of single cells. The polynucleotide comprising an oligo d(T)
CC sequence and a heel sequence 5' can be used for the reverse transcription
CC of mRNA species in a sample. The polynucleotide primer population of
CC claim (4) can be used for the synthesis of second strand cDNA from a
CC population of first strand cDNA species. Single cell cDNA libraries can
CC be made for subsequent detailed analysis of gene expression and the
CC discovery of novel genes. Small samples can be used and allow the
CC utilization of the large amount of sequence data available for further
CC understanding of disease processes and the cellular physiology of complex
CC issues. The invention provides a rapid, robust and reproducible procedure
CC called Three Prime End Amplification (TPEA), optionally with PCR (TPEA-
CC PCR). Prior art methods for the analysis of gene expression within single
CC cells or small tissue samples are limiting. Whilst in situ hybridization
CC techniques provide detailed information about the cellular expression
CC pattern of a gene in intact tissue the technique is laborious and unable
CC to analyze multiple transcripts in a single preparation. The methods
CC presented in the disclosure provide a more straightforward, reproducible
CC and reliable cDNA amplification procedure for small mRNA samples where
CC expression profiling can be conducted. The amplification technique can be
CC carried out in a single tube with a need for only limited manual
CC intervention and large numbers of samples can be analyzed. There is a
CC bias towards more uniform length cDNA molecules ensuring that even
CC relatively low abundance mRNA species are transcribed and optionally
CC amplified at the same level of efficiency as more abundant mRNA species.
CC AAZ89191-289253 represent the primers described in the method of the
CC invention
XX
SQ Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

    Query Match      0.4%; Score 14.8; DB 1; Length 18;
    Best Local Similarity 88.9%; Pred. No. 2.1e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 536 GATCCTGAGCTGCAGGAA 553
DB 18 GAGCCTGAGCTGCTGGAA 1

RESULT 283
AAF88307/c
ID AAF88307 standard; DNA; 18 BP.
XX
AC AAF88307;
XX
DT 22-AUG-2001 (first entry)
XX
XX C. officinalis calendulic acid desaturase primer 1.
DE
XX Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
KW triglyceride; transgenic plant; primer; ss.
XX
XX Calendula officinalis.
OS
XX DE19941609-A1.
PN
XX
```

PD 08-MAR-2001.
XX
XX
XX 01-SEP-1999; 99DE-01041609.
XX
PR 01-SEP-1999; 99DE-01041609.
XX
XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX
XX Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;
XX
XX WPI; 2001-283028/30.
DR
XX
XX New nucleic acid sequence encoding Calendula officinalis calendulic acid
XX
XX desaturase, useful for e.g. producing transgenic plants having oil with
XX
XX an increased unsaturated fatty acid content.,
XX
XX Example 3; Page 10; 22pp; German.
XX
XX This invention describes a novel isolated nucleic acid sequence (I)
XX
XX encoding a Calendula officinalis calendulic acid desaturase polypeptide.
XX
XX The invention also describes (1) a process for producing unsaturated
XX
XX fatty acids, comprising introducing at least one copy of (I) or (II) into
XX
XX an oil-producing organism, growing the organism, isolating oil from the
XX
XX organism and releasing fatty acids from the oil; (2) a process for
XX
XX producing triglycerides with an increased unsaturated fatty acid content,
XX
XX comprising introducing at least one copy of (I) or (II) into an oil-
XX
XX producing organism, growing the organism and isolating oil from the
XX
XX organism; (3) a process for producing saturated fatty acids, comprising
XX
XX introducing at least one nonfunctional copy of (I) or (II) into an oil-
XX
XX producing organism, growing the organism, isolating oil from the organism
XX
XX and releasing fatty acids from the oil; (4) a process for producing
XX
XX triglycerides with an increased saturated fatty acid content, comprising
XX
XX introducing at least one nonfunctional copy of (I) or (II) into an oil-
XX
XX producing organism, growing the organism and isolating oil from the
XX
XX organism; (5) an enzyme capable of converting a diunsaturated fatty acid
XX
XX of to a triunsaturated fatty acid. Transgenic organisms (especially
XX
XX plants) containing one or more copies of (I) are useful for producing
XX
XX oils with an increased unsaturated fatty acid content. Transgenic
XX
XX organisms (especially plants) containing one or more nonfunctional copies
XX
XX of (I) are useful for producing oils with an increased saturated fatty
XX
XX acid content. (I) and fragments of (I) are also useful for isolating
XX
XX genomic sequences by homology screening. This sequence represents a
XX
XX primer used in the isolation of the calendulic acid desaturase described
XX
XX in the method of the invention
XX
SQ Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 42 AATTCAGCGAGAGATCG 59
Db 18 AATCAGCGAGAGACCG 1
RESULT 284
AAS20963
ID AAS20963 standard; DNA; 18 BP.
XX
XX AAS20963;
XX
XX 09-APR-2002 (first entry)
XX
XX PCR primer Igf2r-I2 relating to gene imprinting invention.
XX
XX Human; genomic imprinting; pluripotent mouse embryonic germ cell line;
XX
XX EG; methylated CpG island; DNA methylation; gene imprinting;
XX
XX post-translational modification of histone; cancer; birth defect;
XX
XX diabetes; aberrant imprinting; PCR; primer; ss.
XX
XX Homo sapiens.
XX

PN WO200190313-A2.
XX
XX 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US016253.
XX
XX 22-MAY-2000; 2000US-0206158P.
XX
XX 22-MAY-2000; 2000US-0206161P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Feinberg A, Strichman-Almashanu L, Jiang S;
XX
XX WPI; 2002-083100/11.
XX
XX Forming embryonic germ cells useful as model system to study imprinting
XX
XX involves mating genetically divergent male and female mammal of same
XX
XX species, dissecting and dissociating embryo obtained from pregnant
XX
XX mammal.
XX
XX Disclosure; Page 54; 125pp; English.
XX
XX The present invention relates to a model system for genomic imprinting
XX
XX using pluripotent mouse embryonic germ (EG) cell lines derived from an
XX
XX interspecific cross. Also disclosed is a library containing methylated
XX
XX CpG islands and a method for assaying methylation in one or more
XX
XX imprintable genes. The gene imprinting assay is carried out by single-
XX
XX strand conformation polymorphism (SSCP), quantitative sequencing, single
XX
XX nucleotide primer extension or hot stop PCR. The assays are carried out
XX
XX to determine the post-translational modification of histones. The method
XX
XX further involves identifying a test substance as a candidate drug for
XX
XX treating cancer if the test substance enhances imprinting of a gene whose
XX
XX imprinting is lost in cancer, or if the test substance inhibits
XX
XX imprinting of a gene whose imprinting is gained in cancer. The methylated
XX
XX CpG islands are useful for providing an assessment of the risk of
XX
XX developing cancer, or for providing diagnostic information relative to
XX
XX cancer which involves determining the methylation status of the CpG
XX
XX island in a patient's DNA. The EG cells allow the accession of imprinted
XX
XX genes which are useful for detecting birth defects, diabetes and cancers
XX
XX associated with aberrant imprinting. The EG cell lines represent the
XX
XX first in vitro model system in which genomic imprinting can be followed
XX
XX dynamically and the two alleles can be distinguished. AAS20953-AAS20969
XX
XX represent PCR primers described in the present invention
XX
SQ Sequence 18 BP; 1 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1024 CTCCTCTGCTGGACCATC 1041
Db 1 CTCCTCTGCTGGACCATC 18
RESULT 285
ABT04994
ID ABT04994 standard; DNA; 18 BP.
XX
XX ABT04994;
XX
XX 11-OCT-2002 (first entry)
XX
XX TNFR1 expression modulation related antisense oligo SEQ ID No 24.
XX
XX Antisense compound; tumour necrosis factor receptor 1; liver disease;
XX
XX TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
XX
XX human; ds.
XX
XX Homo sapiens.
XX
XX WO200248168-A1.
XX

CC the gene with intronic primers for the human MLH1 gene and analysing the
 CC sequence to identify any mutants; (3) a method of identifying mutants in
 CC splice donor or acceptor sites of a human MSH2 gene, comprising
 CC sequencing splice donor or acceptor sites of the gene with intronic
 CC primers for the human MSH2 gene and analysing the sequence to identify
 CC any mutants; and (4) a transgenic model system for colorectal cancer
 CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
 CC hMSH2 variants are used to diagnose or determine a patient's
 CC susceptibility to hereditary non-polyposis colorectal cancer.. ABL01648 to
 CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
 CC fragments from the present invention. ABL01832 to ABL01839 represent
 CC mutagenic primers used in the exemplification of the present invention
 XX
 XX SQ Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAAGCCTCAGGATCTC 1240
 |||||
 Db 1 CAAAAGCTTCAGATCTC 18

RESULT 288

ABX80015
 ID ABX80015 standard; cDNA; 18 BP.

XX AC ABX80015;

XX DT 17-APR-2003 (first entry)

XX DE EST polymorphic DNA repeat polynucleotide #340.

XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
 XX Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX OS Homo sapiens.

XX PN US6472154-B1.

XX PD 29-OCT-2002.

XX PF 31-DEC-1999; 99US-00475947.

XX PR 31-DEC-1999; 99US-00475947.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX DR WPI; 2003-208818/20.

XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

XX PS Example; Col 1165; 588pp; English.

XX CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic

CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 XX SQ Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
 |||||
 Db 1 GCAGCAGCAGCCCGCAGCA 18

RESULT 289

AAD56267

ID AAD56267 standard; DNA; 18 BP.

XX AC AAD56267;

XX DT 07-AUG-2003 (first entry)

XX DE Hepatitis E virus target oligonucleotide #2.

XX KW Antiviral; viral infection; antisense therapy; virucide; ss.

XX OS Hepatitis E virus.

XX PN WO2003033657-A2.

XX PD 24-APR-2003.

XX PF 16-OCT-2002; 2002WO-US032868.

XX PR 16-OCT-2001; 2001US-0329815P.

XX PA (AVIB-) AVI BIOPHARMA INC.

XX PI Stein DA, Skilling DE, Iversen PL, Smith AW;

XX DR WPI; 2003-403210/38.

XX PT New antiviral compound directed against RNA viruses, e.g. picornavirus,
 PT comprising morpholino oligomer, supporting sequence complementary to
 PT viral target sequence that spans first open reading frame of virus
 PT genome.

XX PS Example 4; Page 41; 63pp; English.

XX CC The invention relates to antisense antiviral compounds and methods of
 CC their use in inhibition of growth of viruses of the picornavirus, of
 CC calicivirus, togavirus or flavivirus families as in treatment of viral
 CC infection. The antiviral compound is useful for inhibiting replication of
 CC an RNA virus. The method is useful for determining the effectiveness of
 CC treating a picornavirus, calicivirus, togavirus or flavivirus infection.
 CC It is also useful for determining the family or genus of an infecting
 CC picornavirus, calicivirus, togavirus or flavivirus. Determining the
 CC family or genus of an infecting virus is useful for identifying a
 CC specific infecting picornavirus, calicivirus, togavirus or flavivirus.
 CC The invention is used in antisense therapy. The present sequence is
 CC Hepatitis E virus target oligonucleotide used to illustrate the method of
 CC the invention

XX SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1271 GCCATGGAGCCCGTCAG 1288
 Db 1 GCCATGGAGCCCGTCAG 18
 RESULT 290
 AAD56287/c
 ID AAD56287 standard; DNA, 18 BP.
 XX AC AAD56287;
 XX AC
 XX 07-AUG-2003 (first entry)
 XX DE Hepatitis E virus targeting antisense oligonucleotide #2.
 XX DE Antiviral; viral infection; antisense therapy; virucide; antisense; ss.
 XX OS Hepatitis E virus.
 XX PN WO2003033657-A2.
 XX XX
 XX 24-APR-2003.
 XX XX
 XX 16-OCT-2002; 2002WO-US032868.
 XX XX
 XX 16-OCT-2001; 2001US-0329815P.
 XX XX
 XX (AVIB-) AVI BIOPHARMA INC.
 XX XX
 XX Stein DA, Skilling DE, Iversen PL, Smith AW;
 XX WPI; 2003-403210/38.
 XX XX
 XX New antiviral compound directed against RNA viruses, e.g. picornavirus,
 XX comprising morpholino oligomer, supporting sequence complementary to
 XX viral target sequence that spans first open reading frame of virus
 XX genome.
 XX XX
 XX Claim 12; Page 23; 63pp; English.
 XX XX
 XX The invention relates to antisense antiviral compounds and methods of
 XX their use in inhibition of growth of viruses of the picornavirus,
 XX calicivirus, togavirus or flavivirus families as in treatment of viral
 XX infection. The antiviral compound is useful for inhibiting replication of
 XX an RNA virus. The method is useful for determining the effectiveness of
 XX treating a picornavirus, calicivirus, togavirus or flavivirus infection.
 XX It is also useful for determining the family or genus of an infecting
 XX picornavirus, calicivirus, togavirus or flavivirus. Determining the
 XX family or genus of an infecting virus is useful for identifying a
 XX specific infecting picornavirus, calicivirus, togavirus or flavivirus.
 XX The invention is used in antisense therapy. The present sequence is
 XX Hepatitis E virus targeting antisense oligonucleotide used to illustrate
 XX the method of the invention
 XX XX
 XX Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1271 GCCATGGAGCCCGTCAG 1288
 Db 18 GCCATGGAGCCCGTCAG 1
 RESULT 291
 ADC69962
 ID ADC69962 standard; DNA; 18 BP.
 XX AC ADC69962;
 XX AC
 XX 18-DEC-2003 (first entry)
 XX XX

DE DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 451).
 XX XX PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
 KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
 KW cytosine methylation state.
 XX XX Unidentified.
 OS XX
 PN WO2003052135-A2.
 XX XX
 XX 26-JUN-2003.
 XX XX
 XX 10-DEC-2002; 2002WO-EP014026.
 PF XX
 XX 14-DEC-2001; 2001DE-01061625.
 PR XX
 XX (EPIG-) EPIGENOMICS AG.
 PA XX
 XX Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;
 PI Nimmrich I;
 PI WPI; 2003-533029/50.
 DR XX
 XX Detecting and differentiating cytosine methylation state of genomic DNA,
 PT useful for diagnosing, treating prognosticating and/or monitoring lung
 PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
 PT carcinoma.
 XX XX
 XX Claim 15; SEQ ID NO 451; 58pp; English.
 PS XX
 XX This invention relates to a novel method for detecting and
 CC differentiating between lung cell proliferative disorders associated with
 CC at least one gene and/or their regulatory regions. Specifically, it
 CC refers to a method comprising contacting a target nucleic acid in a
 CC biological sample with at least one reagent, wherein the reagent is able
 CC to distinguish between methylated and non-methylated CpG dinucleotides
 CC present in the target DNA. As such, it is possible to further
 CC differentiate and diagnose medical conditions including adenocarcinoma
 CC and squamous cell carcinoma, and their respective adjacent lung tissue.
 CC The present invention describes cytosine methylation and PNA-oligomers
 CC that are useful as probes for determining the cytosine methylation state
 CC of single nucleotide polymorphisms (SNPs) of the target sequence. This
 CC oligonucleotide sequence is a primer oligomer used for the analysis of
 CC CpG positions within genomic DNA, used in an exemplification of the
 CC invention.
 XX XX
 XX Sequence 18 BP; 3 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3583 TATAGTTTGTGGAGT 3600
 Db 1 TTAGGTTTGTGGAGT 18
 RESULT 292
 ADD28828/c
 ID ADD28828 standard; DNA; 18 BP.
 XX AC ADD28828;
 XX AC
 XX 15-JAN-2004 (first entry)
 DT XX
 XX Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:447.
 DE XX
 XX molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX XX
 XX Escherichia coli.
 OS XX

```

PN WO2003050269-A2.
XX 19-JUN-2003.
XX 11-DEC-2002; 2002WO-US039914.
XX 11-DEC-2001; 2001US-0339687P.
XX (UYAR-) UNIV ARIZONA.
XX (KEIM/) KEIM P.
XX (KEYS/) KEYS C.
XX Keim P, Keys C;
XX WPI; 2003-864934/80.
XX Molecular sub-typing system for Escherichia coli, comprises observing and
XX recording variable number tandem repeat arrays in an Escherichia coli DNA
XX sample.
XX Claim 7; SEQ ID NO 447; 166pp; English.
XX The present invention describes a molecular sub-typing system (S) for
XX Escherichia coli, which comprises observing and recording variable number
XX tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
XX described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers
XX (II) for amplifying (1); (3) amplicon comprising (II) and a locus
XX comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
XX of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
XX comprising primers for VNTR loci in E. coli, and amplifying reagents for
XX multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
XX -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
XX primers for amplifying loci comprising VNTR, where the primers have an
XX observable indicator; (b) obtaining single-stranded sample DNA from the
XX E. coli sample to be subtyped; (c) combining the primers, the sample DNA
XX and amplifying reagents under hybridising and amplifying conditions in a
XX PCR instrument to form amplicons comprising the primers and the VNTR; (d)
XX separating the amplicons by size; (e) evaluating numbers and sizes of
XX separated amplicons; and (f) comparing the evaluation to an evaluation of
XX amplicons obtained by PCR from a known E. coli strain. M1 is useful for
XX producing discrete genetic data for an epidemiological database. (1) is
XX useful as a research tool. (S) is useful for subtyping pathogenic E.
XX coli. The present sequence represents an E. coli VNTR loci related
XX amplicon sequence which is used in the exemplification of the present
XX invention.
XX Sequence 18 BP; 0 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1579 ACAACAGCAACAACAGCA 1596
XX Db 18 AAAACAGCAAAAACAGCA 1
XX RESULT 293
XX ADD28830/c
XX ID ADD28830 standard; DNA; 18 BP.
XX AC ADD28830;
XX 15-JAN-2004 (first entry)
XX Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:449.
XX molecular sub-typing system; Escherichia coli;

```

```

KW variable number tandem repeat; VNTR; genetic data;
KW epidemiological database; research; gene; ds.
XX Escherichia coli.
XX WO2003050269-A2.
XX 19-JUN-2003.
XX 11-DEC-2002; 2002WO-US039914.
XX 11-DEC-2001; 2001US-0339687P.
XX (UYAR-) UNIV ARIZONA.
XX (KEIM/) KEIM P.
XX (KEYS/) KEYS C.
XX Keim P, Keys C;
XX WPI; 2003-864934/80.
XX Molecular sub-typing system for Escherichia coli, comprises observing and
XX recording variable number tandem repeat arrays in an Escherichia coli DNA
XX sample.
XX Claim 7; SEQ ID NO 449; 166pp; English.
XX The present invention describes a molecular sub-typing system (S) for
XX Escherichia coli, which comprises observing and recording variable number
XX tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
XX described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers
XX (II) for amplifying (1); (3) amplicon comprising (II) and a locus
XX comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
XX of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
XX comprising primers for VNTR loci in E. coli, and amplifying reagents for
XX multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
XX -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
XX primers for amplifying loci comprising VNTR, where the primers have an
XX observable indicator; (b) obtaining single-stranded sample DNA from the
XX E. coli sample to be subtyped; (c) combining the primers, the sample DNA
XX and amplifying reagents under hybridising and amplifying conditions in a
XX PCR instrument to form amplicons comprising the primers and the VNTR; (d)
XX separating the amplicons by size; (e) evaluating numbers and sizes of
XX separated amplicons; and (f) comparing the evaluation to an evaluation of
XX amplicons obtained by PCR from a known E. coli strain. M1 is useful for
XX producing discrete genetic data for an epidemiological database. (1) is
XX useful as a research tool. (S) is useful for subtyping pathogenic E.
XX coli. The present sequence represents an E. coli VNTR loci related
XX amplicon sequence which is used in the exemplification of the present
XX invention.
XX Sequence 18 BP; 0 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1579 ACAACAGCAACAACAGCA 1596
XX Db 18 AAAACAGCAAAAACAGCA 1
XX RESULT 294
XX ADD28831
XX ID ADD28831 standard; DNA; 18 BP.
XX AC ADD28831;
XX

```


DT 15-JAN-2004 (first entry)
 XX Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:450.
 XX molecular sub-typing system; Escherichia coli;
 XX variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 KW Escherichia coli.
 XX WO2003050269-A2.
 XX 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 XX recording variable number tandem repeat arrays in an Escherichia coli DNA
 XX sample.
 PS Claim 7; SEQ ID NO 450; 166pp; English.
 XX The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli 0157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCAACACAGCA 1596
 Db 1 AAAAAAGCAAAACAGCA 18

RESULT 295

ADD28829
 ID ADD28829 standard; DNA; 18 BP.
 XX AC ADD28829;
 XX 15-JAN-2004 (first entry)
 DT Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:448.
 DE molecular sub-typing system; Escherichia coli;
 XX variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX Escherichia coli.
 OS WO2003050269-A2.
 XX 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 PR (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 DR Molecular sub-typing system for Escherichia coli, comprises observing and
 XX recording variable number tandem repeat arrays in an Escherichia coli DNA
 XX sample.
 PT Claim 7; SEQ ID NO 448; 166pp; English.
 XX The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli 0157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCAACACAGCA 1596

```
Db      1  ||||| ||||| |||||
1 AAAACAGCAAAACACGCA 18

RESULT 296
ABZ97839
ID ABZ97839 standard; DNA; 18 BP.
XX
AC ABZ97839;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human eotaxin oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13081; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cycostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1183 CCCCTCAGCCCGGTTGG 1200

RESULT 297
ADM92720
ID ADM92720 standard; DNA; 18 BP.
XX
AC ADM92720;
XX
DT 03-JUN-2004 (first entry)
XX
DE SNP-containing cardiovascular associated gene primer #50.
XX
KW SNP; single nucleotide polymorphism; cardiovascular associated gene;
KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2003057911-A2.
XX
PD 17-JUL-2003.
XX
PF 07-JAN-2003; 2003WO-EP000060.
XX
PR 08-JAN-2002; 2002EP-00000153.
XX
PA (FARB ) BAYER AG.
XX
PI Stropp U, Schwes S, Kallabis H;
XX
DR WPI; 2003-577532/54.
XX
PT New isolated polynucleotides comprising single nucleotide polymorphisms
PT of the cardiovascular gene, useful for assessing predisposition or
PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,
PT restenosis or stroke.
XX
PS Disclosure; Page 68; 187pp; English.
XX
CC The invention relates an isolated polynucleotide (I) encoded by a
CC cardiovascular associated (CA) gene, having allelic variation contained
CC in a functional surrounding like full length cDNA for CA gene
CC polypeptide, and with or without the CA gene promoter sequence. (I) is a
CC polynucleotide comprising single nucleotide polymorphisms predicting
CC cardiovascular disease. The polynucleotides are useful for assessing
CC predisposition or susceptibility to a cardiovascular disease, e.g.
CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
CC inflammation, myocardial infarction, and stroke. These may also be used
CC to predict personal medication schemes omitting adverse drug reactions,
CC or as probes for detecting genetic polymorphisms and as templates for the
CC recombinant production of normal or variant peptides/polypeptides encoded
CC by the genes. This sequence corresponds to a PCR primer to amplify one of
CC the genes of the invention.
XX
SQ Sequence 18 BP; 1 A; 8 C; 1 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1344 CTTCTGTTTGGCCTTCCC 1361
||||| ||||| |||||
Db      1 CTTCTCTATAGCCCTTCCC 18

RESULT 298
ADM92724
ID ADM92724 standard; DNA; 18 BP.
XX
AC ADM92724;
```

XX	03-JUN-2004 (first entry)
DT	SNP-containing cardiovascular associated gene primer #54.
XX	
DE	SNP; single nucleotide polymorphism; cardiovascular associated gene;
XX	allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
KW	restenosis; arterial inflammation; myocardial infarction; stroke; primer;
KW	ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2003057911-A2.
XX	
PD	17-JUL-2003.
XX	
PF	07-JAN-2003; 2003WO-EP0000060.
XX	
PR	08-JAN-2002; 2002EP-00000153.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Stropp U, Schwes S, Kallabis H;
XX	
DR	WPI; 2003-577532/54.
XX	
PT	New isolated polynucleotides comprising single nucleotide polymorphisms
PT	of the cardiovascular gene, useful for assessing predisposition or
PT	susceptibility to a cardiovascular disease, e.g. atherosclerosis,
PT	restenosis or stroke.
XX	
PS	Disclosure; Page 68; 187pp; English.
XX	
CC	The invention relates an isolated polynucleotide (I) encoded by a
CC	cardiovascular associated (CA) gene, having allelic variation contained
CC	in a functional surrounding like full length cDNA for CA gene
CC	polypeptide, and with or without the CA gene promoter sequence. (I) is a
CC	polynucleotide comprising single nucleotide polymorphisms predicting
CC	cardiovascular disease. The polynucleotides are useful for assessing
CC	predisposition or susceptibility to a cardiovascular disease, e.g.
CC	atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
CC	inflammation, myocardial infarction, and stroke. These may also be used
CC	to predict personal medication schemes omitting adverse drug reactions,
CC	or as probes for detecting genetic polymorphisms and as templates for the
CC	recombinant production of normal or variant peptides/polypeptides encoded
CC	by the genes. This sequence corresponds to a PCR primer to amplify one of
CC	the genes of the invention.
XX	
SQ	Sequence 18 BP; 1 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
	Query Match 0.4%; Score 14.8; DB 1; Length 18;
	Best Local Similarity 88.9%; Pred. No. 2.1e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy	1344 CTTCTGTTTTCCTTCCC 1361
Db	1 CTTCTCTATGCTTCCC 18
RESULT 299	
ADM77392	
ID	ADM77392 standard; DNA; 18 BP.
XX	
AC	ADM77392;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Human fibrocystin (PKHD1) gene DHPLC PCR primer #100.
XX	
KW	human; fibrocystin;
KW	treating autosomal recessive polycystic kidney disease; PKHD1; DHPLC PCR;
XX	ss; primer.
XX	

PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX WPI; 2004-203534/19.
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codons and introns of respiratory disease-relevant genes e.g.,
 PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
 PT disease e.g., asthma.
 XX Claim 2; SEQ ID NO 568; 85pp; English.
 XX The present invention relates to an oligonucleotide anti-sense to e.g.,
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
 CC end of nucleic acid target comprising gene(s) chosen from e.g.
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
 CC oligonucleotide and optionally surfactant operatively linked to the
 CC oligonucleotide. The method is useful for preventing or treating a
 CC respiratory or lung disease, which involves administering to the airways
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is
 CC useful for production of a medicament for the prevention and/or treatment
 CC of a respiratory or lung disease. The respiratory or lung disease is
 CC chosen from airway inflammation, allergy(ies), asthma, impeded
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
 CC obstruction. The present sequence represents an oligonucleotide of the
 CC invention.
 XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1183 CCCCTCAGCCAGGTGG 1200
 Db 1 CCCCTCAGCTCAGTGG 18
 RESULT 303
 ADO45203
 ID ADO45203 standard; DNA; 18 BP.
 XX ADO45203;
 AC ADO45203;
 XX 15-JUL-2004 (first entry)
 DT Human oligonucleotide #569.
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX Homo sapiens.
 OS US2004049022-A1.
 XX 11-MAR-2004.
 PD 25-JUL-2003; 2003US-00627930.
 XX 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.

(TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX WPI; 2004-293804/27.
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX Claim 2; SEQ ID NO 569; 174pp; English.
 XX The invention relates to oligonucleotides anti-sense to an initiation
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
 CC also relates to a method of screening a candidate compound that binds to
 CC one or more nucleic acid target(s) or expressed product(s), for the
 CC prevention and/or treatment of a respiratory or lung disease. The
 CC oligonucleotides are useful for reducing or inhibiting expression of a
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
 CC useful for preventing or treating a respiratory or lung disease. The
 CC respiratory or lung disease is associated with hyper-responsiveness to
 CC and/or increased levels of, adenosine and/or levels of adenosine A
 CC receptor(s), and/or asthma and/or lung allergies associated with
 CC inflammation or an inflammatory disease. The respiratory or lung disease
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
 CC hypertension, lung inflammation, bronchitis, airway obstruction or
 CC bronchoconstriction. This sequence represents an oligonucleotide of the
 CC invention.
 XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1183 CCCCTCAGCCAGGTGG 1200
 Db 1 CCCCTCAGCTCAGTGG 18
 RESULT 304
 ADO45202
 ID ADO45202 standard; DNA; 18 BP.
 XX ADO45202;
 AC ADO45202;
 XX 15-JUL-2004 (first entry)
 DT Human oligonucleotide #568.
 DE Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX Homo sapiens.
XX US2004049022-A1.
XX 11-MAR-2004.
XX 25-JUL-2003; 2003US-00627930.
XX 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUHH/) LU H.
XX (CONG/) CONG H.
XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-293804/27.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX Claim 2; SEQ ID NO 568; 174pp; English.
XX The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1183 CCCCTCAGCCCGGTGG 1200
|||||
Db 1 CCCCTCAGCTCAGTGG 18
RESULT 305
ADR06027
ID ADR06027 standard; DNA; 18 BP.

XX ADR06027;
XX 21-OCT-2004 (first entry)
XX Human TNFR1 antisense oligonucleotide seqid 25.
XX cytostatic; gene therapy; apoptosis inhibitor;
KW radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;
KW human; antisense oligonucleotide; antisense technology; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= Phosphorothioate backbone"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
FT nucleotides"
FT modified_base 15..18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
FT nucleotides"
XX US2004147471-A1.
XX 29-JUL-2004.
XX 06-NOV-2003; 2003US-00702817.
XX 26-JUN-1998; 98US-00106038.
PR 17-JUN-1999; 99WO-US013763.
PR 24-OCT-2000; 2000US-00695451.
XX (ZHAN/) ZHANG H.
XX Zhang H;
XX WPI; 2004-561407/54.
XX Inhibiting radiation-induced apoptosis in a cell or tissue comprises
PT administering to the cell or tissue an antisense oligonucleotide targeted
PT to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
XX Example 10; SEQ ID NO 25; 24pp; English.
XX The invention describes a method of inhibiting radiation-induced
CC apoptosis in a cell or tissue comprising administering to the cell or
CC tissue an antisense oligonucleotide of 8-30 nucleotides in length
CC targeted to a nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
CC for inhibiting radiation-induced apoptosis in a cell or tissue, and for
CC treating diseases associated with the expression of TNFR1. This sequence
CC represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
CC oligonucleotide.
XX Sequence 18 BP; 5 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 977 CAGCAGCACCAGCAGCAG 994
|||||
Db 1 CAGGAGCACCAGCGCAG 18
RESULT 306

KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX
 OS Rattus rattus.

XX WO9523225-A2.

XX PD 31-AUG-1995.

XX PF 23-FEB-1995; 95WO-IB000156.

XX PR 23-FEB-1994; 94US-00201109.

XX PR 29-MAR-1994; 94US-00218934.

XX PR 07-APR-1994; 94US-00222795.

XX PR 15-APR-1994; 94US-00224483.

XX PR 15-APR-1994; 94US-00227958.

XX PR 18-MAY-1994; 94US-00228041.

XX PR 06-JUL-1994; 94US-00245736.

XX PR 15-AUG-1994; 94US-00271280.

XX PR 16-AUG-1994; 94US-00291932.

XX PR 17-AUG-1994; 94US-00291433.

XX PR 19-AUG-1994; 94US-00292620.

XX PR 02-SEP-1994; 94US-00293520.

XX PR 08-SEP-1994; 94US-00300000.

XX PR 23-SEP-1994; 94US-00303039.

XX PR 23-SEP-1994; 94US-00311486.

XX PR 28-SEP-1994; 94US-00311749.

XX PR 03-OCT-1994; 94US-00314397.

XX PR 07-OCT-1994; 94US-00316771.

XX PR 11-OCT-1994; 94US-00319492.

XX PR 04-NOV-1994; 94US-00321993.

XX PR 10-NOV-1994; 94US-00334847.

XX PR 28-NOV-1994; 94US-00337608.

XX PR 16-DEC-1994; 94US-00345516.

XX PR 23-DEC-1994; 94US-00357577.

XX PR 30-JAN-1995; 94US-00363233.

XX PR 95US-00380734.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;

PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;

PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;

PI Tracz D, Usman N, Wincott FE, Woolf T;

XX WPI; 1995-351090/45.

XX Ribozyms having modified bases and methods for producing them - for use

XX in inhibiting disease related genes.

XX Claim 2; Page 201; 407pp; English.

XX The present sequence represents a preferred target sequence for an

XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the

XX nucleotide base position indicated in the DE line. Regions of the mRNA

XX that do not form secondary folding structures and that contain potential

XX hammerhead and hairpin ribozyme cleavage sites were identified by

XX computer analysis. Ribozymes directed against these mRNA sequences were

XX designed and synthesised with modifications that improve their nuclease

XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby

XX inhibit ICAM-1 expression, making them useful for reducing transplant

XX rejection and alleviating symptoms in patients with rheumatoid arthritis,

XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to

XX correct PI field.)

XX Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;

XX Query Match 0.4%; Score 14.4; DB 1; Length 17;

XX Best Local Similarity 75.0%; Pred. No. 2e+02; Indels 0; Gaps 0;

XX Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

XX

XX

XX

XX

XX

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XX

XX

Qy 2349 GGCCACCCTACCTAGG 2364
 |||||:||||:
 Db 1 GGCCCCUACCUAGG 16

RESULT 309

AAT33778/c

ID AAT33778 standard; DNA; 17 BP.

XX AC AAT33778;

XX DT 19-DEC-1996 (first entry)

XX DE Primer/probe (CTA) used in manipulation of ob gene control region.

XX KW Ob gene; modulation; control region; cachexia; anorexia; wasting disease;

XX KW hyperlipidaemia; hypercholesterolaemia; obesity; infertility;

XX KW type II diabetes; ss.

XX OS Synthetic.

XX PN WO9629405-A2.

XX PD 26-SEP-1996.

XX PF 19-MAR-1996; 96WO-US003808.

XX PR 20-MAR-1995; 95US-00408584.

XX PR 05-APR-1995; 95US-00418096.

XX PR 02-AUG-1995; 95US-00510584.

XX PR 30-OCT-1995; 95US-00558588.

XX PR 21-NOV-1995; 95US-0007390P.

XX PR 30-NOV-1995; 95US-0007721P.

XX PR 14-DEC-1995; 95US-0008601P.

XX PA (LIGA-) LIGAND PHARM INC.

XX PA (INSP) INST PASTEUR LILLE.

XX PI Eriggs MR, Auwerx J, De Vos P, Staelen B, Croston GE, Miller SG;

XX WPI; 1996-443181/44.

XX Control regions isolated from human ob gene - useful in systems to

XX identify modulators of ob gene expression, for treatment of anorexia,

XX cachexia, diabetes, and obesity.

XX Disclosure; Page 33; 167pp; English.

XX The control regions of the ob gene can be used to identify compounds

XX which modulate expression of the gene. A host having cachexia, anorexia

XX or any wasting disease characterised by loss of appetite, insufficient

XX food intake or body weight loss can be treated by administering a

XX composition containing a down regulator of ob gene expression. The body

XX weight or fat content of a host can be changed and a host having

XX hyperlipidaemia, hypercholesterolaemia, type II diabetes, or obesity

XX related infertility can be treated by administering a composition

XX containing an up regulator of ob gene expression. Primers/probes used in

XX the amplification/identification of the human ob gene control regions are

XX listed in AAT33760-78

XX Sequence 17 BP; 1 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 14.4; DB 1; Length 17;

XX Best Local Similarity 93.8%; Pred. No. 2e+02; Indels 0; Gaps 0;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AAAX71238
ID AAAX71238 standard; RNA; 17 BP.
XX
AC AAAX71238;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #250.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
XX
PA 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, ecc., in a human patient.
XX
PS Claim 4; Page 104; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 1;
OY 3494 AATTGCTCTAATAGA 3509
DB 1 AAUUGUCUUAUUGA 16
RESULT 311
AAA20589/c
ID AAA20589 standard; RNA; 17 BP.
XX
AC AAA20589;
XX
XX 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3815.
XX
KW Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW
KW hammerhead ribozyme; angiogenic factor; cyrostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus scleriosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX WO9950403-A2.
PN
XX 07-OCT-1999.
PD
XX 24-MAR-1999; 99WO-US006507.
PF
XX 27-MAR-1998; 98US-0079678P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI
XX WPI; 1999-591315/50.
DR
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
PS Claim 55; Page 155; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences.
CC AAA21889 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberosus scleriosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;
OY 1390 CCAACAGCAACAGCAG 1405
DB 17 CCAACAGCAACATCAG 2
RESULT 312
AAA25734/c
ID AAA25734 standard; DNA; 17 BP.
XX
XX AAA25734;
AC
XX 19-JUL-2000 (first entry)
DT

```
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2232.
DE
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
KW
XX Homo sapiens.
OS
XX WO9954459-A2.
PN
XX 28-OCT-1999.
PD
XX 19-APR-1999; 99WO-US008547.
PF
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX Claim 77; Page 88; 148pp; English.
PS
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA25993 to AAA26105 represent their corresponding target sequences.
XX AAA24748 to AAA25992 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 GTGATCAAAAGTGAAT 731
DB 17 GTGATCAAAAGTGAAT 2
RESULT 313
AAA25735/C
ID AAA25735 standard; DNA; 17 BP.
XX
XX AAA25735;
AC
XX 19-JUL-2000 (first entry)
DT
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2233.
DE
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XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX WO9954459-A2.
PN
XX 28-OCT-1999.
PD
XX 19-APR-1999; 99WO-US008547.
PF
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX Claim 77; Page 88; 148pp; English.
PS
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA25993 to AAA26105 represent their corresponding target sequences.
XX AAA24748 to AAA25992 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 GTGATCAAAAGTGAAT 731
DB 16 GTGATCAAAAGTGAAT 1
RESULT 314
ABK00234
ID ABK00234 standard; RNA; 17 BP.
XX
XX ABK00234;
AC
XX 12-MAR-2002 (first entry)
DT
XX Human NOGO Hammerhead Ribozyme #234.
DE
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW
```

cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
inflammatory arthropathy; central nervous system injury;
cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
Parkinson's disease; ataxia; Huntington's disease;
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX
XX 28-FEB-2000; 2000US-0185516P.
XX
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (BLAT/) BLATT L.
XX
XX (MCSW/) MCSWIGGEN J.
XX
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 88; Page 69; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the
XX presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the
XX cell and treat a patient having a condition associated with the level of
XX NOGO. The treatment may further comprise the use of one or more
XX therapies. In particular, the NOGO-targeting nucleic acid may be used to
XX treat central nervous system (CNS) injury and cerebrovascular accident
XX (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
XX chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
XX Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
XX disease, muscular dystrophy, and/or other neurodegenerative disease
XX states which respond to the modulation of NOGO expression. The present
XX sequence is a hammerhead ribozyme of the invention

SQ Sequence 17 BP; 7 A; 4 C; 1 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 1689 TCCTACTTCAGCAAT 1704
Db 2 UCCUACUUCAGAAAU 17
RESULT 315
ABK00235
ID ABK00235 standard; RNA; 17 BP.
XX
XX AC ABK00235;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human NOGO Hammerhead Ribozyme #235.
XX
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
XX KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
XX KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
XX KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
XX KW inflammatory arthropathy; central nervous system injury;
XX KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
XX KW Parkinson's disease; ataxia; Huntington's disease;
XX KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO200159103-A2.
XX
XX PD 16-AUG-2001.
XX
XX PF 09-FEB-2001; 2001WO-US004273.
XX
XX PR 11-FEB-2000; 2000US-0181797P.
XX
XX PR 28-FEB-2000; 2000US-0185516P.
XX
XX PR 06-MAR-2000; 2000US-0187128P.
XX
XX XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PA (BLAT/) BLATT L.
XX
XX PA (MCSW/) MCSWIGGEN J.
XX
XX PA (CHOW/) CHOWRIRA B M.
XX
XX PI Blatt L, Mcswiggen J, Chowrira BM;
XX
XX XX WPI; 2001-607195/69.
XX
XX XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX XX Claim 88; Page 69; 200pp; English.
XX
XX XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the
XX presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the
XX cell and treat a patient having a condition associated with the level of
XX NOGO. The treatment may further comprise the use of one or more
XX therapies. In particular, the NOGO-targeting nucleic acid may be used to
XX treat central nervous system (CNS) injury and cerebrovascular accident
XX (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
XX chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
XX Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
XX disease, muscular dystrophy, and/or other neurodegenerative disease
XX states which respond to the modulation of NOGO expression. The present
XX sequence is a hammerhead ribozyme of the invention

CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention

XX SQ Sequence 17 BP; 7 A; 4 C; 1 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 10; Conservative 5;

QY 1689 TCCTACTTCAGCAAT 1704

DB 1 UCCUACUUCAGAAAU 16

RESULT 316

ABL46891

ID ABL46891 standard; RNA; 17 BP.

AC ABL46891;

DT 27-JUN-2003 (first entry)

XX Human GRID G-cleaver ribozyme substrate oligonucleotide #32.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX Homo sapiens.

XX WO200162911-A2.

XX 30-AUG-2001.

PF 23-FEB-2001; 2001WO-US005957.

PR 24-FEB-2000; 2000US-0184594P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 69; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful

CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0;

QY 1409 CAGCAGCAGCAGC 1424

DB 1 CAGCAGCUGCAGCAGC 16

RESULT 317

ABL46750

ID ABL46750 standard; RNA; 17 BP.

XX ABL46750;

XX 27-JUN-2003 (first entry)

XX Human GRID NCH ribozyme substrate oligonucleotide #204.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX Homo sapiens.

XX WO200162911-A2.

XX 30-AUG-2001.

PF 23-FEB-2001; 2001WO-US005957.

PR 24-FEB-2000; 2000US-0184594P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 66; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0;

QY 1409 CAGCAGCAGCAGC 1424

DB 2 CAGCAGCUGCAGCAGC 17

```
RESULT 318
AAS00452/c
ID AAS00452 standard; DNA; 17 BP.
XX
XX AAS00452;
AC
XX
XX 11-SEP-2003 (revised)
DT 15-MAY-2001 (first entry)
XX
XX Lactococcus lactis pyrG gene nested PCR primer pyrg8b.
DE
XX
XX Pyrg; cytidine triphosphate synthetase; CTP; pyrimidine metabolism; UTP;
KW bacteriophage resistant; lactic acid bacterial culture; starter culture;
KW food industry; feed product; dairy product; fermentation process;
KW probiotic; PCR primer; ss.
XX
XX Lactococcus lactis subsp. cremoris; MG1363.
OS
XX
XX WO200114520-A2.
PN
XX
XX 01-MAR-2001.
PD
XX
XX 10-AUG-2000; 2000WO-DK000446.
PF
XX
XX 19-AUG-1999; 99US-00377152.
PR
XX
XX (CHRH-) CHR HANSEN AS.
PA
XX
XX Wadkov-Hansen SLL, Hammer K, Martinussen J;
PI
XX
XX WPI; 2001-218434/22.
DR
XX
XX Obtaining a derivative of Lactococcus lactis subspecies cremoris having
PT reduced susceptibility to a bacteriophage, useful in food and feed
PT manufacturing, comprises mutating a gene involved in pyrimidine
PT metabolism of a parent bacterium.
XX
XX Example 1; Page 20; 70pp; English.
PS
XX
XX The present sequence for Lactococcus lactis pyrG gene nested PCR primer
CC pyrg8b is 1 of 6 nested PCR primers (AAS00444-AAS00446 and AAS00450-
CC AAS00452) used with partly degenerate primers containing either an EcoRI,
CC HindIII or Sau3AI restriction site (AAS00455-AAS00457) to PCR Lactococcus
CC lactis subspecies cremoris wild type strain MG1363 pyrG gene. The pyrG
CC gene encodes for cytidine triphosphate (CTP) synthetase which is involved
CC in pyrimidine metabolism by converting UTP to CTP. The wild type CTP
CC synthetase is used to construct bacteriophage resistant lactic acid
CC mutants (AAU00432-AAU00434) that have a reduced susceptibility towards
CC attack by at least one kind of bacteriophage comprising subjecting a
CC population of parent lactic acid bacterial cells, which are initially
CC susceptible towards bacteriophage attack, to mutation in a gene involved
CC in the pyrimidine metabolism. The lactic acid bacterial cultures which
CC have significantly reduced susceptibility towards bacteriophage attacks
CC are useful as starter cultures in the manufacture of food and feed
CC products, e.g. dairy products and in other food fermentation processes.
CC These may also be used as probiotics, which when ingested by humans or
CC animals in the form of viable cells confers good health conditions.
CC Another strain of L. lactis, WB383, is a leaky mutant for the pyrG gene
CC (AAS00458) in that these cells do not require cytidine for growth but
CC have a reduced susceptibility to bacteriophages. (Updated on 11-SEP-2003
CC to standardise OS field)
XX
XX Sequence 17 BP; 1 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. NO. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1570 GCAGCAACACACACG 1585
| | | | | | | | | | | | | | | |
Db 17 GCAGCAACACACACTG 2
```

```
RESULT 319
AEN08476
ID AEN08476 standard; DNA; 17 BP.
XX
XX AEN08476;
AC
XX
XX 29-MAY-2002 (first entry)
DT
XX
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8468.
DE
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200192524-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX
XX 21-SEP-2000; 2000US-0234687P.
PR
XX
XX 27-SEP-2000; 2000US-0236359P.
PR
XX
XX 04-OCT-2000; 2000GB-00024263.
PR
XX
XX 30-JAN-2001; 2001WO-US000661.
PR
XX
XX 30-JAN-2001; 2001WO-US000662.
PR
XX
XX 30-JAN-2001; 2001WO-US000663.
PR
XX
XX 30-JAN-2001; 2001WO-US000664.
PR
XX
XX 30-JAN-2001; 2001WO-US000665.
PR
XX
XX 30-JAN-2001; 2001WO-US000666.
PR
XX
XX 30-JAN-2001; 2001WO-US000667.
PR
XX
XX 30-JAN-2001; 2001WO-US000668.
PR
XX
XX 30-JAN-2001; 2001WO-US000669.
PR
XX
XX 30-JAN-2001; 2001WO-US000670.
PR
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX
XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 8468; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX
XX The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
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```
XX SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 602 GAACCTGGAGACATCA 617
Db 1 GACCTGGAGACATCA 16

RESULT 320
ABN07209
ID ABN07209 standard; DNA; 17 BP.
XX AC ABN07209;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7201.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 7201; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
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```
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCCTATGAGC 337
Db 2 GACCTTGCCGATGAGC 17

RESULT 321
ABN07210
ID ABN07210 standard; DNA; 17 BP.
XX AC ABN07210;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7202.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 7202; 214pp; English.
XX
```

CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCTGATGAC 337
 |||||
 DB 1 GACCTTGCGATGAC 16

RESULT 322
 ABN08475
 ID ABN08475 standard; DNA; 17 BP.
 AC
 XX ABN08475;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8467.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 FA (ABOM-) ABOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 8467; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACGGAGAACATGA 617
 |||||
 DB 2 GAGCTGGAGAACATGA 17

RESULT 323
 ABV9862
 ID ABV9862 standard; DNA; 17 BP.
 XX
 AC ABV9862;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 575.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI2339051-A2.
 XX
 PD 11-SEP-2002.
 XX
 XX 28-JAN-2002; 2002EP-00001165.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.


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PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 575; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2553 CCTGACGCTCTGCAGG 2568
Db 1 CCCAGACGCTCTGCAGG 16
RESULT 324
ABV89861
ID ABV89861 standard; DNA; 17 BP.
XX AC ABV89861;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 574.
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-00001165.
XX PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 574; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2553 CCTGACGCTCTGCAGG 2568
Db 2 CCCAGACGCTCTGCAGG 17
RESULT 325
ACN12567/c
ID ACN12567 standard; RNA; 17 BP.
XX AC ACN12567;
XX 22-APR-2004 (first entry)
XX WNV minus strand Zinzyne substrate SEQ ID NO 12570.
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX viricide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyne; ss.
XX OS West Nile Virus.
XX WO200268637-A2.
XX 06-SEP-2002.

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PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX Claim 23; SEQ ID NO 12570; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||
17 AACCCCTGCTCAACTC 2

RESULT 326
ACN04426
ID ACN04426 standard; RNA; 17 BP.
XX
XX ACN04426;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Zinzyme substrate SEQ ID NO 4429.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
XX Amberzyme; Zinzyme; 88.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX Claim 23; SEQ ID NO 12570; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||
17 AACCCCTGCTCAACTC 2

RESULT 327
ABT34779/c
ID ABT34779 standard; DNA; 17 BP.
XX
XX ABT34779;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID NO 416.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 82; 720pp; French.

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XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 4429; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 5 A; 8 C; 1 G; 0 T; 3 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||
2 AACCCCTGCTCAACUC 17

RESULT 327
ABT34779/c
ID ABT34779 standard; DNA; 17 BP.
XX
XX ABT34779;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID NO 416.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 82; 720pp; French.

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XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 XX Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2778 AGCTAAGCACACAGAT 2793
 |||||
 DB 17 AGCTAAGCAACAGAT 2

RESULT 328
 ADB05009/C
 ID ADB05009 standard; DNA; 17 BP.
 XX ADB05009;
 XX 20-NOV-2003 (first entry)
 XX Human MDZ12 scanning oligonucleotide SEQ ID 5995.
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX
 XX EP1281758-A2.
 XX
 XX 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX Example 8; SEQ ID NO 5995; 103pp; English.
 XX

CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 AGCTTCTCTCTCTACA 1383
 |||||
 DB 17 AGCTTCTCTCTCTACA 2

RESULT 329
 ADB05010/C
 ID ADB05010 standard; DNA; 17 BP.
 XX ADB05010;
 XX 20-NOV-2003 (first entry)
 XX Human MDZ12 scanning oligonucleotide SEQ ID 5996.
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS
 XX
 XX EP1281758-A2.
 XX
 XX 05-FEB-2003.
 XX 30-JUL-2002; 2002EP-00016874.
 XX 02-AUG-2001; 2001US-00922181.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX Example 8; SEQ ID NO 5996; 103pp; English.
 XX

The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX

CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 AGCCTTCTCTCTCTACA 1383
 |||||
 Db 16 AGGCTTCTCTCTCTACA 1

RESULT 330
 ACID62073/c

ID ACID62073 standard; RNA; 17 BP.

AC ACID62073;

DT 23-SEP-2003 (first entry)

DE HCV minus strand DNazyme substrate sequence #384.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0286876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLATT) BLATT L.

PA (MACEJ) MACEJAK D.

PA (MCSW) MCSWIGGEN J.

PA (MORR) MORRISSEY D.

PA (PAVC) PAVCO P.

PA (LEEP) LEE P.

PA (DRAP) DRAPER K.

PA (ROBE) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Claim 1; Page 281; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV. The compounds
 CC that modulate the expression and/or replication of HCV. The compounds
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675

|||||
 Db 16 AAGGTCACCTTTGCCA 1

RESULT 331

ACC64185

ID ACC64185 standard; DNA; 17 BP.

XX ACC64185;

AC ACC64185;

DT 01-JUN-2003 (first entry)

XX Murine oligonucleotide associated with tumour suppression, SEQ ID 1432.

DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;

KW tumour suppression; tumour reversion; apoptosis; virus resistance;

KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;

KW schizophrenia; ss.

XX Mus musculus.

OS WO2003025176-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

PI WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.

XX Disclosure; Page 198; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-

CC ACC68806), which are associated with tumour suppression, tumour

CC reversion, apoptosis and virus resistance. The oligonucleotides are

CC useful as (1) as probes and primers for detecting, identifying,

CC quantifying and/or amplifying nucleic acid, e.g. as one component of a

CC gene chip; in vitro as (anti)sense reagents; and (2) for production of

CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3255 ATTCTTGTTTAAATC 3270
|||
Db 2 ATCTTGTTTAAATC 17

RESULT 332
ADC37826
ID ADC37826 standard; DNA; 17 BP.

XX AC ADC37826;

XX 18-DEC-2003 (first entry)

XX Human AMLPia scanning 17-mer oligonucleotide SEQ ID NO:175.

XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.

XX Synthetic.

OS Homo sapiens.

XX WO2003037931-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035129.

XX 01-NOV-2001; 2001US-0334773P.

XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX Shannon M, Phan T;

XX WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.

XX Example 2; SEQ ID NO 175; 172pp; English.

XX The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.

XX Sequence 17 BP; 6 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1506 AGCAACAGCAGCAGAG 1521
|||
Db 1 AGCAACAGCAGCAGG 16

RESULT 333

ADB45768/c
ID ADB45768 standard; DNA; 17 BP.

XX AC ADB45768;

XX 18-DEC-2003 (first entry)

XX Tumour suppression/reversion associated nucleotide #6091.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
diagnosis.

XX OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX NPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 744; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors) the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules.
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3182 TGGACTACATGAAGAT 3197
|||||
Db 17 TGGACTACATGAAGAT 2

RESULT 334

ADI50387

ID ADI50387 standard; DNA; 17 BP.

XX AC ADI50387;

WPI; 2003-250498/25.

Best Local Similarity 93.8%; Pred. NO. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3330 ATCCAAATTATCCAAA 3345
|||||
Db 2 ATCCAAATTATCCAAA 17

RESULT 339
ADL47232/c
ID ADL47232 standard; RNA; 17 BP.
XX
AC ADL47232;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor zinyyme substrate sequence #219.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor zinyyme; substrate; ds.
XX
OS Unidentified.
XX
FN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 9; SEQ ID NO 765; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor zinyyme substrate sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. NO. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2650 CCAGAGGGCAGTGGCT 2665
|||||
Db 17 CCAGAGGGCAGTGGCT 2

RESULT 340
ADL46972/c
ID ADL46972 standard; RNA; 17 BP.
XX
AC ADL46972;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor inozyme substrate sequence #405.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor inozyme; substrate; ds.
XX
OS Unidentified.
XX
FN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
DR WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 9; SEQ ID NO 505; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor inozyme substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 7 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Indels 1; Gaps 0;

QY 2649 CCCAGAGCGCAGTGGC 2664
 DB 16 CCCAGAGCGCAGTGGC 1

RESULT 341

ADM54108
 ID ADM54108 standard; mRNA; 17 BP.

XX AC ADM54108;

DT 03-JUN-2004 (first entry)

DE Human GR1D mRNA substrate sequence #383.

XX Human; ss; GR1D; Grb2-related with insert domain; hammerhead ribozyme;
 KW NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNazyme; Inozyme;
 KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

XX OS Homo sapiens.

XX US2003134806-A1.

XX 17-JUL-2003.

PF 23-FEB-2001; 2001US-00792818.

PR 10-FEB-2000; 2000US-0181594P.

XX (JARV/) JARVIS T.

PA (CARL/) CARLOWITZ I V.

PA (MCSW/) MCSWIGGEN J.

PA (HAMB/) HAMBLIN P A.

PA (ELLI/) ELLIS J H.

XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;

XX WPI; 2003-829646/77.

XX New nucleic acid molecule that down-regulates expression of Grb2-related
 PT with insert domain (GR1D) gene, useful for treating a condition
 PT associated with the level of GR1D, e.g. tissue/graft rejection and
 PT leukemia.

XX Claim 4; SEQ ID NO 383; 74pp; English.

XX The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Grb2-related with insert domain (GR1D) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNazyme,
 CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 CC including the novel nucleic acid molecule, reducing GR1D activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC treating a patient having a condition associated with the level of GR1D
 CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GR1D gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GR1D gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GR1D, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.

XX Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Mismatches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGC 1424
 DB 2 CAGCAGCUGCAGCAGC 17

RESULT 342

ADI85415/C

ID ADI85415 standard; RNA; 17 BP.

XX AC ADI85415;

DT 03-JUN-2004 (first entry)

DE HCV DNazyme substrate sequence #2661.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
 KW HCV infection; type I interferon; DNazyme.

XX Hepatitis C virus.

OS US2003125270-A1.

XX 03-JUL-2003.

PF 18-DEC-2000; 2000US-00740332.

PR 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
 PT especially in combination with type I interferon therapy.

XX Claim 1; SEQ ID NO 2661; 198pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
 CC the binding arms of the enzymatic nucleic acid molecule comprises
 CC sequences complementary to any of the defined substrate sequences given
 CC in the specification. The nucleic acid molecule may be administered for
 CC the treatment of HCV infections, especially in combination with type I
 CC interferons. The present sequence represents a HCV DNazyme substrate
 CC sequence.

XX Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Mismatches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675

DB 16 AAGGTCACCTTTGACA 1

RESULT 343

ADR27873

ID ADR27873 standard; DNA; 17 BP.

XX AC ADR27873;

DT 04-NOV-2004 (first entry)

DE Murine VE-statin b PCR primer, SEQ ID 13.

XX Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;
 KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;
 KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; PCR;
 KW primer; ss; mouse.
 XX Mus musculus.
 OS FR2851249-Al.
 PN 20-AUG-2004.
 PD 17-FEB-2003; 2003FR-00001875.
 PF 17-FEB-2003; 2003FR-00001875.
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 XX Soncin F, Mattot V;
 PI WPI; 2004-618122/60.
 DR Using VE-statins to inhibit recruitment of perivascular smooth muscle
 PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,
 PT related nucleic acids and antibodies.
 XX Claim 10; SEQ ID NO 13; 63pp; French.
 XX The present invention relates to a method for preparing a composition for
 CC inhibiting recruitment of perivascular cells of smooth muscle type using
 CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,
 CC soluble factors secreted by endothelial cells of the blood vessels, block
 CC recruitment of perivascular smooth muscle cells (but do not affect their
 CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide
 CC fragments, nucleic acids encoding them and vectors containing this
 CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
 CC and restenosis, including in gene therapy. The VE-statin nucleic acids
 CC can also be used to produce transgenic animals (for studying the VE-
 CC statin proteins and genes); the VE-statins are used to screen for
 CC specific (ant)agonists, and antibodies specific for VE-statins can be
 CC used to determine expression profiles, particularly for diagnosis of
 CC diseases associated with VE-statins. The present sequence is a primer
 CC used to illustrate the invention.
 XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1084 TGGTCAGCAGACATTC 1099
 Db 1 TGGCAGCAGACATTC 16
 |||||
 RESULT 344
 ACN70300
 ID ACN70300 standard; DNA; 17 BP.
 XX ACN70300;
 AC 02-DEC-2004 (first entry)
 XX Human GDMPLP-1 probe SEQ ID NO:7202.
 DE Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX Homo sapiens.
 OS US2004137589-Al.
 XX PN

PD 15-JUL-2004.
 XX 26-NOV-2003; 2003US-00723361.
 PF 26-MAY-2000; 2000US-0207456P.
 XX 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0286860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 7202; 0pp; English.
 XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and
 CC 65% identity to (SI). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 322 GACCTTCCTATGAGC 337
 Db 1 GACCTTCCTATGAGC 16
 |||||
 RESULT 345
 ACN71565
 ID ACN71565 standard; DNA; 17 BP.
 XX ACN71565;
 AC 02-DEC-2004 (first entry)
 XX Human GDMPLP-1 probe SEQ ID NO:8467.
 DE
 XX

KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX Homo sapiens.
XX OS
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0268660P.
XX 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
XX (JIVY/) JI Y.
XX (PENN/) PENN S G.
XX (HANZ/) HANZEL D K.
XX (RANK/) RANK D.
XX (CHEN/) CHEN W.
XX (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon MB;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
XX Disclosure; SEQ ID NO 8467; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 602 GAACGGAGAACATGA 617
DB 2 GAGCTGAGAACATGA 17
XX
RESULT 346
ACN70299

ID ACN70299 standard; DNA; 17 BP.
XX ACN70299;
XX 02-DEC-2004 (first entry)
XX DT
XX DE Human GDMPLP-1 probe SEQ ID NO:7201.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX Homo sapiens.
XX OS
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0268660P.
XX 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
XX (JIVY/) JI Y.
XX (PENN/) PENN S G.
XX (HANZ/) HANZEL D K.
XX (RANK/) RANK D.
XX (CHEN/) CHEN W.
XX (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon MB;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
XX Disclosure; SEQ ID NO 7201; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 2e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

QY 322 GACCTTGCTGATGAC 337
ACN71566
|||
DB 2 GACCTTGGCGATGAC 17
|||
RESULT 347
ACN71566
ID ACN71566 standard; DNA; 17 BP.
XX
AC ACN71566;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPLP-1 probe SEQ ID NO:8468.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYY/) GU Y.
PA (JIYY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
DR
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 8468; Opp; English.
XX
CC The invention relates to a novel polypeptide (1) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 602 GAACCTGGAGAACATGA 617
|||
DB 1 GAGCTGGAGAACATGA 16
|||
RESULT 348
AAV51900/c
ID AAV51900 standard; DNA; 18 BP.
XX
AC AAV51900;
XX
DT 02-FEB-1999 (first entry)
XX
DE Zea mays genome reverse PCR primer #196.
XX
KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW hybridisation; plant; hybrid certification; genetic contribution;
KW progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS Synthetic.
OS Zea mays.
XX
PN WO9824796-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021782.
XX
PR 02-DEC-1996; 96US-0032069P.
PR 07-MAR-1997; 97US-00813507.
XX
PA (APFY-) AFFYMETRIX INC.
XX
PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
XX WPI; 1998-333252/29.
XX
PT Brassica species allele-specific oligonucleotide probes and primers -
PT useful for plant breeding.
XX
PS Example 1; Page 53; 65pp; English.
XX
CC AAV51705-V52008 are reverse PCR primers used to amplify fragments of the
CC Zea mays genome in order to detect polymorphic markers. Such markers can
CC be used in the construction of allele-specific primers and probes for
CC amplification or hybridisation, e.g. to determine common or disparate
CC ancestry between 2 or more plants, to monitor the genetic contribution of
CC an ancestral plant, to trace the progeny of proprietary plants, in
CC certification of a hybrid plant or to identify the progeny of a back-
CC crossed plant with an ancestral plant
XX
SQ Sequence 18 BP; 0 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1532 GCCCAACAGCAGCAGC 1547
|||
DB 18 GCCCAACAGCAGCAGC 3
|||
RESULT 349
AAX10193/c

ID AAX10193 standard; DNA; 18 BP.
 XX
 AC AAX10193;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Human biallelic polymorphic marker downstream primer #499.
 XX
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KW treatment; marker; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9820165-A2.
 XX
 PD 14-MAY-1998.
 XX
 PF 05-NOV-1997; 97WO-US020313.
 XX
 PR 06-NOV-1996; 96US-0030455P.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA
 XX Lander ES, Wang D, Hudson T;
 PI WPI; 1998-286974/25.
 XX
 DR New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.
 XX
 PS Claim 16; Page 213; 310pp; English.
 XX
 CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the
 CC isolation of various biallelic polymorphic markers found in the human
 CC genome (represented in AAX10269-X12937). These primers can be used in a
 CC method for determining polymorphic forms in an individual for use in e.g.
 CC forensics, paternity testing or for phenotypic typing for diseases such
 CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
 CC hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria.
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases
 XX
 SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2647 TTCCCAGAGGCGAGTG 2662
 | | | | | | | | | | | | | | | | | | | | | |
 Db 16 TTCCCAGAGGCGAGTG 1
 RESULT 350
 AAZ41191/c
 ID AAZ41191 standard; DNA; 18 BP.
 XX
 AC AAZ41191;
 XX
 DT 26-JAN-2000 (first entry)

XX Human AKT-1 phosphorothioate antisense oligonucleotide SEQ ID NO:343.
 DE
 XX Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9953101-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008268.
 XX
 PR 13-APR-1998; 98US-0081483P.
 PR 28-APR-1998; 98US-00067638.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Cowser LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
 PI Chasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX WPI; 1999-620446/53.
 XX
 DR Identifying compounds which modulate expression of nucleic acids, used to
 PT provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity.
 XX
 PS Example 30; Page 113; 264pp; English.
 CC
 CC A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of the
 CC compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the tNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the tNA according to defined criteria; and (2) a method of defining a set
 CC of compounds that modulate the expression of a tNA sequence via binding
 CC of the compounds with the tNA. The methods can be used for the generation
 CC and identification of synthetic compounds having defined physical,
 CC chemical or bioactive properties. Information gathered from assays of
 CC such compounds is used to identify nucleic acid sequences that are
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 18 BP; 0 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 73 GAAGCAGCGGAGGAGGAG 88
 | | | | | | | | | | | | | | | | | | | | | |
 Db 18 GAAGCAGCGGAGGAGGAG 3
 RESULT 351
 AAZ22207/c
 ID AAZ22207 standard; DNA; 18 BP.
 XX
 AC AAZ22207;
 XX
 DT 26-NOV-1999 (first entry)

DE Human Akt-1 mRNA inhibiting antisense oligo ISIS #28890.
 XX Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis; infection;
 KW inflammation; tumor formation; ss.
 KW Synthetic.
 OS Homo sapiens.
 XX US5958773-A.
 XX 28-SEP-1999.
 XX 17-DEC-1998; 98US-00212771.
 XX 17-DEC-1998; 98US-00212771.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowsett LM;
 XX WPI; 1999-561048/47.
 XX Antisense compounds complementary to Akt-1 useful for, e.g. diagnostics,
 PT therapeutics and as research reagents.
 XX Claim 3; Col 39; 32pp; English.
 XX The invention provides antisense compounds of 8-30 nucleotides that
 CC inhibit the expression of human Akt-1. The antisense compounds may be
 CC used for diagnostics, therapeutics (for modulating the expression of Akt-
 CC 1), prophylaxis (e.g. to prevent or delay infection, inflammation, or
 CC tumor formation), as research reagents (e.g. to distinguish between
 CC members of a biological pathway) and in kits. Sequences AA22197-236
 CC represent phosphorothioate oligonucleotides used for antisense inhibition
 CC of Akt-1 mRNA
 XX
 XX Sequence 18 BP; 0 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 73 GAAGCAGCGGAGGAG 88
 Db 18 GAAGCAGCGGAGGAG 3
 RESULT 352
 AAA48769
 ID AAA48769 standard; DNA; 18 BP.
 XX
 XX AAA48769;
 AC
 XX 08-SEP-2000. (first entry)
 DT
 XX Human G-alpha-16 antisense oligonucleotide ISIS# 20826.
 DE
 XX Human; G-alpha-16; G protein; cytostatic; hyperproliferative disorder;
 KW cancer; inflammation; infection; antisense inhibition; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200032817-A1.
 XX
 XX 08-JUN-2000.
 PD
 XX 25-AUG-1999; 98WO-US019613.
 XX
 XX 03-DEC-1998; 98US-00205143.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Cowsett LM;
 PI

XX WPI; 2000-412354/35.
 DR
 XX A new antisense compound for inhibiting the expression of human G-alpha-
 PT 16 and treating, preventing or delaying infections, inflammation or
 PT hyperproliferative disorders such as cancer.
 XX
 XX Claim 3; Page 73; 100pp; English.
 PS
 XX The present sequence is an antisense oligonucleotide used to modulate
 CC expression of G-alpha-16. G-alpha-16 is a human G protein which interacts
 CC differentially with several receptor types including members of the
 CC opioid and chemokine receptor families. A series of antisense
 CC oligonucleotides have been designed to target different regions of the
 CC human G-alpha-16 RNA. They may be used to inhibit the expression of G-
 CC alpha-16 in human cells and tissues and thus to treat diseases associated
 CC with G-alpha-16, such as hyperproliferative disorders, especially cancer.
 CC Infections, inflammation or tumour formation can be prevented or delayed.
 CC The compounds can be used in research and diagnostics in sandwich and
 CC other assays. Note: The sequence has a phosphorothioate backbone and may
 CC be either an oligodeoxynucleotide or a chimeric oligonucleotide
 CC containing 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS
 CC number given above corresponds to the oligodeoxynucleotide sequence
 XX
 XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1532 GCCCAACAGCAGCAGC 1547
 Db 3 GCCCAACAGCAGCAGC 18
 RESULT 353
 AAH02259
 ID AAH02259 standard; DNA; 18 BP.
 XX
 XX AAH02259;
 AC
 XX 24-JUL-2001 (first entry)
 DT
 XX
 XX aph(3')-Via resistance gene detection nucleotide sequence SEQ ID NO:2252.
 DE
 XX Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitica;
 KW microorganism; diagnosis; translation elongation factor ru; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KW primer; ss.
 KW
 XX Unidentified.
 OS
 XX WO200123604-A2.
 XX
 XX 05-APR-2001.
 PD
 XX 28-SEP-2000; 2000WO-CA001150.
 PF
 XX 28-SEP-1999; 99CA-02283458.
 XX
 XX 19-MAY-2000; 2000CA-02307010.
 XX
 XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 PA
 XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 XX WPI; 2001-245006/25.
 XX
 XX Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitica species in a test sample.

CC stands for ATP-Binding Cassette), which are used to identify agents (A)
 CC that modulate transcription of nucleic acids placed under control of the
 CC promoter. (A) is potentially useful for treating or preventing defects in
 CC lipid metabolism and defects in mechanisms involved in the immune
 CC response and inflammation. The promoters can also be used in gene therapy
 CC to control expression of therapeutic genes. Analysis of the promoter
 CC sequences can be used diagnostically, particularly to identify subjects
 CC at risk of lipid metabolism disorders. The present sequence is a PCR
 CC primer for human ABCA7, used to illustrate the invention
 XX
 SQ Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 GCACAGCAGCAGCAGC 1522
 DB 18 GCACAGCAGCAGCAGC 3

RESULT 356
 ADK95201
 ID ADK95201 standard; DNA; 18 BP.

XX
 AC ADK95201;

XX
 DT 06-MAY-2004 (first entry)

XX
 DE Primer of the invention #921.

XX
 KW human; single nucleotide polymorphism; SNP; ss; primer.

OS Synthetic.

XX
 FN JP2003259875-A.

XX
 PD 16-SEP-2003.

XX
 PF 08-MAR-2002; 2002JP-00064373.

XX
 PR 08-MAR-2002; 2002JP-00064373.

XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX
 DR WPI; 2004-093977/10.

XX
 PT Novel polynucleotide useful for PCR amplification along with two DNA
 PT fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.

XX
 PS Claim 2; SEQ ID NO 4230; 2627pp; Japanese.

XX
 CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.

XX
 SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 CAGCAGCAGCAGCAGC 1001
 DB 3 CAGCAGCAGCAGCAGC 18

RESULT 357
 ADM69867/c
 ID ADM69867 standard; DNA; 18 BP.

XX
 AC ADM69867;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Plant gene polymorphism marker related primer, SEQ ID 746.
 XX
 KW Primer; variation mapping; mutation mapping; plant;
 KW gene polymorphism marker; ss.
 XX
 OS Synthetic.

XX
 FN JP2003289885-A.

XX
 PD 14-OCT-2003.

XX
 PF 31-JAN-2003; 2003JP-00024620.

XX
 PR 01-FEB-2002; 2002JP-00025338.

XX
 PA (RIKA) RIKAGAKU KENKYUSHO.

XX
 PA (SAIM-) SAI MEDIA KK.

XX
 PA (MATS/) MATSUI M.

XX
 PA (NAKA/) NAKAZAWA M.

XX
 DR WPI; 2004-126231/13.

XX
 PT A primer set and method useful for mapping at least the
 PT variation/mutation part of a plant gene using a gene polymorphism marker.

XX
 PS Claim 7; SEQ ID NO 746; 120pp; Japanese.

XX
 CC The present invention relates to a primer set and method for mapping at
 CC least the variation/mutation part of a plant gene using a gene
 CC polymorphism marker. A mutation site of the plant gene is mapped by
 CC utilizing a genetic polymorphism marker as follows: (a) Genomic DNA is
 CC prepared from a plant homozygously having a mutation to be an object of
 CC the mapping; (b) A forward primer 1 containing a base corresponding to
 CC the gene polymorphic maker of one ecotype plant, a forward primer 2
 CC containing a base corresponding to the genetic polymorphism of the other
 CC ecotype plant and a reverse primer 3 based on the base sequence common
 CC with both the ecotype plants are prepared; (c) two kinds of
 CC oligonucleotides emitting fluorescence of different colors when the
 CC genetic polymorphism marker is detected are prepared; (d) an
 CC amplification reaction of the genomic DNA is carried out in the presence
 CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
 CC the fluorescence intensity emitted from the resultant reactional product
 CC is detected and (f) the position on the genome of the mutation site is
 CC determined from the results of detection. The present sequence is a
 CC primer, used to illustrate the invention.

XX
 SQ Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2463 CACCACAGAGAACATC 2478
 DB 16 CACCACAGAGACCATC 1

RESULT 358
 ADN06360
 ID ADN06360 standard; DNA; 18 BP.

XX
 AC ADN06360;

XX
 DT 15-JUL-2004 (first entry)

XX
 DE Human FLAP related microsatellite marker SEQ ID NO:8.

XX
 KW leukotriene synthesis inhibitor; myocardial infarction;

PI	Ohtaki T, Masuda Y, Takatsu Y;	
XX		
DR	WPI; 2003-646310/61.	
XX		
PT	Angiogenesis inhibitors for treatment and prevention of cancer, ovarian	
PT	diseases and inflammatory disease.	
XX		
PS	Example 3; SEQ ID NO 7; 308pp; Japanese.	
XX		
CC	The invention relates to a novel angiogenesis inhibitor comprising a	
CC	compound that inhibits the activity of an amino acid sequence given in	
CC	the specification. Angiogenesis-related proteins Bv8, ZAQ and ISE were	
CC	utilised within the method of the invention. The molecules of the	
CC	invention demonstrate cytostatic and antiinflammatory activities whilst	
CC	the method may be useful for treatment and prevention of cancer, ovarian	
CC	diseases, diabetic retinopathy and inflammatory disease. The current	
CC	sequence is that of the angiogenesis inhibitor-related PCR primer of the	
CC	invention.	
XX		
XX	Sequence 26 BP; 1 A; 9 C; 6 G; 10 T; 0 U; 0 Other;	
XX		
XX	Query Match 0.4%; Score 14.4; DB 1; Length 26;	
XX	Best Local Similarity 75.0%; Pred. No. 5.1e+02;	
XX	Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	1931 CTTCTTCTCCAGCAGCAGATGCTG 1954	
DB	1 CTACTTCTGCTGCGCTGCTG 24	
XX		
XX	RESULT 363	
XX	ACA99718/c	
ID	ACA99718 standard; DNA; 17 BP.	
XX		
AC	ACA99718;	
XX		
DT	28-JUL-2003 (first entry)	
XX		
XX	G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #211.	
XX		
KW	Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;	
KW	G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003031621-A2.	
XX		
XX	17-APR-2003.	
PF	11-OCT-2002; 2002WO-US032599.	
XX		
XX	12-OCT-2001; 2001US-0329000P.	
XX		
PA	(AMSH) AMERSHAM BIOSCIENCES SV CORP.	
XX		
PI	Zhang J;	
XX		
DR	WPI; 2003-381720/36.	
XX		
XX	New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,	
PT	investigating and/or treating disorders associated with aberrant	
PT	expression or activity of GPCR-A-1, such as tumors and cancers.	
XX		
PS	Example 2; SEQ ID NO 235; 156pp; English.	
XX		
XX	The invention describes an isolated nucleic acid encoding a G protein	
CC	coupled receptor (GPCR), mutations of which cause cancer, comprising a	
CC	2225 or 1921 base pair sequence, or their degenerate variants, encoding a	
CC	409 residue amino acid sequence, all given in the specification, with or	
CC	without conservative amino acid substitutions, or complements of the	
CC	sequence of them. The encoding nucleic acid is not more than 100 kb in	
CC	length. The methods and compositions of the present invention are useful	
CC	for diagnosing, investigating and/or treating disorders associated with	
CC	aberrant expression or activity of GPCR-A-1, such as tumors and cancers.	
XX		
XX	Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;	
XX		
XX	Query Match 0.4%; Score 14; DB 1; Length 17;	
XX	Best Local Similarity 100.0%; Pred. No. 2.3e+02;	
XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2660 GTGGCTCTCTCTAA 2673	
DB	15 GTGGCTCTCTCTAA 2	
XX		
XX	RESULT 364	
XX	ACA99717/c	
ID	ACA99717 standard; DNA; 17 BP.	
XX		
AC	ACA99717;	
XX		
DT	28-JUL-2003 (first entry)	
XX		
XX	G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #210.	
XX		
KW	Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;	
KW	G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003031621-A2.	
XX		
XX	17-APR-2003.	
XX		
XX	11-OCT-2002; 2002WO-US032599.	
XX		
XX	12-OCT-2001; 2001US-0329000P.	
XX		
PA	(AMSH) AMERSHAM BIOSCIENCES SV CORP.	
XX		
PI	Zhang J;	
XX		
DR	WPI; 2003-381720/36.	
XX		
XX	New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,	
PT	investigating and/or treating disorders associated with aberrant	
PT	expression or activity of GPCR-A-1, such as tumors and cancers.	
XX		
PS	Example 2; SEQ ID NO 235; 156pp; English.	
XX		
XX	The invention describes an isolated nucleic acid encoding a G protein	
CC	coupled receptor (GPCR), mutations of which cause cancer, comprising a	
CC	2225 or 1921 base pair sequence, or their degenerate variants, encoding a	
CC	409 residue amino acid sequence, all given in the specification, with or	
CC	without conservative amino acid substitutions, or complements of the	
CC	sequence of them. The encoding nucleic acid is not more than 100 kb in	
CC	length. The methods and compositions of the present invention are useful	
CC	for diagnosing, investigating and/or treating disorders associated with	
CC	aberrant expression or activity of GPCR-A-1, such as tumors and cancers.	
CC	This sequence represents an oligonucleotide used to analyse the gene	
CC	encoding human G-protein coupled receptor GPCR-A-1	
XX		
XX	Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;	
XX		
XX	Query Match 0.4%; Score 14; DB 1; Length 17;	
XX	Best Local Similarity 100.0%; Pred. No. 2.3e+02;	
XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2660 GTGGCT	

```

RESULT 365
ACA99716/c
ID ACA99716 standard; DNA; 17 BP.
XX
AC ACA99716;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #209.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
FN WO2003031621-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032599.
XX
PR 12-OCT-2001; 2001US-0329000P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-381720/36.
XX
XX
New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
investigating and/or treating disorders associated with aberrant
expression or activity of GPCR-A-1, such as tumors and cancers.
Example 2; SEQ ID NO 232; 156pp; English.
The invention describes an isolated nucleic acid encoding a G protein
coupled receptor (GPCR), mutations of which cause cancer, comprising a
2225 or 1921 base pair sequence, or their degenerate variants, encoding a
409 residue amino acid sequence, all given in the specification, with or
without conservative amino acid substitutions, or complements of the
sequence of them. The encoding nucleic acid is not more than 100 kbase in
length. The methods and compositions of the present invention are useful
for diagnosing, investigating and/or treating disorders associated with
aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
This sequence represents an oligonucleotide used to analyse the gene
encoding human G-protein coupled receptor GPCR-A-1
Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2660 GTGGCTCTCTCTAA 2673
Db 16 GTGGCTCTCTCTAA 3
RESULT 366
ACA99715/c
ID ACA99715 standard; DNA; 17 BP.
XX
AC ACA99715;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #208.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
XX
WO2003031621-A2.
17-APR-2003.
11-OCT-2002; 2002WO-US032599.
12-OCT-2001; 2001US-0329000P.
(AMSH ) AMERSHAM BIOSCIENCES SV CORP.
Zhang J;
WPI; 2003-381720/36.
New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
investigating and/or treating disorders associated with aberrant
expression or activity of GPCR-A-1, such as tumors and cancers.
Example 2; SEQ ID NO 233; 156pp; English.
The invention describes an isolated nucleic acid encoding a G protein
coupled receptor (GPCR), mutations of which cause cancer, comprising a
2225 or 1921 base pair sequence, or their degenerate variants, encoding a
409 residue amino acid sequence, all given in the specification, with or
without conservative amino acid substitutions, or complements of the
sequence of them. The encoding nucleic acid is not more than 100 kbase in
length. The methods and compositions of the present invention are useful
for diagnosing, investigating and/or treating disorders associated with
aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
This sequence represents an oligonucleotide used to analyse the gene
encoding human G-protein coupled receptor GPCR-A-1
Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2660 GTGGCTCTCTCTAA 2673
Db 17 GTGGCTCTCTCTAA 4
RESULT 367
ADC37815
ID ADC37815 standard; DNA; 17 BP.
XX
AC ADC37815;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:164.
XX
KW human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
XX AMLP1a; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX

```

PT New isolated nucleic acid molecule encoding a human angiotensin-like
PT protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 164; 172pp; English.
XX
CC The present invention describes the human angiotensin-like protein 1
CC (AMLP1). human AMLP1 has cytosolic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1, which is used in an example from the
CC present invention.
XX
SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
DB 4 GCAGCAGCAGCAAC 17
RESULT 368
ADF78423/C
ID ADF78423 standard; DNA; 17 BP.
XX
AC ADF78423;
XX
DT 26-FEB-2004 (first entry)
XX
DE Chromosomal abnormality detection-related APC small deletion DNA 169.
XX
KW chromosomal abnormality; maternal locus; genetic disorder; foetus;
KW mutation; translocation; transversion; monosomy; trisomy 21;
KW chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;
KW chromosome addition; chromosome amplification; chromosome translocation;
KW chromosome rearrangement; single nucleotide polymorphism detection;
KW SNP detection; pregnant female; APC; adenomatous polyposis coli; ds.
XX
OS Homo sapiens.
XX
PN WO2003074723-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006198.
XX
PR 01-MAR-2002; 2002US-0360232P.
PR 11-MAR-2002; 2002US-00093618.
PR 08-MAY-2002; 2002US-0378354P.
XX
PA (DHALL/) DHALLAN R.
XX
PI Dhallan R;
XX
PT WPI; 2003-845073/78.
XX
PS Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
PT invasively in a fetus, comprises forming a ratio of amounts of alleles at
PT a locus of interest and a different heterozygous locus.
XX
XX Example 7; Page 164; 164pp; English.
XX
CC This invention relates to a novel method of detecting chromosomal
CC abnormalities by determining the sequence of alleles of a locus of
CC interest from template DNA, determining which alleles are present and
CC comparing to amounts of alleles at a different, selected heterozygous
CC locus (for example on another chromosome or a maternal locus); relative
CC amounts are expressed as a ratio indicating presence or absence of the

CC abnormality. The method is useful for the detection of genetic disorders,
CC especially in a foetus, including chromosomal abnormalities and
CC mutations, for example translocations, transversions, monosomies,
CC trisomies (for example trisomy 21 in which an additional copy of
CC chromosome 21 results in Down's Syndrome) and other aneuploidies,
CC deletions, additions, amplifications, translocations and rearrangements.
CC It can be used to detect any alterations in a gene sequence, especially
CC single nucleotide polymorphisms (SNPs), and may be used to detect
CC numerous abnormalities simultaneously, for example if several SNPs are
CC associated with a particular disease. The method provides a rapid, non-
CC invasive method for determining the sequence of DNA from a foetus using a
CC sample from a pregnant female, for example to detect genetic disorders as
CC above or to determine if a foetus is a carrier of a disease or
CC predisposed to a disease.

XX SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3174 TGTTTCAGGTGGACT 3187
DB 14 TGTTTCAGGTGGACT 1

RESULT 369
ADH53228/C
ID ADH53228 standard; DNA; 17 BP.
XX
AC ADH53228;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human APC (adenomatous polyposis coli) DNA fragment 165.
XX
KW sequence determination; recognition site; restriction endonuclease;
KW human; APC; adenomatous polyposis coli; chromosome 5q21-22;
KW colorectal cancer; ds.
XX
OS Homo sapiens.
XX
PN WO2003074740-A1.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006376.
XX
PR 01-MAR-2002; 2002US-0360232P.
PR 11-MAR-2002; 2002US-00093618.
PR 08-MAY-2002; 2002US-0378354P.
XX
PA (DHALL/) DHALLAN R.
XX
PI Dhallan R;
XX
PT WPI; 2003-756772/71.
XX
PS Determining a sequence of a locus of interest comprises replicating a
PT region of DNA comprising a locus of interest from a template
PT polynucleotide by using a first and a second primer.
XX
XX Example 5; Page 141; 190pp; English.
XX
CC The invention relates to a novel method for determining the sequence of a
CC locus of interest which comprises replicating a region of DNA comprising
CC a locus of interest from a template polynucleotide by using a first and a
CC second primer where the second primer contains a sequence that generates
CC a recognition site for a restriction enzyme such that digestion with the
CC restriction enzyme generates a 5' overhang containing the locus of
CC interest. The method may be useful for determining the sequences of
CC multiple loci of interest concurrently and for determining the sequence
CC of a mutant allele in the presence of a normal allele. The current

CC sequence is that of the human APC (adenomatous polyposis coli) DNA
 CC fragment of the invention which is located on chromosome 5q21-22 and in
 CC which mutations are associated with colorectal cancer.
 XX
 SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3174 TGTTGAGTGGACT 3187
 DB 14 TGTTGAGTGGACT 1

RESULT 370
 ADI50862
 ID ADI50862 standard; DNA; 17 BP.
 XX
 AC ADI50862;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID3365.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosatic; virucide; neuroprotective; nontropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 3365; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;

CC sequence is that of the human APC (adenomatous polyposis coli) DNA
 CC fragment of the invention which is located on chromosome 5q21-22 and in
 CC which mutations are associated with colorectal cancer.
 XX
 SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 536 GATCCTGAGCTGCA 549
 DB 1 GATCCTGAGCTGCA 14

RESULT 371
 ADI47898/C
 ID ADI47898 standard; DNA; 17 BP.
 XX
 AC ADI47898;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID401.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosatic; virucide; neuroprotective; nontropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 401; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, indentifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1042 ACCAGGTCCTTTG 1055
 DB 17 ACCAGGTCCTTTG 4

RESULT 372

ADR97999/c
 ID ADR97999 standard; DNA; 17 BP.
 AC ADR97999;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human APC DNA fragment containing deletion at codon 1371.
 DE
 XX ds; chromosomal abnormality; detection; foetus; translocation;
 KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;
 KW amplification; prenatal diagnosis; SNP; single nucleotide polymorphism;
 KW human; chromosome 5q21-22; adenomatous polyposis coli; mutation.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO2004079011-A1.
 XX
 XX 16-SEP-2004.
 XX
 XX 29-AUG-2003; 2003WO-US027308.
 XX
 XX 28-FEB-2003; 2003WO-US006198.
 XX
 XX (RAVG-) RAVGEN INC.
 XX
 XX Dhallan R;
 XX
 XX WPI; 2004-677127/66.
 XX
 XX Detecting a chromosomal abnormality, e.g. translocations, transversions,
 PT monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises
 PT determining the sequence of alleles of a locus of interest in the sample
 PT from template DNA.
 XX
 XX Example 7; Page 156; 429pp; English.
 XX
 XX This invention describes a novel method for detecting a chromosomal
 CC abnormality in a sample which comprises determining the sequence of
 CC alleles of a locus of interest in a sample from template DNA where
 CC determining the sequence of the alleles comprises amplifying the locus of
 CC interest, hybridising the amplified loci to GeneChip array, washing
 CC GeneChip array, staining the GeneChip array with detectable reagents, and
 CC scanning GeneChip array. The amplification method is self-sustained
 CC sequence reaction, ligase chain reaction, rapid amplification of cDNA
 CC ends, PCR and ligase chain reaction. O-beta phage amplification, strand
 CC displacement amplification, or splice overlap extension PCR, preferably
 CC PCR. The determination of the sequence of the alleles comprises
 CC amplifying the locus of interest, fragmenting the amplicon, hybridising
 CC fragmented amplicons to CodeLink Arrays, extension reaction to
 CC incorporate a nucleotide and detecting incorporated nucleotides. The
 CC amplicon fragmentation is by exonuclease digestion. Detecting a
 CC chromosomal abnormality in a sample comprises determining the sequence of
 CC alleles of a locus of interest from template DNA, where determining the
 CC sequence of the alleles comprises using Beadarray Technology. The
 CC determination of the sequence of the alleles may also be done by
 CC amplifying the locus of interest, dephosphorylation of the unused
 CC reagents, in vitro transcription reaction of the products, RNase A
 CC cleavage of the products, mixing the products with CleanResin,
 CC transferring products to SpectroCHIP, and analysing the SpectroCHIP. The
 CC dephosphorylation reaction is with shrimp alkaline phosphatase.
 CC Alternatively, the determination of the sequence of the alleles comprises
 CC amplifying the locus of interest, dephosphorylation of the unused
 CC reagents, hybridising a primer to the locus of interest, incorporating a
 CC nucleotide, mixing the products with CleanResin, transferring products to
 CC SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer
 CC is adjacent to the locus of interest. The determination of the sequence
 CC of the alleles may also comprise amplifying the locus of interest,
 CC treating the products with exonuclease, single stranded DNA is annealed
 CC to an oligonucleotide, incorporating a nucleotide using the annealed
 CC template and primer, and detecting the incorporated nucleotide. The
 CC method is useful for detecting a chromosomal abnormality in a sample.

CC Specifically, the method is useful for detecting chromosomal
 CC abnormalities in a fetus including translocations, transversions,
 CC monosomies, trisomies, and other aneuploidies, deletions, additions,
 CC amplifications, and arrangements. The method of the invention can also be
 CC used for prenatal diagnosis. This sequence represents a fragment of the
 CC human adenomatous polyposis coli (APC) gene which contains a nucleotide
 CC deletion.
 XX

SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3174 TGTTCAGGTGGACT 3187
 |||||
 DB 14 TGTTCAGGTGGACT 1

RESULT 373

ADS08683/C

ID ADS08683 standard; DNA; 17 BP.

XX

AC ADS08683;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human DNA oligonucleotide #172.

XX

KW Human; nucleic acid detection; cell lysis; chromosomal abnormality;
 KW cancer; carcinoma; bladder; breast; bronchus; colon; kidney; liver; lung;
 KW oesophagus; gall bladder; ovary; pancreas; stomach; cervix; thyroid;
 KW prostate; skin; small cell lung cancer; squamous cell carcinoma;
 KW leukaemia; lymphoma; myelodysplastic syndrome; fibrosarcoma;
 KW rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma; schwannoma;
 KW melanoma; seminoma; teratocarcinoma; osteosarcoma; ds.

XX Homo sapiens.

OS Synthetic.

XX

PN WO2004078994-A2.

XX

PD 16-SEP-2004.

XX

PF 01-MAR-2004; 2004WO-US006337.

XX

PR 28-FEB-2003; 2003WO-US006198.

XX

XX (RAVG-) RAVGEN INC.

XX

PI Dhallan R;

XX

XX WPI; 2004-662434/64.

XX

PT Detecting presence or absence of nucleic acid, containing mutation,
 PT involves isolating nucleic acid from sample containing cell lysis
 PT inhibitor, and detecting presence or absence of nucleic acid.

XX Example 7; Page 165; 440pp; English.

XX The invention relates to a method for detecting a nucleic acid, involving
 CC isolating a nucleic acid from a sample, where an agent that impedes cell
 CC lysis was added to the sample, and detecting the presence or absence of
 CC the nucleic acid. The invention also relates to a method for detecting of
 CC chromosomal abnormalities in a DNA sample and determining the sequence of
 CC foetal DNA from a sample of a pregnant female. The nucleic acid contains
 CC at least one mutation chosen from a single point mutation, multiple point
 CC mutations, an insertion, a frameshift, a truncation, a deletion, a
 CC duplication and a transversion. The method is useful for detecting
 CC nucleic acid in a sample obtained from a source chosen from bacteria,
 CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,
 CC non-humans, multi-cellular parasites, animals and archaeobacteria. The
 CC method is useful for detecting, diagnosing or monitoring a disease such

as cancer chosen from carcinoma of the bladder, breast, bronchus, colon, kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach, cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-cell lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage, acute and chronic myelogenous leukaemias, myelodysplastic syndrome and promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and rhabdomyosarcoma, tumours of the central and peripheral nervous system, astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma, teratocarcinoma and osteosarcoma. The method is also useful for monitoring response to treatment chosen from surgery, radiation, lifestyle change, dietary protocol and supplementation and administration of a drug. The drug is chosen from chemotherapeutic agents, antibacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents. This sequence represents a DNA oligonucleotide used in the scope of the invention.

SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 TGTTCAGGTGGACT 3187
 Db 14 TGTTCAGGTGGACT 1

RESULT 374
 AA244310/C
 ID AA244310 standard; DNA; 30 BP.

XX AC AA244310;

XX DT 04-APR-2000 (first entry)

XX DE Human SCA7 primer 1.

XX KW SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;
 KW repeat expansion detection; RED analysis; detection; primer; ss.

XX OS Homo sapiens.

XX XX CA2245310-A.

XX PD 19-FEB-1999.

XX PF 19-AUG-1998; 98CA-02245310.

XX PR 19-AUG-1997; 97US-0056170P.

XX PA (MINU) UNIV MINNESOTA.

XX PI Koob MD, Ranum LP;

XX DR WPI; 2000-098181/09.

XX PT Identifying individuals at risk of developing spinocerebellar ataxia type
 XX 7 by analyzing trinucleotide repeat regions of spinocerebellar ataxia
 XX type 7 gene.

XX PS Disclosure; Page 43; 66pp; English.

XX CC This invention describes a novel method for identifying individuals at
 CC risk for developing spinocerebellar ataxia type 7 (SCA7). The method
 CC comprises analyzing the CAG repeat region of a SCA7 gene to detect CAG
 CC repeats, where individuals at risk have at least 30 CAG repeats and those
 CC not at risk have less than 19 CAG repeats. The method is useful for
 CC identifying individuals at risk of developing SCA7 and also those at risk
 CC of developing SCA1, 2, 3 or 6. The use of genomic DNA in the repeat

CC expansion detection (RED) analysis allows isolation of any potential
 CC trinucleotide repeat expansion regardless of the expression pattern.
 CC Utilization of different oligonucleotides in the RED assay allows any of
 CC the possible trinucleotide repeats to be detected, and the cycled nature
 CC of the reaction makes it extremely sensitive. This sequence represents a
 CC primer used to amplify the human SCA7 gene which is described in the
 CC method of the invention

SQ Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14; DB 1; Length 30;
 Best Local Similarity 66.7%; Pred. No. 6e+02;
 Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954

Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 375

AAS13781/C
 ID AAS13781 standard; DNA; 30 BP.

XX AC AAS13781;

XX DT 08-MAY-2002 (first entry)

XX DE Simple sequence repeat, SSR, #52.

XX KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW cereal profiling; grass profiling; seed batch purity testing.

XX OS Synthetic.

XX PN NZ509193-A.

XX PD 25-MAY-2001.

XX PF 03-JAN-2001; 2001NZ-00509193.

XX PR 24-DEC-1999; 99AU-00004906.

XX PR 04-MAY-2000; 2000AU-00007310.

XX PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

XX PA (UYSC-) UNIV SOUTHERN CROSS.

XX PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.

XX PA (UYAD-) UNIV ADELAIDE.

XX PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

XX PI Forster JW, Jones ES;

XX WPI; 2001-512563/56.

XX PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
 PT core elements isolated from ryegrass and fescue, useful for selecting of
 PT genes in grass or cereal breeding or profiling grass or cereal species
 PT varieties.

XX PS Claim 13; Page 53; 72pp; English.

XX CC The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a
 CC method for DNA profiling grass or cereal species varieties by assessing
 CC variation between SSR varieties and testing the purity of grass or cereal

CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a ryegrass or fescue SSR
XX
SQ Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTCTCCAGCAGCAGATGCTG 1954

DB 30 CRGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 376

AAV81598/c

ID AAV81598 standard; DNA; 17 BP.

XX AAV81598;

XX 11-MAY-1999 (first entry)

XX Oligonucleotide used in PNA-DNA-PNA chimeric macromolecule.

XX PNA; peptide nucleic acid; nuclease resistance; diagnostic; ss.

XX Synthetic.

XX WO9514706-A1.

XX 01-JUN-1995.

XX 23-NOV-1994; 94WO-US013523.

XX 24-NOV-1993; 93US-00158352.

XX (ISIS-) ISIS PHARM INC.

XX Cook PD;

XX WPI; 1995-206893/27.

XX New chimeric macromolecules contg. DNA and peptide nucleic acid segments
PT - with good nuclease stability and binding affinity, also activating
PT RNaseH, useful for treating disease, in diagnosis and for identifying
PT chemotherapeutic agents.
XX
XX Disclosure; Page 50; 68pp; English..

XX The patent discloses new macromolecules of formula PNA-DNA-PNA, in which
CC DNA comprises at least one 2'-deoxynucleotide and each PNA comprises at
CC least one peptide nucleic acid subunit. These compounds have increased
CC resistance to nuclease and increased specific binding affinity, and they
CC can activate RNaseH for target strand cleavage. They can hybridise
CC specifically to a nucleic acid strand (especially RNA) and are useful (1)
CC for treating diseases associated with undesirable production of protein,
CC (2) for in-vitro modification of sequence-specific nucleic acid (by
CC contacting a test solution with the macromolecule and RNaseH), or (3) for
CC in-vivo enhancement of polynucleotide hybridisation and RNase activity.
CC They can also be used diagnostically and for screening chemotherapeutic
CC agents
XX

SQ Sequence 17 BP; 2 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CGGAATTCAGCGAGAA 54

Db 17 CTGAATGCAGCGAGAA 1

RESULT 377

AAAX63806/c

ID AAX63806 standard; RNA; 17 BP.

XX AAX63806;

XX 20-JUL-1999 (first entry)

XX Rabbit stromelysin hammerhead target SEQ ID NO:438.

XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.

XX Oryctolagus cuniculus.

XX WO9618736-A2.

XX 20-JUN-1996.

XX 22-NOV-1995; 95WO-US015516.

XX 13-DEC-1994; 94US-00354920.

XX 23-DEC-1994; 94US-00363253.

XX 23-DEC-1994; 94US-00363254.

XX 17-FEB-1995; 95US-00390850.

XX 20-APR-1995; 95US-00426124.

XX 02-MAY-1995; 95US-00432874.

XX 04-MAY-1995; 95US-00434509.

XX 07-JUL-1995; 95US-0000951P.

XX 07-JUL-1995; 95US-0000974P.

XX 07-AUG-1995; 95US-00512861.

XX 05-OCT-1995; 95US-00541365.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;

XX Mcwiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;

XX Karpelsky A, Thompson JD, Modak A, Burgin A;

XX WPI; 1996-300653/30.

XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.

XX Example 1; Page 153; 307pp; English.

XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention

XX

SQ Sequence 17 BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 560 AATGAACCTGACCAACAT 576
 | | | | | | | | | | | | | | | | | | |
 Db 17 ACTGAAGTGACCAACAT 1

RESULT 378
 AAX63820/C
 ID AAX63820 standard; RNA; 17 BP.
 XX AC AAX63820;
 DT 20-JUL-1999 (first entry)
 DE Rabbit stromelysin hammerhead target SEQ ID NO:452.

XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 XX OS Oryctolagus cuniculus.
 XX PN W09618736-A2.
 XX PD 20-JUN-1996.
 XX PF 22-NOV-1995; 95WO-US015516.
 XX PR 13-DEC-1994; 94US-00354920.
 XX PR 23-DEC-1994; 94US-00363253.
 XX PR 23-DEC-1994; 94US-00363254.
 XX PR 17-FEB-1995; 95US-00390850.
 XX PR 20-APR-1995; 95US-00426124.
 XX PR 02-MAY-1995; 95US-00432874.
 XX PR 04-MAY-1995; 95US-00434509.
 XX PR 07-JUL-1995; 95US-0000951P.
 XX PR 07-JUL-1995; 95US-0000974P.
 XX PR 07-AUG-1995; 95US-00512861.
 XX PR 05-OCT-1995; 95US-00541365.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 XX PI Mcswiggen J, Gustofson J, Ugan N, Wincott F, Matulic-Adamic J;
 XX PI Karpelesky A, Thompson JD, Modak A, Burgin A;
 XX WPT; 1996-300653/30.
 XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
 the treatment of arthritis, induction of graft tolerance or treatment of
 auto-immune diseases.
 XX Example 1; Page 153; 307pp; English.
 XX The present invention describes a novel enzymatic nucleic acid (ENA)
 having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 can inhibit collagenase and stromelysin production in the synovial
 membrane of joints for the treatment or prevention of arthritis,
 particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 be used to treat antigen presenting cells of a donor to induce tolerance
 in a recipient to an alloantigen of a donor. They can also be used for
 enhancing graft tolerance or for treating autoimmune disease, and for
 treating allergies and other inflammatory conditions. The ENA's can also
 be used in diagnosis. Ribozyme therapy impacts on the expression of

CC stromelysin without introducing the non-specific effects upon gene
 expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the
 CC present invention
 XX SQ Sequence 17 BP; 2 A; 3 C; 6 G; 0 T; 6 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1432 GCAGCAGCAACAGCAGC 1448
 | | | | | | | | | | | | | | | | | | |
 Db 17 GCAGCATCAACAGCATC 1

RESULT 379
 AAX68730
 ID AAX68730 standard; RNA; 17 BP.
 XX AC AAX68730;
 DT 28-JUL-1999 (first entry)
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #25.
 XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX OS Homo sapiens.
 XX PN W09715662-A2.
 XX PD 01-MAY-1997.
 XX PF 25-OCT-1996; 96WO-US017480.
 XX PR 26-OCT-1995; 95US-0005974P.
 XX PR 11-JAN-1996; 96US-00584040.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (CHIR) CHIRON CORP.
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPT; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 XX rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 47; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate the
 XX synthesis, expression and/or stability of a mRNA encoding 1 or more
 XX receptors of vascular endothelial growth factor (VEGF). A patient
 XX (preferably human) having a condition associated with the level of the
 XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 XX treated by administering the nucleic acid molecule or the expression
 XX vector to the patient. AAX67275 to AAX75752 represent specific examples
 XX of nucleic acid molecules from the present invention
 XX SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 52.9%; Pred. No. 2.5e+02;

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Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TGCTACTTCTCAGCGG 2182
   ||:| :||:|||||
Db 1 DGUCGUCUCACAGG 17

RESULT 380
AAAG69120/c
ID AAG69120 standard; RNA; 17 BP.
XX
XX
AC AAG69120;
XX
XX
DT 28-JUL-1999 (first entry)
XX
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #415.
XX
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX
DR WPI; 1997-259017/23.
XX
XX
Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
stability - useful for treating e.g. tumour angiogenesis, psoriasis,
rheumatoid arthritis, etc., in a human patient.
XX
XX
PS Claim 4; Page 59; 218pp; English.
XX
XX
The present invention describes nucleic acid molecules which modulate the
synthesis, expression and/or stability of a mRNA encoding 1 or more
receptors of vascular endothelial growth factor (VEGF). A patient
(preferably human) having a condition associated with the level of the
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
treated by administering the nucleic acid molecule or the expression
vector to the patient. AAG67275 to AAX75752 represent specific examples
of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 7 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 AGGAGCCAGGAGACT 445
   |||||
Db 17 AGGAGCCAGGAGAGT 1

RESULT 381
AAX74700
ID AAX74700 standard; RNA; 17 BP.
XX
XX

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AC AAX74700;
XX
XX
DT 28-JUL-1999 (first entry)
XX
XX
DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #228.
XX
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX
OS Mus sp.
XX
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX
DR WPI; 1997-259017/23.
XX
XX
Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
stability - useful for treating e.g. tumour angiogenesis, psoriasis,
rheumatoid arthritis, etc., in a human patient.
XX
XX
PS Claim 4; Page 162; 218pp; English.
XX
XX
The present invention describes nucleic acid molecules which modulate the
synthesis, expression and/or stability of a mRNA encoding 1 or more
receptors of vascular endothelial growth factor (VEGF). A patient
(preferably human) having a condition associated with the level of the
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
treated by administering the nucleic acid molecule or the expression
vector to the patient. AAX67275 to AAX75752 represent specific examples
of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. NO. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCGAAATCTCAGACCC 2773
   ||:| :||:|||||
Db 1 GGCUGACUCUCAGACCC 17

RESULT 382
AAX68731
ID AAX68731 standard; RNA; 17 BP.
XX
XX
AC AAX68731;
XX
XX
DT 28-JUL-1999 (first entry)
XX
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #26.
XX
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX

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XX OS Homo sapiens.
XX PA WO9715662-A2.
XX PN
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 47; 218pp; English.
XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX75725 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Oy 2167 GTCTACTTCTCAGCGGA 2183
Db 1 GUCUGUCUCACAGGA 17
RESULT 383
AAX71615/c
ID AAX71615 standard; RNA; 17 BP.
XX AC AAX71615;
XX DT 28-JUL-1999 (first entry)
XX DE Human KDR VEGF receptor hammerhead ribozyme substrate #627.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.

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XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 116; 218pp; English.
XX SQ Sequence 17 BP; 1 A; 6 C; 3 G; 0 T; 7 U; 0 Other;
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGGAGGAGAGCTCA 1
RESULT 384
AAX69119/c
ID AAX69119 standard; RNA; 17 BP.
XX AC AAX69119;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #414.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.

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Db      1  UCAUGUCUUGAUUCAA 17

RESULT 387
AAAX74483
ID  AAX74483 standard; RNA; 17 BP.
XX
XX  AC  AAX74483;
XX
XX  DT  28-JUL-1999  (first entry)
XX
XX  DE  Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #11.
XX
XX  KW  Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW  KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW  tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW  fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW  foetal liver kinase 1; ss.
XX
OS  Mus sp.
XX
XX  PN  WO9715662-A2.
XX
XX  PD  01-MAY-1997.
XX
XX  PF  25-OCT-1996; 96WO-US017480.
XX
XX  PR  26-OCT-1995; 95US-0005974P.
XX  PR  11-JAN-1996; 96US-00584040.
XX
XX  PA  (RIBO-) RIBOZYME PHARM INC.
XX  PA  (CHIR ) CHIRON CORP.
XX
XX  PI  Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX  DR  WPI; 1997-259017/23.
XX
XX  PT  Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT  stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT  rheumatoid arthritis, etc., in a human patient.
XX
XX  PS  Claim 4; Page 155; 218pp; English.
XX
XX  CC  The present invention describes nucleic acid molecules which modulate the
CC  synthesis, expression and/or stability of a mRNA encoding 1 or more
CC  receptors of vascular endothelial growth factor (VEGF). A patient
CC  (preferably human) having a condition associated with the level of the
CC  fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC  receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC  angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC  treated by administering the nucleic acid molecule or the expression
CC  vector to the patient. AAX57275 to AAX5752 represent specific examples
CC  of nucleic acid molecules from the present invention
XX
XX  SQ  Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
      Query Match 0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 52.9%; Pred. No. 2.5e+02;
      Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY  2166 TGCTACTTCACACGGG 2182
      :||:|::|::|::|
Db  1  UGUCUGUCUUCACACGG 17

RESULT 388
AAV39600
ID  AAV39600 standard; cDNA; 17 BP.
XX
XX  AC  AAV39600;
XX
XX  DT  28-SEP-1998  (first entry)
XX
XX

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DE  Pentaplex tc-PROBE apolipoprotein A IV oligonucleotide SEQ ID NO:90.
XX
XX  KW  Mass spectrometry; diagnosis; detection; biological sample; infection;
KW  genetic disease; chromosomal abnormality; identification; heredity;
KW  pathogenic organism; telomerase activity; oncogene mutation;
KW  cancer-specific sequence; primer; ss.
XX
XX  OS  Synthetic.
XX
XX  PN  WO9820166-A2.
XX
XX  PD  14-MAY-1998.
XX
XX  PF  06-NOV-1997; 97WO-US020444.
XX
XX  PR  06-NOV-1996; 96US-00744481.
XX  PR  06-NOV-1996; 96US-00744590.
XX  PR  06-NOV-1996; 96US-00746036.
XX  PR  06-NOV-1996; 96US-00746055.
XX  PR  23-JAN-1997; 97US-00786988.
XX  PR  23-JAN-1997; 97US-00787639.
XX  PR  19-SEP-1997; 97US-00933792.
XX  PR  08-OCT-1997; 97US-00947801.
XX
XX  PA  (SEQU-) SEQUENOM INC.
XX
XX  PI  Koester H, Tang K, Fu D, Siebert CW, Little DP, Higgins GS;
XX  PI  Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
XX  PI  Lough DM;
XX
XX  DR  WPI; 1998-286975/25.
XX
XX  PT  Sequencing nucleic acid by mass spectrometric analysis - for detecting
XX  PT  nucleic acids, telomerase activity, oncogene mutations, or cancer-
XX  PT  specific sequences, for diagnosis of disease.
XX
XX  PS  Example 24; Page 199; 478pp; English.
XX
XX  CC  A process has been developed for determining the sequence of a target
XX  CC  nucleic acid. The process comprises: (i) generating at least two
XX  CC  fragments (F) from the target nucleic acid; and (ii) analysing F by mass
XX  CC  spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically
XX  CC  claimed primers for use in the mass spectrometric analysis of the above
XX  CC  process. The process is used to detect genetic diseases (e.g.
XX  CC  haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's
XX  CC  disease, cystic fibrosis and many others) or chromosomal abnormalities
XX  CC  (or predisposition); infections and cancers; also for establishing
XX  CC  identity and heredity. Particular applications are diagnosis of
XX  CC  neuroblastoma, detecting telomerase, determining family relationships and
XX  CC  HLA compatibility, and in genetic fingerprinting. Compared with known
XX  CC  methods using MS, this process requires fewer specific reagents and is
XX  CC  better suited to automation. Extended primers are shorter; primer
XX  CC  annealing is more efficient and the process allows detection of many
XX  CC  sequences simultaneously. The present sequence represent an
XX  CC  oligonucleotide used in an example from the present invention
XX
XX  SQ  Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
      Query Match 0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 2.5e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1399 ACAGCAGCAACAGCAGC 1415
      |||||
Db  1  ACAGCAGCAACAGCATC 17

RESULT 389
AAV95022/c
ID  AAV95022 standard; RNA; 17 BP.
XX
XX  AC  AAV95022;
XX
XX

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DT 24-FEB-1999 (first entry)
XX
DE Mouse IL-2 receptor g-chain substrate position 1012.
XX
KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX
OS Mus sp.
XX
PN WO9824913-A2.
XX
PD 11-JUN-1998.
XX
PF 02-DEC-1997; 97WO-US021748.
XX
PR 03-DEC-1996; 96US-00758306.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Mcswiggen JA;
XX
DR WPI; 1998-333332/29.
XX
RW Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,
XX autoimmune disease and allergies.
XX
PS Claim 4; Page 43; 61pp; English.
XX
CC The present sequence invention describes ribozymes targetted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 252 TTGGGGAGATCTCTCT 268
DB 17 TTGGGGGAATCTCGCT 1

RESULT 390
AAV08617
ID AAV08617 standard; DNA; 17 BP.
XX
AC AAV08617;
XX
DT 15-FEB-1999 (first entry)
XX
DE Primer ACP/9RB for human ACE gene.
XX
KW PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;
KW polymorphic pattern; blood pressure; electrocardiographic profile;
KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
KW hypertension; cardiovascular disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9845477-A2.
XX
PD 15-OCT-1998.
XX
PF 01-APR-1998; 98WO-IB000475.
XX
PR 04-APR-1997; 97US-0042930P.
XX

PF 01-APR-1998; 98WO-IB000475.
XX
PR 04-APR-1997; 97US-0042930P.
XX
PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstroem PHR;
XX
DR WPI; 1998-568361/48.
XX
RW Assessing cardiovascular status in humans by polymorphic analysis - of
RW genes for angiotensin converting enzyme, angiotensinogen and angiotensin
RW II receptor, used to diagnose predisposition to disease and to predict
RW effect of therapy.
XX
PS Example 1; Page 29; 71pp; English.
XX
CC This sequence represents a PCR primer for the human ACE (angiotensin
CC converting enzyme) gene, and can be used in the method of the invention.
CC The method is for assessing cardiovascular status in humans by
CC determining the sequence of at least one polymorphic site in the ACE
CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1
CC angiotensin II receptor) genes, and comparing the polymorphic pattern
CC with that in patients with predetermined markers of status. The method is
CC used to assess blood pressure or electrocardiographic profile, to
CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),
CC hypertension, atherosclerosis or stroke. They can also be used to predict
CC response to treatments with ACE inhibitors, angiotensin II receptor
CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
CC etc. It is also used to identify susceptibility to cardiovascular
CC disease. Libraries of nucleic acids containing polymorphic positions in
CC the 3 genes, and libraries of targets corresponding to the peptides from
CC the genes are used to screen for cardiovascular agents. The nucleic acids
CC contained in the library can be used as source of probes
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGGCGGCAGCAGCAACA 17

RESULT 391
AAV08623
ID AAV08623 standard; DNA; 17 BP.
XX
AC AAV08623;
XX
DT 15-FEB-1999 (first entry)
XX
DE Primer ACP/16RT for human ACE gene.
XX
KW PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;
KW polymorphic pattern; blood pressure; electrocardiographic profile;
KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
KW hypertension; cardiovascular disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9845477-A2.
XX
PD 15-OCT-1998.
XX
PF 01-APR-1998; 98WO-IB000475.
XX
PR 04-APR-1997; 97US-0042930P.
XX

```

PA (EURO-) EURONA MEDICAL AB.
 XX Norberg LT, Andersson MK, Lindstroem PHR;
 XX WPI; 1998-568361/48.
 XX
 XX Assessing cardiovascular status in humans by polymorphic analysis - of
 PT genes for angiotensin converting enzyme, angiotensinogen and angiotensin
 PT II receptor, used to diagnose predisposition to disease and to predict
 PT effect of therapy.
 XX
 XX Example 1; Page 29; 71pp; English.
 XX
 XX This sequence represents a PCR primer for the human ACE (angiotensin
 CC converting enzyme) gene, and can be used in the method of the invention.
 CC The method is for assessing cardiovascular status in humans by
 CC determining the sequence of at least one polymorphic site in the ACE
 CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1
 CC angiotensin II receptor) genes, and comparing the polymorphic pattern
 CC with that in patients with predetermined markers of status. The method is
 CC used to assess blood pressure or electrocardiographic profile, to
 CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),
 CC hypertension, atherosclerosis or stroke. They can also be used to predict
 CC response to treatments with ACE inhibitors, angiotensin II receptor
 CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
 CC etc. It is also used to identify susceptibility to cardiovascular
 CC disease. Libraries of nucleic acids containing polymorphic positions in
 CC the 3 genes, and libraries of targets corresponding to the peptides from
 CC the genes are used to screen for cardiovascular agents. The nucleic acids
 CC contained in the library can be used as source of probes
 XX
 XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1427 CAGCAGCAGCAGCAACA 1443
 DB 1 CGCGCGCAGCAGCAACA 17
 RESULT 392
 AAA20848
 ID AAA20848 standard; RNA; 17 BP.
 XX
 AC AAA20848;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4074.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US006507.
 XX
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 XX Claim 55; Page 171; 305pp; English.
 XX
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21589 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberculous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 XX Sequence 17 BP; 10 A; 1 C; 3 G; 0 T; 3 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 2.5e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 938 AACACAGATAGCTGCTAA 954
 DB 1 AACACAGAUAGAUGAUA 17
 RESULT 393
 AAA22595/c
 ID AAA22595 standard; RNA; 17 BP.
 XX
 AC AAA22595;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5821.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 XX 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US006507.
 XX
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX


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PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 99US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
DR Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 230; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequences
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6 or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3090 AAAGAGAGAAAGGGAAGA 3106
DB 17 AAAGAGAGAAAGGGAAGA 1
XX
RESULT 394
AAA38251
ID AAA38251 standard; DNA; 17 BP.
XX
AC AAA38251;
XX
XX 21-AUG-2000 (first entry)
XX
XX Human ACE regulatory region PCR primer, SEQ ID NO:51.
XX
XX Angiotensin-converting enzyme gene; ACE; regulatory region; polymorphism;
XX polymorphic marker; cardiovascular disease; myocardial infarction;
XX unstable angina; hypertension; atherosclerosis; stroke; prognosis;
XX drug screening; treatment outcome; human; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200022166-A2.
XX
XX 20-APR-2000.
XX
XX

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PF 13-OCT-1999; 99WO-IB001678.
XX
XX 14-OCT-1998; 98US-0104286P.
PR 14-OCT-1998; 98US-0104302P.
XX
XX (EURO-) EURONA MEDICAL AB.
XX
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
XX
XX WPI; 2000-318010/27.
XX
XX Assessing cardiovascular status in humans involves comparing test
XX polymorphic pattern comprising polymorphic positions within genes
XX encoding specific proteins, with reference polymorphic pattern.
XX
XX Example 1; Page 51; 126pp; English.
XX
XX The invention relates to a novel method of assessing the cardiovascular
XX status in an individual and to newly identified polymorphisms in the
XX genes encoding angiotensin-converting enzyme (ACE), angiotensin II
XX receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
XX aldosterone synthase, endothelin receptor type A and beta-adrenergic
XX receptors 1 and 2. The method comprises determining the sequence at one
XX or more polymorphic positions within these genes, and comparing the
XX pattern of polymorphisms from the individual with a reference polymorphic
XX pattern obtained from a population of individuals exhibiting a
XX predetermined cardiovascular disease status. The polymorphic markers are
XX useful for determining the predisposition of an individual to
XX cardiovascular disorders such as myocardial infarction, unstable angina,
XX hypertension, atherosclerosis and stroke. They are also useful for
XX predicting the likely cardiovascular status of a patient given a
XX treatment regimen comprising administration of cardiovascular drugs
XX (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
XX blockers) or calcium channel blockers). One or more polymorphic markers
XX provides a basis for predicting the outcome of a treatment regimen.
XX Fragments of the genes comprising a polymorphic site may be used as
XX primers and probes for detecting genetic polymorphisms or in molecular
XX library arrays for high throughput screening. The genes, and the proteins
XX they encode are useful in the screening of potential cardiovascular
XX drugs. Determination of an individual's polymorphic pattern reduces or
XX eliminates trial and error in selecting a treatment for a particular
XX individual cardiovascular patient. It also provides the ability to
XX eliminate patients from clinical trials who are predicted to be non-
XX responsive, or at a risk for an adverse response, to a particular
XX treatment regimen. Adverse results in an early trial can be evaluated to
XX identify polymorphic patterns so that the adverse results can be
XX correlated with a sub-population of the test population, permitting
XX exclusion of such sub-populations from the treatment group. Beneficial
XX drugs can be approved for use in the appropriate population, thereby
XX decreasing the number of patients required for a clinical trial which in
XX turn decreases the duration and cost of such trials. Sequences AAA38240-
XX A38251 represent PCR primers used in an exemplification of the invention
XX to amplify short fragments of the human ACE gene regulatory region
XX (AAA38329) for sequence determination
XX
XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1427 CAGCAGCGCAGCAGCAACA 1443
DB 1 CGCGCGCAGCAGCAACA 17
XX
RESULT 395
AAA38245
ID AAA38245 standard; DNA; 17 BP.
XX
XX AAA38245;
AC
XX
XX 21-AUG-2000 (first entry)
XX
XX

```


XX Human ACE regulatory region PCR primer, SEQ ID NO:45.
DE Angiotensin-converting enzyme gene; ACE; regulatory region; polymorphism;
XX polymorphic marker; cardiovascular disease; myocardial infarction;
KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;
KW drug screening; treatment outcome; human; PCR primer; ss.
XX Homo sapiens.
OS
XX WO200022166-A2.
PN
XX 20-APR-2000.
PD
XX
XX 13-OCT-1999; 99WO-IB001678.
PF
XX 14-OCT-1998; 98US-0104286P.
PR
XX 14-OCT-1998; 98US-0104302P.
PR
XX (EURO-) EURONA MEDICAL AB.
PA
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
PI WPI; 2000-318010/27.
XX
XX Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern.
XX
XX Example 1; Page 50; 126pp; English.
PS
XX The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be non-
CC responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. Sequences AAA38240-
CC A38251 represent PCR primers used in an exemplification of the invention
CC to amplify short fragments of the human ACE gene regulatory region
CC (AAA38329) for sequence determination
XX

Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGGCGGCAGCAGCAACA 17
RESULT 396
AAA25616/C
ID AAA25616 standard; DNA; 17 BP.
XX
XX AAA25616;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2114.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX WO9954459-A2.
FN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 85; 148pp; English.
PS
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 2 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1384 CTACACCCCAACGCAAC 1400
Db 17 CTACACCCCAATACCAAC 1

RESULT 397
AAA25020/c
ID AAA25020 standard; DNA; 17 BP.
XX
XX
AC AAA25020;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1518.
XX
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US008547.
XX
XX 20-APR-1998; 98US-0082404P.
XX
XX 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
XX Claim 77; Page 65; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 458 AAGCACATGATGGCCA 474
||||| ||| ||||| |||||

RESULT 397
AAC61245
ID AAC61245 standard; DNA; 17 BP.
XX
XX AAC61245;
XX
XX 30-JAN-2001 (first entry)
XX
XX Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 51.
KW Human; genetic polymorphism; disease diagnosis; treatment; cancer;
KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200056922-A2.
XX
XX 28-SEP-2000.
XX
XX 23-MAR-2000; 2000WO-GB001102.
XX
XX 23-MAR-1999; 99US-0136046P.
XX
XX 23-MAR-1999; 99WO-IB000497.
XX
XX 24-MAR-1999; 99US-0126243P.
XX
XX 23-DEC-1999; 99US-00471890.
XX
XX (GEMI-) GEMINI GENOMICS AB.
XX
XX Lindstrom PHR, Norberg LT, Jonasson L, Olaisson E, Sanders R;
XX
XX WPI; 2000-638268/61.
XX
XX Assessing disease status in individual by determining sequence(s) at one
PT or more polymorphic positions within the human genes encoding the
PT protein(s) involved in physiological pathway associated with treatment
PT regime.
XX
XX Example 1; Page 58; 141pp; English.
XX
XX The present invention is related to methods for determining the
CC polymorphic pattern of an individual and using the results to determine
CC their risk of a number of diseases, including cancer, cardiovascular
CC diseases, glaucoma and nervous system disorders such as depression and
CC neurodegenerative diseases. In addition, the methods can be used to
CC determine the effects of different types of treatment for individuals,
CC and thus enables appropriate therapies to be prescribed. The PCR primers
CC shown in sequences AAC61201-C61371 were all used to demonstrate the
CC methods of the invention
XX
XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGCGCGCAGCAGCAACA 17

RESULT 399
AAC61245
ID AAC61245 standard; DNA; 17 BP.
XX
XX AAC61245;
XX
XX 30-JAN-2001 (first entry)
XX
XX Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 45.
XX
```

KW Human; genetic polymorphism; disease diagnosis; treatment; cancer;
 KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
 XX Homo sapiens.
 XX WO200056922-A2.
 XX 28-SEP-2000.
 XX 23-MAR-2000; 2000WO-GB001102.
 XX 23-MAR-1999; 99US-0126046P.
 XX 23-MAR-1999; 99WO-IB000497.
 XX 24-MAR-1999; 99US-0126243P.
 XX 23-DEC-1999; 99US-00471890.
 XX (GEMI-) GEMINI GENOMICS AB.
 XX Lindstrom PHR, Norberg LT, Jonsson L, Olaisson E, Sanders R.
 XX WPI; 2000-638268/61.
 XX Assessing disease status in individual by determining sequence(s) at one
 PT or more polymorphic positions within the human genes encoding the
 PT protein(s) involved in physiological pathway associated with treatment
 PT regime.
 XX Example 1; Page 57; 141pp; English.
 XX The present invention is related to methods for determining the
 CC polymorphic pattern of an individual and using the results to determine
 CC their risk of a number of diseases, including cancer, cardiovascular
 CC diseases, glaucoma and nervous system disorders such as depression and
 CC neurodegenerative diseases. In addition, the methods can be used to
 CC determine the effects of different types of treatment for individuals,
 CC and thus enables appropriate therapies to be prescribed. The PCR primers
 CC shown in sequences AAC61201-C61371 were all used to demonstrate the
 CC methods of the invention
 XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1427 CAGCAGCAGCAGCA 1443
 DB 1 CGGCGCAGCAGCA 17
 RESULT 400
 AAF07477/c
 ID AAF07477 standard; DNA; 17 BP.
 XX AAF07477;
 AC AAF07477;
 XX 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #3734.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US009721.
 XX 12-APR-1999; 99US-0129390P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 18; Page 117; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor. EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of
 erythropoietin, granulocyte colony stimulating factor protein and
 interferon alpha

PA (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 54; Page 141; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of
 erythropoietin, granulocyte colony stimulating factor protein and
 interferon alpha

Sequence 17 BP; 6 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 3351 CTGTGGTGTCAATGTGT 3367
 DB 17 CTGTGGAGTAAATGTGT 1
 RESULT 401
 AAF05460
 ID AAF05460 standard; DNA; 17 BP.
 XX AAF05460;
 AC AAF05460;
 XX 16-FEB-2001 (first entry)
 XX Hammerhead ribozyme substrate #2679.
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO200061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US009721.
 XX 12-APR-1999; 99US-0129390P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 18; Page 117; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor. EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of

```
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3369 ATTAATTGTTGTAATA 3385
Db 1 ATTCATTGTTGTAATA 17

RESULT 402
AAFO4887/c
ID AAFO4887 standard; DNA; 17 BP.
XX
AC AAFO4887;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2403.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 4; Page 110; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3100 GCGAGACAAATTACAA 3116
Db 17 GTGAGACAAATTGACAA 1

RESULT 403
AAFO4439/c
ID AAFO4439 standard; DNA; 17 BP.
XX
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```
AC AAF04439;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1955.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 4; Page 100; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3100 GCGAGACAAATTACAA 3116
Db 17 GTGAGACAAATTGACAA 1

RESULT 404
AAC73225
ID AAC73225 standard; DNA; 17 BP.
XX
AC AAC73225;
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #39 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
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PR 23-JUN-1999; 99US-0140359P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (APFY-) APFYMETRIX INC.
XX
XX Pan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
XX Example 7; Page 51; 70pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
XX Sequence 17 BP; 1 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 815 TCTGCCCTCTGCACCTC 831
Db 1 TCTGCCCTCTGCACCTC 17
RESULT 405
AAD09710
ID AAD09710 standard; DNA; 17 BP.
XX
XX AAD09710;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cryptosporidium parvum S60 gene sequencing PCR primer, S15.R9.
XX
XX S60 antigen; protozoacide; vaccine; intestinal infection; diarrhoea;
XX AIDS; Acquired Immune Deficiency Syndrome; cancer; PCR primer; as.
XX
XX Cryptosporidium parvum.
XX
XX WO200140248-A1.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-AU001492.
XX
XX 01-DEC-1999; 99AU-00004400.
XX
XX (MACQ-) MACQUARIE RES LTD.
XX
XX Winter G, Slade MB, Williams KL, Gooley AA;
XX WPI; 2001-408274/43.
XX
XX Novel nucleic acids encoding antigenic polypeptides of Cryptosporidium
XX useful in antigenic preparations for immunizing animals against
XX Cryptosporidium.
XX
XX Example; Fig 6; 72pp; English.
XX

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```

CC The invention relates to Cryptosporidium parvum S60 potential vaccine
CC antigen and its corresponding DNA molecule. S60 antigens are used in
CC vaccine preparations for immunising animals, preferably human, against
CC Cryptosporidium. The S60 protein is processed into two glycoproteins S15
CC and S45. This S45 and S15 glycoproteins behave as a single membrane
CC glycoprotein S60. S60 vaccine antigen is used for treating intestinal
CC infections such as diarrhoea in immunosuppressed patients e.g., AIDS
CC (Acquired Immune Deficiency Syndrome), cancer patients and recipients of
CC transplants. The present DNA sequence is PCR primer which is used for
CC sequencing Cryptosporidium parvum S60 gene
XX
XX Sequence 17 BP; 1 A; 2 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2394 TTGGAGCTGGATCTGTT 2410
Db 1 TTGGTGGGGGATCTGTT 17
RESULT 406
AAH94700/C
ID AAH94700 standard; RNA; 17 BP.
XX
XX AAH94700;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human Chk1 ribozyme substrate SEQ ID NO: 125.
XX
XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
XX RNA cleavage; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157206-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US003504.
XX
XX 03-FEB-2000; 2000US-0179983P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (FATT) FATTAEY A R.
XX
XX Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
XX WPI; 2001-496922/54.
XX
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
XX molecules, which downregulates expression of a checkpoint kinase-1 gene,
XX useful for treating colorectal, lung, breast or prostate cancers.
XX
XX Claim 4; Page 54; 115pp; English.
XX
XX The present invention provides nucleic acid molecules capable of
XX downregulating the expression of the human checkpoint kinase-1 (chk1)
XX gene. These may be antisense or ribozyme sequences, and are useful in the
XX treatment of diseases associated with conditions affected by Chk1 levels,
XX including cancer. The present sequence is an oligonucleotide described in
XX the exemplification of the invention
XX
XX Sequence 17 BP; 1 A; 7 C; 3 G; 0 T; 6 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 666 AGCAAGCCAGGAGC 682

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XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 83; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an inozyme of the invention
XX
SQ Sequence 17 BP; 7 A; 4 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1687 GCTCTACTCTACGACAA 1703
| :|:|:|:|:|:|:|:|:|
Db 1 GAUCCUACUUCAGAAA 17
RESULT 410
ABK00766
ID ABK00766 standard; RNA; 17 BP.
AC ABK00766;
XX
XX 12-MAR-2002 (first entry)
XX
DE Human NOGO Inozyme #36.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX
XX 28-FEB-2000; 2000US-0185516P.
XX
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
CC Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
CC constructs, which down regulate expression of a CD20 gene or neurite
CC growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
CC central nervous system injury.
XX
CC Claim 88; Page 78; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an inozyme of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 7 G; 0 T; 1 U; 0 Other;


```

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGC 1427
DB 1 GCGGCAGCAGCAGCAGC 17

RESULT 411
ID ABK02892/c
XX ABK02892 standard; RNA; 17 BP.
AC ABK02892;
XX
DT 12-MAR-2002 (first entry)
DE Human CD20 Hammerhead ribozyme #191.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
WPI; 2001-607195/69.
XX
DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 30; Page 143; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a RNA motif) or
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more

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CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
XX
SQ Sequence 17 BP; 1 A; 3 C; 1 G; 0 T; 12 U; 0 Other;

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Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3416 TAAAAAGGTAATAGAA 3432
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DB 17 TAAAAAGGTAATAGAA 1
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RESULT 412
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ABK02895/c
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ID ABK02895 standard; RNA; 17 BP.
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XX AC ABK02895;
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XX DT 12-MAR-2002 (first entry)
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```
XX DE Human CD20 Hammerhead ribozyme #194.
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KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX

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OS Homo sapiens.
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OS Synthetic.
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XX PN WO200159103-A2.
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XX PD 16-AUG-2001.
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XX PF 09-FEB-2001; 2001WO-US004273.
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XX PR 11-FEB-2000; 2000US-0181797P.
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XX PR 28-FEB-2000; 2000US-0185516P.
```

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XX PR 06-MAR-2000; 2000US-0187128P.
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XX (RIBO-) RIBOZYME PHARM INC.
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XX (BLAT/) BLATT L.
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XX (MCSW/) MCSWIGGEN J.
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XX (CHOW/) CHOWRIRA B M.
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XX Blatt L, Mcswiggen J, Chowrira BM;
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XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

XX Claim 30; Page 143; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targetting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targetting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a hammerhead ribozyme of the invention

XX

SQ Sequence 17 BP; 4 A; 3 C; 0 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3201 ATGCTTAAAAATGGAAA 3217

Db 17 ATGTTTAAAAAAGGAAA 1

RESULT 413

ABK00767

ID ABK00767 standard; RNA; 17 BP.

AC ABK00767;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human NOGO Inozyme #37.

XX

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX

PD 16-AUG-2001.

XX

XX 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWIRA B M.

XX

PI Blatt L, Mcswiggen J, Chowira BM;

XX

XX WPI; 2001-607195/69.

XX

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX

XX Claim 88; Page 78; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targetting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targetting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a hammerhead ribozyme of the invention

XX

SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCACGACGACGACGACG 1427

Db 1 GCACGACGACGACGACG 17

RESULT 414
ABK01792
ID ABK01792 standard; RNA; 17 BP.
AC
XX ABK01792;
DT 12-MAR-2002 (first entry)
XX
DE Human NIGO Zinzyne #114.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 88; Page 97; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NIGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with an RNA motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-
XX targeting nucleic acid is used to cleave RNA of the NIGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NIGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NIGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NIGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NIGO expression. The present
CC sequence is a zinzyme molecule of the invention
XX

SQ Sequence 17 BP; 4 A; 6 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
Db 1 CGGCAGCAGCAGCAGCA 17
|||||

RESULT 415

ABK01549

ID ABK01549 standard; RNA; 17 BP.

AC ABK01549;

XX 12-MAR-2002 (first entry)

XX Human NIGO G-Cleaver #5.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX


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XX DT 27-JUN-2003 (first entry)
XX DE Human GRID zinzyme substrate oligonucleotide #58.
XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;
XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
XX KW leukaemia; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200162911-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-US005957.
XX PR 24-FEB-2000; 2000US-0184594P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX DR WPI; 2001-550088/61.
XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
XX PT (GRID) gene comprises using antisense and enzymatic nucleic acid
XX PT molecules such as hammerhead ribozymes.
XX PS Claim 4; Page 72; 108pp; English.
XX CC The present invention relates to oligonucleotides that downregulate the
XX CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
XX CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
XX CC for modulating the expression of GRID, to treat conditions such as
XX CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
XX CC administered in conjunction with other therapies such as radiation,
XX CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
XX CC used to illustrate the invention
XX SQ Sequence 17 BP; 4 A; 9 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACACGACGACGACCA 999
DB 1 CCCCUGCAGCAGCACCA 17

RESULT 418
ABL46825
ID ABL46825 standard; RNA; 17 BP.
XX AC ABL46825;
XX DT 27-JUN-2003 (first entry)
XX DE Human GRID NCH ribozyme substrate oligonucleotide #279.
XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;
XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
XX KW leukaemia; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200162911-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-US005957.

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XX PR 24-FEB-2000; 2000US-0184594P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX DR WPI; 2001-550088/61.
XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
XX PT (GRID) gene comprises using antisense and enzymatic nucleic acid
XX PT molecules such as hammerhead ribozymes.
XX PS Claim 4; Page 68; 108pp; English.
XX CC The present invention relates to oligonucleotides that downregulate the
XX CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
XX CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
XX CC for modulating the expression of GRID, to treat conditions such as
XX CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
XX CC administered in conjunction with other therapies such as radiation,
XX CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
XX CC used to illustrate the invention
XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2508 CACCAAACTGGGCTCT 2524
DB 1 CAACAAGCUGGGCCUCU 17

RESULT 419
ABA93692/c
ID ABA93692 standard; DNA; 17 BP.
XX AC ABA93692;
XX DT 29-APR-2002 (first entry)
XX DE GAPDH cDNA PCR primer #1.
XX KW Neomycin resistance; viral vector; plasmid; pSub201; CMV promoter;
XX KW reversed terminal repetitive sequence; polyclonal site; pRc/CMV;
XX KW cytomegalovirus promoter; GAPDH; PCR primer; ss.
XX OS Homo sapiens.
XX PN CN1322840-A.
XX PD 21-NOV-2001.
XX PF 20-JUN-2001; 2001CN-00118841.
XX PR 20-JUN-2001; 2001CN-00118841.
XX PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX PI Zhu L, Shi G, Liu Y;
XX DR WPI; 2002-148632/20.
XX PT Glandular associated viral vector for mediating gene transfer, comprises
XX PT a reversed terminal repetitive sequence of plasmid pSub201.
XX PS Example 3; Page 16; 29pp; Chinese.
XX CC The present invention describes a viral vector as a 7146 base pair
XX CC plasmid including a reversed terminal repetitive sequence of plasmid

```

CC pSub201 and a CMV promoter, polyclonal site and neomycin resistance gene
 CC of plasmid pRC/CMV. A gene transferred by the vector of the present
 CC invention may be expressed stably in a host cell for a long period. The
 CC present sequence represents a PCR primer for GAPDH, which is used in an
 CC example from the present invention

XX Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 793 CCCCGCCTTCTCCATGG 809

Db 17 CCCAGCCTTCTCCATGG 1

RESULT 420

ABN00672

ID ABN00672 standard; DNA; 17 BP.

XX

AC ABN00672;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:664.

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PR 30-JAN-2001; 2001WO-US000661.

XX

PR 30-JAN-2001; 2001WO-US000662.

XX

PR 30-JAN-2001; 2001WO-US000663.

XX

PR 30-JAN-2001; 2001WO-US000664.

XX

PR 30-JAN-2001; 2001WO-US000665.

XX

PR 30-JAN-2001; 2001WO-US000666.

XX

PR 30-JAN-2001; 2001WO-US000667.

XX

PR 30-JAN-2001; 2001WO-US000668.

XX

PR 30-JAN-2001; 2001WO-US000669.

XX

PR 05-FEB-2001; 2001US-0266860P.

XX

PA (AEOM-) AEOMICA INC.

XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

XX WPI; 2002-179446/23.

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 664; 214pp; English.

CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 664 TCACCAAGCCAGAGGA 680

Db 1 TCAGCCAGCCAGAGAA 17

RESULT 421

ABN10755

ID ABN10755 standard; DNA; 17 BP.

XX

AC ABN10755;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10747.

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PR 30-JAN-2001; 2001WO-US000661.

XX

PR 30-JAN-2001; 2001WO-US000662.

XX

PR 30-JAN-2001; 2001WO-US000663.

XX

PR 30-JAN-2001; 2001WO-US000664.

XX

PR 30-JAN-2001; 2001WO-US000665.

XX

PR 30-JAN-2001; 2001WO-US000666.

XX

PR 30-JAN-2001; 2001WO-US000667.

XX

PR 30-JAN-2001; 2001WO-US000668.

XX

PR 30-JAN-2001; 2001WO-US000669.

XX

PR 05-FEB-2001; 2001US-0266860P.

XX

PA (AEOM-) AEOMICA INC.

XX

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

XX WPI; 2002-179446/23.

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX Disclosure; SEQ ID NO 664; 214pp; English.

PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10747; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 3 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1771 TGTGGTAGCCCGAACA 1787
Db 1 TGTGGTTGCCCTGAACA 17

RESULT 422
ABN00673
ID ABN00673 standard; DNA; 17 BP.
XX
XX AC ABN00673;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:665.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000SE-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (ABOM-) ABOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 665; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 665 CAGCAAGCCAGAGGAG 681
Db 1 CAGCCAGCCAGAGAG 17

RESULT 423
ABN01880
ID ABN01880 standard; DNA; 17 BP.
XX
XX AC ABN01880;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1872.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 1872; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1022 CCTCTCTGCTGGACC 1038
 DB 1 CCTCTCTGCTGGACC 17
 RESULT 424
 ABN07810
 ID ABN07810 standard; DNA; 17 BP.
 XX
 AC ABN07810;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7802.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 XX WO200192524-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 7802; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCA 1425
 DB 1 CAGCAGCAGCAGCAGCA 17
 RESULT 425

CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1187 TCAGCCAGGCTGGGCA 1203
 Db 1 TCAGCCAAAGGTGGCA 17
 RESULT 427
 ABN02741
 ID ABN02741 standard; DNA; 17 BP.
 XX
 AC ABN02741;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2733.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 FI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 2733; 214pp; English.
 XX
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 765 CTCCTCAGCTGAGGCC 781
 Db 1 CTAGCGAGCTGAGGCC 17
 RESULT 428
 ABN07811
 ID ABN07811 standard; DNA; 17 BP.
 XX
 AC ABN07811;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7803.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 FI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WIPI; 2002-179446/23.
XX
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
XX Disclosure; SEQ ID NO 7803; 214pp; English.
XX
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 7 A; 4 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1425 AGCAGCAGCAGCAGCA 1441
Db 1 AGCAGCAGCTGAAGCA 17
XX
XX
XX RESULT 429
ABK25807/C
XX ID ABK25807 standard; DNA; 17 BP.
XX
XX AC ABK25807;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Stress tolerance conferring genome altering oligonucleotide #275.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW increased stearate production; reduced palmitate production; albino plant;
KW photosynthetic process.
XX
XX Cucurbita sp.
OS Synthetic.
XX
XX WO2001192512-A2.
XX
XX PD 06-DEC-2001.
XX

PF 01-JUN-2001; 2001WO-US017672.
XX
XX 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNIV DELAWARE.
PA
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
XX WIPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
XX Claim 7; Page 112; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
XX Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 928 CCAGCAGCTCAACAGA 944
Db 17 CCAGCTGCTCAACCGA 1
XX
XX
XX RESULT 430
ABK25808
XX ID ABK25808 standard; DNA; 17 BP.
XX
XX AC ABK25808;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Stress tolerance conferring genome altering oligonucleotide #276.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;

RESULT 432
ABK27199/c
ID ABK27199 standard; DNA; 17 BP.
XX
AC ABK27199;
XX
DT 09-APR-2002 (first entry)
XX
DE Reduced linolenic acid production genome altering oligonucleotide #95.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; herbicide resistance; disease resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO2001192512-A2.
XX
XX 06-DEC-2001.
PD
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
PI
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
XX Claim 7; Page 196; 220pp; English.
PS
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 AGCAGCTCAACAGATA 946
Db ||||| ||||| |||||
17 AGCAGCTCAAGCAGCTA 1
RESULT 433
ABK25787/c
ID ABK25787 standard; DNA; 17 BP.
XX
AC ABK25787;
XX
DT 09-APR-2002 (first entry)
XX
DE Stress tolerance conferring genome altering oligonucleotide #255.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; herbicide resistance; disease resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Cucumis sativus.
OS Synthetic.
XX
PN WO2001192512-A2.
XX
PD 06-DEC-2001.
XX
XX 01-JUN-2001; 2001WO-US017672.
PF
XX 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNIV DELAWARE.
PA
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
PI
XX WPI; 2002-106307/14.
DR
XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
XX Claim 7; Page 111; 220pp; English.
PS
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide

CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCA 944
 DB 17 CCAGCTGCTCAACCGA 1
 RESULT 434
 ID ABK25788 standard; DNA; 17 BP.
 XX
 AC ABK25788;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Stress tolerance conferring genome altering oligonucleotide #256.
 XX
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.
 XX
 OS Cucumis sativus.
 OS Synthetic.
 XX
 FN WO200192512-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-US017672.
 XX
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC, Kim J;
 XX
 DR WPI; 2002-106307/14.
 XX
 PT New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.
 XX
 PS Claim 7; Page 111; 220pp; English.
 XX
 CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises

CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCA 944
 DB 1 CCAGCTGCTCAACCGA 17

RESULT 435
 ABN97699
 ID ABN97699 standard; cDNA; 17 BP.
 XX
 AC ABN97699;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human NEDD-1 scanning 17-mer sequence #209.
 XX
 KW NEDD-1; cytosolic; human; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200226818-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US030287.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 01-JUN-2001; 2001US-00872462.
 XX
 PA (AEOM-) AEOMICA INT.
 XX
 PI Gu Y, Corrigan A;
 XX
 DR WPI; 2002-426011/45.
 XX

PT Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,
 PT treating or preventing a disorder associated with decreased or increased
 PT expression or activity of the polypeptide.
 XX


```
XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2675 CAGTTAACACCGAGT 2691
|||||
Db 1 CAGTTAAGACCATCATG 17

RESULT 438
ABN97696
ID ABN97696 standard; cDNA; 17 BP.
XX
AC ABN97696;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human NEDD-1 scanning 17-mer sequence #206.
XX
KW NEDD-1; cytosstatic; human; ss.
XX
OS Homo sapiens.
XX
PN WO200226818-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030287.
XX
PR 27-SEP-2000; 2000US-0236359P.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 01-JUN-2001; 2001US-00872462.
XX
PA (AEOM-) AEOMICA INT.
XX
PI Gu Y, Corrigan A;
XX
DR WPI; 2002-426011/45.
XX
PT Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,
PT treating or preventing a disorder associated with decreased or increased
PT expression or activity of the polypeptide.
XX
PS Example 4; Page 159; 190pp; English.
XX
CC This invention relates to an isolated polynucleotide encoding human NEDD-
CC 1, which is cytosstatic in its action. The polynucleotide is useful for
CC diagnosing or monitoring diseases caused by mutation in human NEDD-1, and for
CC diagnosing or monitoring diseases caused by altered expression of human
CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and
CC primers, and to direct expression or synthesis of epitopic or immunogenic
CC protein fragments. The proteins are useful as therapeutic supplement in
CC patients with specific deficiency in human NEDD-1 production, and for
CC treating subjects preferably with defects in NEDD-1. The present sequence
CC is a nucleotide sequence related to human NEDD-1
XX
SQ Sequence 17 BP; 7 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2673 ACCAGTTAACACCGAGT 2689
|||||
Db 1 ACCAGTTAAGACCATCA 17

RESULT 439
ABN97697
ID ABN97697 standard; cDNA; 17 BP.
XX
AC ABN97697;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human NEDD-1 scanning 17-mer sequence #207.
XX
KW NEDD-1; cytosstatic; human; ss.
XX
OS Homo sapiens.
XX
PN WO200226818-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030287.
XX
PR 27-SEP-2000; 2000US-0236359P.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 01-JUN-2001; 2001US-00872462.
XX
PA (AEOM-) AEOMICA INT.
XX
PI Gu Y, Corrigan A;
XX
DR WPI; 2002-426011/45.
XX
PT Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,
PT treating or preventing a disorder associated with decreased or increased
PT expression or activity of the polypeptide.
XX
PS Example 4; Page 159; 190pp; English.
XX
CC This invention relates to an isolated polynucleotide encoding human NEDD-
CC 1, which is cytosstatic in its action. The polynucleotide is useful for
CC diagnosing or monitoring diseases caused by mutation in human NEDD-1, and for
CC diagnosing or monitoring diseases caused by altered expression of human
CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and
CC primers, and to direct expression or synthesis of epitopic or immunogenic
CC protein fragments. The proteins are useful as therapeutic supplement in
CC patients with specific deficiency in human NEDD-1 production, and for
CC treating subjects preferably with defects in NEDD-1. The present sequence
CC is a nucleotide sequence related to human NEDD-1
XX
SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2674 CCAGTTAACACCGAGT 2690
|||||
Db 1 CCAGTTAAGACCATCATG 17
```



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RESULT 440
ABS74998
ID ABS74998 standard; DNA; 17 BP.
XX
XX
AC ABS74998;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 524.
XX
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
XX Homo sapiens.
OS
XX US2002102252-A1.
PN
XX 01-AUG-2002.
PD
XX 06-APR-2001; 2001US-00827998.
PF
XX 26-MAY-2000; 2000US-0207456P.
PR
XX (GUY/) GU Y.
XX (SHAN/) SHANNON M E.
PA
XX Gu Y, Shannon ME;
PI
XX WPI; 2002-697817/75.
DR
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
PT
XX Example 2; Page 144; 353pp; English.
PS
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 17 BP; 10 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 473 CAAATGACCCCAAGAGAA 489
DB 1 CAAAGGAACCAAGAGAA 17
|||||
RESULT 441
ABV90854/C
ID ABV90854 standard; DNA; 17 BP.
XX
AC ABV90854;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1567.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW

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KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
FN EPI239051-A2.
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (ABOM-) AEOMICA INC.
XX
PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1567; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 9% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 5 A; 6 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2211 TTCAGNATATGGGATG 2227
DB 17 TTCGAAATGGGGATG 1
|||||
RESULT 442
ABV89860
ID ABV89860 standard; DNA; 17 BP.
XX
AC ABV89860;
XX
XX 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 573.

```


XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 573; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2551 AGCCCTGAGCTGTGAG 2567
DB 1 ACCCCAGAGCTGTGAG 17
RESULT 443
ABV90268/C
ID ABV90268 standard; DNA; 17 BP.
XX
AC ABV90268;
XX

DT 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 981.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
XX
XX EP1239051-A2.
XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 981; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 1 A; 5 C; 1 G; 10 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3090 AAAGAAGAAAGGGAAGA 3106
DB 17 AACACAGATAGGGAAGA 1
RESULT 444
ABV98959
ID ABV98959 standard; DNA; 17 BP.

XX AC ABV89859;
XX DT 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 572.
XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX KW gene therapy; transgenic; ss.
XX OS Homo sapiens.
XX PN EP1239051-A2.
XX PD 11-SEP-2002.
XX PF 28-JAN-2002; 2002EP-00001165.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 10-OCT-2001; 2001US-0328205P.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M;
XX DR WPI; 2002-684061/74.
XX KW Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX PS Example 2; SEQ ID NO 572; 60pp + Sequence Listing; English.
XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (II) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2550 AAGCCCTGAGCTGCTGCA 2566
Db 1 AACCCTGAGCTGCTGCA 17
|||||

RESULT 445
ID ABK56440/c
XX AC ABK56440 standard; RNA; 17 BP.
XX AC ABK56440;
XX DT 02-JUL-2002 (first entry)
XX DE Human CLCA1 gene enzymatic nucleic acid #811.
XX KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX KW acetylcysteine.
XX OS Homo sapiens.
XX PN WO200211674-A2.
XX PD 14-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US024970.
XX PR 09-AUG-2000; 2000US-0224383P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (SYNT) SYNTEX USA LLC.
XX PA (THOM) THOMPSON J.
XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX DR WPI; 2002-217145/27.
XX KW Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX PS Claim 4; Page 71; 152pp; English.
XX CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition comprises
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX SQ Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 269 GCAGGACAGGTGGCT 285
Db 17 GCAGGAAAGCTGGCT 1
|||||

RESULT 446
ID ABK55961
ABK55961 standard; RNA; 17 BP.

XX AC ABK55961;
 XX DT 02-JUL-2002 (first entry)
 XX DE Human CLCA1 gene enzymatic nucleic acid #332.
 XX DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 XX KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 XX KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 XX KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 XX KW acetylcysteine.
 XX OS Homo sapiens.
 XX PN WO200211674-A2.
 XX PD 14-FEB-2002.
 XX PF 09-AUG-2001; 2001WO-US024970.
 XX PR 09-AUG-2000; 2000US-0224383P.
 XX PR (RIBO-) RIBOZYME PHARM INC.
 XX PA (SYNT) SYNTAX USA LLC.
 XX PA (THOM/) THOMPSON J.
 XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 XX PI Grupe A;
 XX WPI; 2002-217145/27.
 XX DR Enzymatic polynucleotide that down regulates expression of chloride
 XX PT channel calcium activated gene, useful for treating Chronic obstructive
 XX PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XX PS Claim 4; Page 58; 152pp; English.
 XX CC The invention relates to enzymatic nucleic acid molecules that down
 XX CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 XX CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 XX CC useful as pharmaceutical agents for treating conditions such as chronic
 XX CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 XX CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 XX CC that are related to or will respond to the levels of CLCA1 in a cell or
 XX CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 XX CC hence, are useful for treatment of a patient having a condition
 XX CC associated with the level of CLCA1, where the invention further comprises
 XX CC the use of one or more therapies under conditions suitable for the
 XX CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 XX CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 XX CC nucleic acids of the invention are also used as diagnostic tools to
 XX CC examine genetic drift and mutations within diseased cells or to detect
 XX CC the presence of CLCA1 RNA in a cell. This sequence represents an
 XX CC enzymatic nucleic acid molecule of the invention
 XX SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 2.5e-02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1648 CCAGCCTTGCTAAGGT 1664
 ||||| :||:||||:
 DB 1 CCAGGCAUUGCUAAGGU 17
 RESULT 447
 AAD36054
 ID AAD36054 standard; DNA; 17 BP.
 XX AC AAD36054;
 XX

DT 09-AUG-2002 (first entry)
 DE Human cMLCK DNA amplifying primer 3.
 KW Human; cardiac myosin light chain kinase; cMLCK; tricuspid valve;
 KW cardiac dysfunction; systolic dysfunction; mitral valve prolapse;
 KW diastolic dysfunction; cardiac hypertrophy; tricuspid insufficiency;
 KW coronary heart disease; myocardial infarction; mitral insufficiency;
 KW valvular heart disease; congestive heart failure; mitral valve;
 KW cardiomyopathy; cardiac; PCR; primer; ss.
 OS Homo sapiens.
 XX PN WO200224889-A2.
 XX PD 28-MAR-2002.
 XX PF 12-SEP-2001; 2001WO-US028639.
 XX PR 12-SEP-2000; 2000US-0232246P.
 XX PR 13-SEP-2000; 2000US-0232456P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Epstein ND, Haseanzadeh S, Winitzky S, Davis JS;
 XX DR WPI; 2002-394135/42.
 XX PT New isolated cardiac myosin light chain kinase (cMLCK) protein, useful
 XX PT for identifying cMLCK modulators that are used for treating cardiac
 XX PT dysfunction e.g. systolic or diastolic dysfunction, myocardial
 XX PT infarction.
 XX PS Example 1; Page 31; 105pp; English.
 XX CC The invention relates to cDNA, protein sequence and genomic structure of
 XX CC the human cardiac isoform of myosin light chain kinase (cMLCK) and
 XX CC mutations in cMLCK gene that are associated with cardiac dysfunction. The
 XX CC invention also relates to methods for identifying agents that modulate
 XX CC cMLCK activity. cMLCK is useful for detecting enhanced susceptibility of
 XX CC a subject to cardiac dysfunction. cMLCK is useful for screening for an
 XX CC agent that modulates its biological activity. The method is useful for
 XX CC enhancing or preserving cardiac function in a subject having cardiac
 XX CC dysfunction, and harbouring a mutation in cMLCK allele. The method is
 XX CC useful for enhancing or preserving cardiac function in a subject having
 XX CC cardiac dysfunction such as systolic dysfunction, diastolic dysfunction,
 XX CC cardiac hypertrophy, cardiomyopathy, coronary heart disease, myocardial
 XX CC infarction, or congestive heart failure, or for preserving cardiac
 XX CC function, or cardiac dysfunction which comprises valvular heart disease
 XX CC such as mitral valve disease, tricuspid valve disease, mitral
 XX CC insufficiency, tricuspid insufficiency, or mitral valve prolapse. The
 XX CC method is useful for treating cardiac dysfunction, e.g., systolic or
 XX CC diastolic dysfunction, coronary heart disease, cardiac hypertrophy,
 XX CC cardiomyopathy, myocardial infarction, or congestive heart failure. The
 XX CC present sequence is a PCR primer used to amplify human cMLCK DNA
 XX SQ Sequence 17 BP; 5 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e-02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 845 TCAGTCCCTCAGAGCCA 861
 ||||| |||||
 DB 1 TCAGACCCCGAGAGCCA 17
 RESULT 448
 ACN03097/c
 ID ACN03097 standard; RNA; 17 BP.
 XX AC ACN03097;
 XX

DT 22-APR-2004 (first entry)
 XX WNV Inozyme substrate SEQ ID NO 3100.
 XX
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 XX
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 3100; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 1 A; 3 C; 5 G; 0 T; 8 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2698 GAGACCCATGACCAAA 2714
 Db 17 GAGCCACATGACCAAA 1
 RESULT 449
 ACN01188/C
 ID ACN01188 standard; RNA; 17 BP.
 XX
 XX ACN01188;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1178.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI; 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 1178; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 2 A; 3 C; 5 G; 0 T; 7 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2700 GACCCATGACCAATG 2716
 Db 17 GCCACATGACCAATG 1
 RESULT 450
 ACN05943/C
 ID ACN05943 standard; RNA; 17 BP.
 XX
 XX ACN05943;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Amberzyme substrate SEQ ID NO 5946.
 DE
 XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX

PD 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 DR New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT Claim 23; SEQ ID NO 5946; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-J' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 4 A; 0 C; 8 G; 0 T; 5 U; 0 Other;
 SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3704 CCACATCTCTACTTC 3720
 DB ||| ||||| |||||
 17 CCAAAATCTCCACTTC 1
 RESULT 451
 ACN14376
 ID ACN14376 standard; RNA; 17 BP.
 AC ACN14376;
 XX 22-APR-2004 (first entry)
 DT WNV minus strand Amberzyme substrate SEQ ID NO 14379.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 DR New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT Claim 23; SEQ ID NO 14379; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-J' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 8 A; 5 C; 2 G; 0 T; 2 U; 0 Other;
 SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. NO. 2.5e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2699 AGACCCATGACCAAT 2715
 DB ||| ||||| |||||
 1 AGCCACAUGAACCAAU 17
 RESULT 452
 ACN01465
 ID ACN01465 standard; RNA; 17 BP.
 XX ACN01465;
 XX 22-APR-2004 (first entry)
 DT WNV Inozyme substrate SEQ ID NO 1455.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 1455; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 10 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2532 GAACAGGCAACAGCA 2548

Db 1 GAACAAACAAACAGCGA 17

RESULT 453

ACN12785/C

ID ACN12785 standard; RNA; 17 BP.

AC ACN12785;

XX 22-APR-2004 (first entry)

DE WNV minus strand Zinzyme substrate SEQ ID NO 12788.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; 88.

XX West Nile Virus.

OS WO200268637-A2.

PN 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 12788; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1212 TCCTCATGCGCAAAAG 1228

Db 17 TCCTCATGCGCGGAG 1

RESULT 454

ACN02990

ID ACN02990 standard; RNA; 17 BP.

AC ACN02990;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 2993.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; 88.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 2993; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 17 BP; 8 A; 2 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2813 TCAGGAACAGGTTGAA 2829
:|||||:|||||
Db 1 UCAGAGACAGGAUGAA 17

RESULT 455
ACN05859/c
ID ACN05859 standard; RNA; 17 BP.
XX
AC ACN05859;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Amberzyme substrate SEQ ID NO 5862.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.

XX
OS West Nile Virus.
XX
FN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
PS WPI; 2002-706994/76.
XX
CC New nucleic acid molecule that modulates replication of West Nile Virus
CC (WNV), useful for treating a condition related to WNV infection e.g.
CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 5862; 495pp; English.

XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX

SQ Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2115 TGGCAACCCAGTTTCA 2131
|||||
Db 17 TGGCACACCCAGTTGCA 1

RESULT 456
ACN09716/c
ID ACN09716 standard; RNA; 17 BP.
XX
AC ACN09716;

XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Inozyme substrate SEQ ID NO 9719.

XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.

XX
OS West Nile Virus.

XX
FN WO200268637-A2.

XX
PD 06-SEP-2002.

XX
PF 19-OCT-2001; 2001WO-US048350.

XX
PR 20-OCT-2000; 2000US-0242411P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

XX
PA (BLAT/) BLATT L.

XX
PA (MCSW/) MCSWIGGEN J A.

XX
PI Blatt L, Mcswiggen JA;

XX
PS WPI; 2002-706994/76.

XX
CC New nucleic acid molecule that modulates replication of West Nile Virus
CC (WNV), useful for treating a condition related to WNV infection e.g.
CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX
PS Claim 23; SEQ ID NO 9719; 495pp; English.

XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 17 BP; 3 A; 6 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3040 TGACTGGATGAAAGACA 3056


```
Db      17 TGAATGGATGGAGACA 1
|||||
RESULT 457
ACN09847
ID ACN09847 standard; RNA; 17 BP.
XX
AC ACN09847;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Inozyme substrate SEQ ID NO 9850.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 9850; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 3666 TTTCTTCCCCCATATTCA 3682
Db 1 UUUUUUUCCCAUUCUCA 17
:::|||||:
RESULT 458
ACN10151/c
ID ACN10151 standard; RNA; 17 BP.
XX
ACN10151;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Inozyme substrate SEQ ID NO 10154.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 10154; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 0 T; 8 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2813 TCAGGAACAGGTTGAA 2829
Db 17 TCAGGACACGAGTTGAA 1
|||||
RESULT 459
ACN06089/c
ID ACN06089 standard; RNA; 17 BP.
XX
AC ACN06089;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV Amberzyme substrate SEQ ID NO 6092.
XX
```


KW WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyne; ss.

XX West Nile Virus.

OS WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC. (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA; WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 6092; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 2 A; 2 C; 5 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 2.5e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 617 ATCAATGCCACCATAAA 633

DB 17 AACGATGCCACCATAAA 1

RESULT 460

ACN07144/C

ID ACN07144 standard; RNA; 17 BP.

XX ACN07144;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7147.

XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyne; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC. (BLAT/) BLATT L. (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA; WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7147; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 8 A; 0 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 2.5e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3656 TTTCTTCCCATATTCA 3682

DB 17 TTTCTTCCCATTTCTCA 1

RESULT 461

ACN01189/C

ID ACN01189 standard; RNA; 17 BP.

XX ACN01189;

XX 22-APR-2004 (first entry)

XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1179.

XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyne; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

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PR 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX Claim 23; SEQ ID NO 1179; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 2 A; 2 C; 5 G; 0 T; 8 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2699 AGACCCATGACCAAT 2715
DB 17 AGCCACATGAACCAAT 1
RESULT 462
ACN11320
ID ACN11320 standard; RNA; 17 BP.
XX ACN11320;
AC ACN11320;
XX 22-APR-2004 (first entry)
XX WNV minus strand Inozyme substrate SEQ ID NO 11323.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX Claim 23; SEQ ID NO 11323; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 8 A; 5 C; 2 G; 0 T; 2 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. NO. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 617 ATCAATGCCACATAAA 633
DB 1 AACGAUGCCACCAAAA 17
RESULT 463
ACN03400
ID ACN05400 standard; RNA; 17 BP.
XX ACN05400;
AC ACN05400;
XX 22-APR-2004 (first entry)
XX
XX WNV DNazyme substrate SEQ ID NO 5403.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX

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CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 4 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2532 GAACAGCAACAGCA 2548
DB 17 GAACAAACAGCA 1

RESULT 466
ACN11653
ID ACN11653 standard; RNA; 17 BP.
XX
AC ACN11653;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Inozyme substrate SEQ ID NO 11656.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyne; ss.
XX
OS West Nile Virus.
XX
XX WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Meswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 11656; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, and zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-J' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2115 TGGCAACCCAGTTTCA 2131
DB 1 UGGCACACCCAGUGUCA 17

RESULT 467
ACD00549/C
ID ACD00549 standard; DNA; 17 BP.
XX
AC ACD00549;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #1022.
XX
XX Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
XX WO2003031621-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032599.
XX
PR 12-OCT-2001; 2001US-0329000P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Zhang J;
XX
XX WPI; 2003-381720/36.
XX
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT investigating and/or treating disorders associated with aberrant
PT expression or activity of GPCR-A-1, such as tumors and cancers.
XX
XX Example 2; SEQ ID NO 1046; 156pp; English.
XX
XX The invention describes an isolated nucleic acid encoding a G protein
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC 409 residue amino acid sequence, all given in the specification, with or
CC without conservative amino acid substitutions, or complements of the
CC sequence of them. The encoding nucleic acid is not more than 100 kb in
CC length. The methods and compositions of the present invention are useful
CC for diagnosing, investigating and/or treating disorders associated with
CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
CC This sequence represents an oligonucleotide used to analyse the gene
CC encoding human G-protein coupled receptor GPCR-A-1
XX
SQ Sequence 17 BP; 4 A; 0 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2367 CAAGTAATAATAACAAT 2383
DB 17 CAATCATATAACAAT 1

RESULT 468
ABT37547/c
ID ABT37547 standard; DNA; 17 BP.
XX
AC ABT37547;
XX
DT 12-JUN-2003 (first entry)
XX

DE Tumour suppression related human fukutin oligo SEQ ID No 3184.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004208.
 XX 17-SEP-2001; 2001FR-00011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; Page 406; 720pp; French.
 PS The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3417 AAAAAGGCTATAGAC 3433
 DB 17 AAAAAGGTAAGATC 1
 RESULT 469
 ABT37040
 ID ABT37040 standard; DNA; 17 BP.
 XX AC ABT37040;
 XX 12-JUN-2003 (first entry)
 DE Tumour suppression related human fukutin oligo SEQ ID No 2677.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004208.
 XX 17-SEP-2001; 2001FR-00011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; Page 406; 720pp; French.
 PS The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 536 GATCCTGAGCTGCAGGA 552
 DB 1 GATCCTGAGCTGCCGAA 17
 RESULT 470
 ABT37508
 ID ABT37508 standard; DNA; 17 BP.
 XX AC ABT37508;
 XX 12-JUN-2003 (first entry)
 DE Tumour suppression related human fukutin oligo SEQ ID No 3145.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004208.
 XX 17-SEP-2001; 2001FR-00011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; Page 346; 720pp; French.
 PS The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 536 GATCCTGAGCTGCAGGA 552
 DB 1 GATCCTGAGCTGCCGAA 17
 RESULT 470
 ABT37508
 ID ABT37508 standard; DNA; 17 BP.
 XX AC ABT37508;
 XX 12-JUN-2003 (first entry)
 DE Tumour suppression related human fukutin oligo SEQ ID No 3145.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

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KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 401; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, or the complement
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1909 GATCATCGACAGAAAC 1925
XX ||||| ||||| |||||
XX 1 GATCCTGGACAGAAAC 17
XX
XX Db
XX
XX RESULT 471
XX ABT35272/c
XX ID ABT35272 standard; DNA; 17 BP.
XX
XX AC ABT35272;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 909.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1747 ACAACAGACAGAGATC 1763
XX ||||| ||||| |||||
XX 17 ACAACAGACATAGATC 1
XX
XX Db
XX
XX RESULT 472
XX ABT37737/c
XX ID ABT37737 standard; DNA; 17 BP.
XX
XX AC ABT37737;
XX
XX DT 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3374.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
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XX WO2003025175-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004208.
 XX 17-SEP-2001; 2001FR-00011978.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313353/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX Disclosure; Page 428; 720pp; French.
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2186 AGAATGCCATCATTTATC 2202
 ||||| ||||| ||||| ||||| |||||
 Db 17 AGAAGGCCATCATGATC 1
 RESULT 473
 ACA06321
 ID ACA06321 standard; RNA; 17 BP.
 XX ACA06321;
 AC ACA06321;
 XX 03-JUN-2003 (first entry)
 DT NFKB sub-unit modulating inozyme substrate #140.
 DE Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 XX G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX Homo sapiens.
 OS US2002177568-A1.
 XX 28-NOV-2002.
 PD 23-MAY-2001; 2001US-00864785.
 PF 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 DR Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX Claim 3; Page 29; 72pp; English.
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX Sequence 17 BP; 2 A; 9 C; 5 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.5e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1176 AGGCGGCGCCCTCAGCC 1192
 ||||| ||||| ||||| ||||| |||||
 Db 1 AGGCAGGCGCCCGCCG 17
 RESULT 474
 ACA06547
 ID ACA06547 standard; RNA; 17 BP.
 XX

CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 SQ Sequence 17 BP; 2 A; 10 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.5e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 756 CCTCAGGCTCTCTCTCAG 772
 Db 1 CCCCAGGCCCUCCUCAG 17
 RESULT 476
 ID ACA07772 standard; RNA; 17 BP.
 AC ACA07772;
 XX
 XX ACA07772;
 XX
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE NFKB sub-unit modulating zinzyme substrate #171.
 XX
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; Breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2002177568-A1.
 XX
 XX 28-NOV-2002.
 XX
 XX 23-MAY-2001; 2001US-00864785.
 XX
 XX 07-DEC-1992; 92US-00987132.
 XX 18-MAY-1994; 94US-00245466.
 XX 15-AUG-1994; 94US-00291932.
 XX 23-DEC-1996; 96US-00777916.
 XX
 XX (STIN// STINCHOMB D T.
 XX (MCSW// MCSWIGGEN J.
 XX (DRAP// DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 XX
 XX WPI; 2003-340953/32.
 XX
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 XX a sequence encoding a subunit of nuclear factor kappa B useful for
 XX treating cancer, inflammatory disorders and autoimmune diseases.
 XX

PS Claim 3; Page 40; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1407 AACGACGACGACGACG 1423
 Db 17 AACTGCAGCTGCACGACG 1
 RESULT 477
 ID ADB05972
 XX ADB05972 standard; DNA; 17 BP.
 AC ADB05972;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 DE Human MD212b scanning oligonucleotide SEQ ID 6958.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EPI281758-A2.
 XX
 XX 05-FEB-2003.
 XX
 XX 30-JUL-2002; 2002EP-00016874.
 XX
 XX 02-AUG-2001; 2001US-00922181.
 XX
 XX (ABOM-) AEDOMICA INC.
 XX
 XX Shannon M, Gu Y, Nguyen C;
 XX
 XX WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 XX manufacturing a medicament for treating or preventing a disorder
 XX associated with decreased or increased expression or activity of MD23,
 XX MD24, MD27 or MD212, e.g. cancer.
 XX

CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2942 TTGACTTCTCAGCCA 2958
Db 17 TTGACTTCTCAGCCA 1
RESULT 479
ADB02404/c
ID ADB02404 standard; DNA; 17 BP.
XX AC ADB02404;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD24 scanning oligonucleotide SEQ ID 3390.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 3390; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.

XX PS Example 8; SEQ ID NO 6958; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 4 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1664 TCACCTTCCCACTTCA 1680
Db 1 TCACCTTCCCACTTAA 17
RESULT 478
ADB00149/c
ID ADB00149 standard; DNA; 17 BP.
XX AC ADB00149;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1135.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1135; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

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CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 976 GCACGACGACACGACG 992
Db 17 GCTCCAGCACGACGACG 1

RESULT 480
ADA99981
ID ADA99981 standard; DNA; 17 BP.
AC ADA99981;
XX
DT 20-NOV-2003 (first entry)
DE Human MD23 scanning oligonucleotide SEQ ID 970.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 970; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 5 A; 7 C; 4 G; 1 T; 0 U; 0 Other;

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 976 GCACGACGACACGACG 992
Db 17 GCTCCAGCACGACGACG 1

RESULT 482
ADB00150/c
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Qy 2578 CCCACACGGTACACCTG 2594
Db 1 CCCACACGGAGACCTG 17

RESULT 481
ADA99394/c
ID ADA99394 standard; DNA; 17 BP.
AC ADA99394;
XX
DT 20-NOV-2003 (first entry)
DE Human MD23 scanning oligonucleotide SEQ ID 383.
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 383; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 976 GCACGACGACACGACG 992
Db 17 GCTCCAGCACGACGACG 1

RESULT 482
ADB00150/c
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ID	ADB00150 standard; DNA; 17 BP.	KW	Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX		KW	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
AC	ADB00150;	KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX		XX	developmental disorder; ss.
DT	20-NOV-2003 (first entry)	OS	Homo sapiens.
XX		XX	
DE	Human MD23 scanning oligonucleotide SEQ ID 1136.	PN	EP1281758-A2.
XX		XX	
KW	Cytostatic; immunostimulant; gene therapy; vaccine; human;	XX	
KW	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;	PD	05-FEB-2003.
KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	XX	
KW	developmental disorder; ss.	PF	30-JUL-2002; 2002EP-00016874.
XX		XX	
OS	Homo sapiens.	PR	02-AUG-2001; 2001US-00922181.
XX		XX	
PN	EP1281758-A2.	PA	(AEOM-) AEOMICA INC.
XX		XX	
XX	05-FEB-2003.	XX	Shannon M, Gu Y, Nguyen C;
PD		PI	WPI; 2003-423107/40.
XX		XX	
XX	30-JUL-2002; 2002EP-00016874.	DR	
XX		XX	
XX	02-AUG-2001; 2001US-00922181.	PT	New zinc finger-containing proteins and nucleic acids, useful in
PR		XX	manufacturing a medicament for treating or preventing a disorder
XX		PT	associated with decreased or increased expression or activity of MD23,
XX		PT	MD24, MD27 or MD212, e.g. cancer.
PA	(AEOM-) AEOMICA INC.	XX	
XX		XX	Example 8; SEQ ID NO 1136; 103pp; English.
PI	Shannon M, Gu Y, Nguyen C;	XX	
XX		XX	WPI; 2003-423107/40.
DR		XX	
XX		CC	The present invention relates to novel human zinc finger-containing
XX		CC	proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC		CC	encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC		CC	MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC		CC	15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC		CC	or in manufacturing a medicament for treating or preventing a disorder
CC		CC	associated with decreased or increased expression or activity of MD23,
CC		CC	MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC		CC	acids and proteins are also useful for diagnosing or monitoring a disease
CC		CC	caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC		CC	acids can also be used as probes to detect and characterize gross
CC		CC	alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC		CC	useful in constructing microarrays for measuring gene expression. The
CC		CC	proteins are useful as therapeutic agents for gene therapy or as
CC		CC	vaccines. The present sequence was used to illustrate the invention.
XX		XX	
XX	Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;	SQ	
			Query Match 0.4%; Score 13.8; DB 1; Length 17;
			Best Local Similarity 88.2%; Pred. No. 2.5e+02;
			Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	2941 TTTTGACTTCTCAGCC 2957	QY	2939 GCTTTGACTTCTCAGC 2955
Db	17 TTTTGACTTCTCAGCC 1	Db	17 GGTTTTGACTTCGTCAG 1
RESULT 483		RESULT 484	
ADB00152/c		ADA99390/c	
ID	ADB00152 standard; DNA; 17 BP.	ID	ADA99390 standard; DNA; 17 BP.
XX		XX	
AC	ADB00152;	AC	ADA99390;
XX		XX	
XX	20-NOV-2003 (first entry)	XX	20-NOV-2003 (first entry)
DT		DT	
XX		XX	
XX	Human MD23 scanning oligonucleotide SEQ ID 1138.	XX	Human MD23 scanning oligonucleotide SEQ ID 379.
DE		DE	
XX		XX	
KW	Cytostatic; immunostimulant; gene therapy; vaccine; human;	KW	Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;	KW	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW	developmental disorder; ss.	XX	developmental disorder; ss.
XX		XX	
OS	Homo sapiens.	XX	Homo sapiens.
XX		XX	
PN	EP1281758-A2.	PN	EP1281758-A2.

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XX PD 05-FEB-2003.
XX XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX XX
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX XX
XX PI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX XX
XX PS Example 8; SEQ ID NO 379; 103pp; English.
XX XX
XX CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX XX
XX SQ Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 CAGCACCAGCAGCAGCA 996
DB 17 CAGCACCAGCAGCTCCA 1
RESULT 495
ADB02405/c
ID ADB02405 standard; DNA; 17 BP.
XX AC ADB02405;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD24 scanning oligonucleotide SEQ ID 3391.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.

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XX PI Shannon M, Gu Y, Nguyen C;
XX XX
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX XX
XX PS Example 8; SEQ ID NO 3391; 103pp; English.
XX XX
XX CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX XX
XX SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 975 TGCACGACGACGACGAG 991
DB 17 TGCTCCAGCAGCAGCAG 1
RESULT 486
ADA99395/c
ID ADA99395 standard; DNA; 17 BP.
XX AC ADA99395;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 384.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,

```

PT MD24, MD27 or MDZ12, e.g. cancer.
 XX Example 8; SEQ ID NO 384; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 975 TGCAGCAGCAGCAGCAG 991
 DB 17 TGGTCCAGCAGCAGCAG 1
 RESULT 487
 ABZ61649/C
 ID ABZ61649 standard; RNA; 17 BP.
 XX
 AC ABZ61649;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human H-Ras DNazyme target #440.
 XX
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200297114-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US016840.
 XX
 XX 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswiggen J;
 PI
 XX WPI; 2003-140484/13.
 DR
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 PS Claim 58; Page 119; 185pp; English.
 XX
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
 CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 237 TCAGAGAAATTCGTGTT 253
 DB 17 TCAGAGAAATTCGTGTT 1
 RESULT 488
 ACDS1476/C
 ID ACDS1476 standard; RNA; 17 BP.
 XX
 AC ACDS1476;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HBV hammerhead ribozyme substrate sequence #585.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 XX WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 XX
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 DR
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 XX Example 1; Page 147; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HBV
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberyne sequences
CC disclosed in the present invention
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1154 GTAATGGCTAACTACAT 1170
Db 17 GTAATGATTACTACAT 1
||||| |||||||
RESULT 489
ACD61082/c
ID ACD61082 standard; RNA; 17 BP.
XX
AC ACD61082;
XX
DT 24-SEP-2003 (first entry)
XX
DE HCV DNazyme substrate sequence #2156.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEF/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 272; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 4 A; 2 C; 6 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 693 CCTCCTTACCCTGGAG 709
Db 17 CATCCTTACCCTAGAG 1
||||| |||||||
RESULT 490
ACD54845/c
ID ACD54845 standard; RNA; 17 BP.
XX
AC ACD54845;
XX
DT 24-SEP-2003 (first entry)
XX
DE HBV DNazyme substrate sequence #149.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
XX

PR	05-DEC-2001; 2001US-0337055P.
XX	(RIBO-) RIBOZYME PHARM INC.
PPA	(BLAT/) BLATT L.
PPA	(MACE/) MACEJAK D.
PPA	(MCSW/) MCSWIGGEN J.
PPA	(MORR/) MORRISSEY D.
PPA	(PAVC/) PAVCO P.
PPA	(LEEP/) LEE P.
PPA	(DRAP/) DRAPER K.
PPA	(ROBE/) ROBERTS E.
XX	
PPI	Blatt L., Macejak D., Mcswiggen J., Morrissey D., Pavco P., Lee P;
PPI	Draper K., Roberts E;
XX	
XX	WPI; 2003-229207/22.
XX	
PPT	Novel compound useful for treating cirrhosis, liver failure,
PPT	Hepatocellular carcinoma, or condition associated with hepatitis C virus
PPT	infection.
XX	
PS	Example 1; Page 189; 387pp; English.
XX	
CC	The present invention relates to nucleic acid molecules which modulate
CC	the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC	Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC	and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC	inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC	are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC	transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC	as oligonucleotides that specifically bind the Enhancer I region of HBV
CC	DNA. The nucleic acids may be used to modulate the expression of HBV
CC	genes and HBV viral replication. Also disclosed is a method for screening
CC	compounds and/or potential therapies directed against HBV, and compounds
CC	that modulate the expression and/or replication of HCV. The compounds and
CC	methods of the invention are useful for the treatment of degenerative and
CC	disease states related to HBV and HCV infection, replication and gene
CC	expression such as cirrhosis, liver failure, and hepatocellular
CC	carcinoma. The present sequence represents a substrate for one of the HBV
CC	ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences
CC	disclosed in the present invention
XX	
SQ	Sequence 17 BP; 5 A; 2 C; 2 G; 0 T; 8 U; 0 Other;
	Query Match 0.4%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1153 AGTAATCGCTAACTACA 1169
Db	17 AGTAATGATTAACTACA 1
RESULT 491	
ACC73351	
ID	ACC73351 standard; DNA; 17 BP.
XX	
AC	ACC73351;
XX	
DT	15-JUL-2003 (first entry)
XX	
DE	Mycobacterium gastrii specific probe GAS-01.
XX	
KW	Microarray; probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
OS	Mycobacterium gastrii.
XX	
XX	WO2003031654-A1.
FN	
PD	17-APR-2003.
XX	
PF	09-OCT-2002; 2002WO-KR001885.
XX	

CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 7 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3013 TTTATTGAAGACAGGC 3029
 DB 17 TTTATTGAAGTCAGATC 1
 |||||
 |||||

RESULT 493
 ACC65076
 ID ACC65076 standard; DNA; 17 BP.
 XX
 AC ACC65076;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2323.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 302; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2756 GGTCTGAATCTCAGACC 2772
 DB 1 GATCTGAATCTCAGAAC 17
 |||||
 |||||

RESULT 494
 ACC65169
 ID ACC65169 standard; DNA; 17 BP.
 XX
 AC ACC65169;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2416.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 313; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1982 GATCAGATAAACCGACA 1998
 DB 1 GATCAGATAAACCATCA 17
 |||||
 |||||

RESULT 495
 ACC65958/c
 ID ACC65958 standard; DNA; 17 BP.
 XX
 AC ACC65958;
 XX

```

DT 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3205.
DE
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX Disclosure; Page 405; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 GCAGAGCCCTCAGGATC 1238
Db 17 GGAAAGCCCCCAGGATC 1

RESULT 496
ACC68010
ID ACC68010 standard; DNA; 17 BP.
XX
XX ACC68010;
AC
XX
XX 01-JUL-2003 (first entry)
DT Murine oligonucleotide associated with tumour suppression, SEQ ID 5257.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
PN
XX 27-MAR-2003.
PD

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```

XX 17-SEP-2002; 2002WO-IB004210.
PF
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX Disclosure; Page 645; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1909 GATCATGCGAGCAGAAC 1925
Db 1 GATCATGCGAGCAGAGC 17

RESULT 497
ACC65917/c
ID ACC65917 standard; DNA; 17 BP.
XX
XX ACC65917;
AC
XX
XX 01-JUL-2003 (first entry)
DT Murine oligonucleotide associated with tumour suppression, SEQ ID 3164.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT

```

XX Disclosure; Page 400; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour CC reversal, apoptosis and virus resistance. The oligonucleotides are CC useful as (1) as probes and primers for detecting, identifying, CC quantifying and/or amplifying nucleic acid, e.g. as one component of a CC gene chip; in vitro as (anti)sense reagents; and (2) for production of CC recombinant polypeptides. The oligonucleotides are useful for preparation CC of pharmaceuticals for prevention and/or treatment of viral diseases that CC are characterised by development of tumours or cell degeneration, CC specifically cancer but also Alzheimer's disease and schizophrenia.

XX Sequence 17 BP; 2 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 998 CAGCCTACCACTGTC 1014
||||| ||||| |||

Db 17 CAGCCAACCACTGATC 1

RESULT 498
ADA15895
ID ADA15895 standard; DNA; 17 BP.

XX ADA15895;

XX 20-NOV-2003 (first entry)

DE Primer for amplification of GAPDH DNA #SEQ ID 74.

XX Human; beta-actin; GAPDH; loop-mediated isothermal amplification; LAMP;
KW Glyceraldehyde-3-phosphate dehydrogenase; cancer; metastasis;
KW genetic engineering; PCR; primer; ss.

XX Homo sapiens.

OS WO2003070935-A1.

PN 28-AUG-2003.

PD 13-FEB-2003; 2003WO-JP001474.

PP 20-FEB-2002; 2002JP-00043866.

PR 20-FEB-2002; 2002JP-00043867.

XX (SYSM-) SYSMEX CORP.

XX Tada S;

PI WPI; 2003-679880/64.

XX Primers for nucleic acid amplification in detecting housekeeping gene
PT mRNAs to confirm amplification of beta-actin and glyceraldehyde-3-
PT phosphate dehydrogenase useful in diagnosis of cancer.

XX Claim 5; Page 26; 90pp; Japanese.

XX The invention relates to primers for nucleic acid amplification for
CC detecting a housekeeping gene and/or a housekeeping gene-related mRNA by
CC the Loop-mediated isothermal amplification (LAMP) method. Particularly
CC referred to are primers for the amplification of beta-actin or GAPDH. The
CC primers of the invention are for nucleic acid amplification in detecting
CC housekeeping gene mRNAs, e.g. to confirm amplification of beta-actin and
CC glyceraldehyde-3-phosphate dehydrogenase (GAPDH), which are useful in
CC diagnosis of cancer and metastasis. By applying such primers, the
CC amplification of beta-actin and GAPDH can be used to confirm the presence
CC or absence of a tumour marker, e.g. cytokeratin, which can be used in the
CC control of data correction in the LAMP method, particularly in genetic

CC engineering, molecular biology and clinical medicine including disease
CC diagnosis. Using this method, diagnosis is fast (within 15 minutes) and
CC highly reliable. The required primers were designed based upon the gene
CC domain of e.g. beta-actin. After reaction by the reverse transcriptase-
CC loop-mediated isothermal amplification (RT-LAMP) method, the
CC amplification product was detected to confirm amplification of beta-actin
CC in the samples. The current sequence represents a primer for the
CC amplification of human GAPDH.

XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 793 CCCGCACTTCCTCCATGG 809
||||| ||||| |||||

Db 1 CCCAGCCTTCCTCCATGG 17

RESULT 499
ADB43213
ID ADB43213 standard; DNA; 17 BP.

XX ADB43213;

XX 18-DEC-2003 (revised)

DT 04-DEC-2003 (first entry)

XX Tumour suppression/reversion associated nucleotide #3536.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

XX Homo sapiens.

OS WO2003040369-A2.

PN 15-MAY-2003.

PD 17-SEP-2002; 2002WO-IB004219.

PP 17-SEP-2001; 2001FR-00011981.

PR (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 445; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2966 GATACATGGGCCCTGC 2982
DB 1 GATCACTTGGGCCCTGC 17
RESULT 500
ADB41766
ID ADB41766 standard; DNA; 17 BP.
XX
AC ADB41766;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2089.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 276; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC

CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1909 GATCATGGAGAGAAAC 1925
DB 1 GATCATGGAGAGAAAC 17
RESULT 501
ADB40208/C
ID ADB40208 standard; DNA; 17 BP.
XX
AC ADB40208;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #531.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 94; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX

SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2756 GGTCTGAATCTCAGACC 2772
 DB 17 GTTCTGAATCTCAGATC 1

RESULT 502
 ADB41665/c
 ID ADB41665 standard; DNA; 17 BP.
 XX AC ADB41665;
 XX AC ADB41665;
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX Tumour suppression/reversion associated nucleotide #1988.
 DE cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX Homo sapiens.
 OS
 XX WO2003040369-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-441574/41.
 DR
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS Disclosure; Page 264; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1896 CTCTACAGAGGCAGATC 1912
 DB 17 CTCTGAGAGGCAGATC 1

RESULT 503
 ADB43678/c
 ID ADB43678 standard; DNA; 17 BP.
 XX AC ADB43678;
 XX AC ADB43678;
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX Tumour suppression/reversion associated nucleotide #4001.
 DE cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX Homo sapiens.
 OS
 XX WO2003040369-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI
 XX WPI; 2003-441574/41.
 DR
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 PS Disclosure; Page 499; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 6 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 3486 AACTCCTTAATTGCTC 3502
DB 17 AACTCCTTAATATGATC 1

RESULT 504
ADB42015
ID ADB42015 standard; DNA; 17 BP.
XX
AC ADB42015;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2338.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Teلمان A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
DR New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 305; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.Se+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 536 GATCCTGAGCTGCAGGA 552
DB 1 GATCCTGAGCTGCCGAA 17
```

```
RESULT 505
ADC70444/C
ID ADC70444 standard; DNA; 17 BP.
XX
AC ADC70444;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tn3O-T PCR primer used to amplify target sequences of known mutants.
XX
KW Tn3O-T; PCR; primer; ss; transposon; mutant; parallel screening;
KW microbial; medical; industrial; agricultural; plate screen.
XX
OS Unidentified.
XX
PN US6528257-B1.
XX
PD 04-MAR-2003.
XX
PF 07-JUL-2000; 2000US-00612555.
XX
PR 07-JUL-2000; 2000US-00612555.
XX
PA (COUL ) COUNCIL SCI & IND RES.
XX
PI Sharma VM, Ganesan K;
XX WPI; 2003-695435/66.
XX
DR Simultaneously monitoring of the abundance of individual mutants of a
PT microbe in mixed populations, comprises generating a population of
PT mutants of a microbe having a genome by the random insertion of a known
PT transposon in the genome.
XX
PS Example 4; SEQ ID NO 13; 10pp; English.
XX
CC This invention relates to an improved and efficient method for
CC simultaneous monitoring of the abundance of individual mutants of a
CC microbe in mixed populations. Specifically, it comprises the random
CC insertion of a known transposon into the genome and quantitatively
CC tracing the abundance of identified mutants to follow their fitness under
CC various environmental conditions. The present invention describes a
CC method useful for parallel screening of large number of mutated genes and
CC for discovering the functions of microbial genes that have medical,
CC industrial and/ or agricultural importance. This improved method is
CC easier and faster, and furthermore is able to detect subtle differences
CC in phenotype to allow the isolation of mutants without a plate screen.
CC This oligonucleotide sequence is the PCR primer Tn3O-T used to amplify
CC the target sequences of known mutants in an exemplification of the
CC invention.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.Se+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2753 AGGGGCTCTGAATCTCAG 2769
DB 17 AGGGGCTCTGACGCTCAG 1

RESULT 506
ADC38460
ID ADC38460 standard; DNA; 17 BP.
XX
AC ADC38460;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:809.
```

XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 XX 01-NOV-2002; 2002WO-US035129.
 PF
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 XX Shannon M, Phan T;
 XX
 XX WPI; 2003-430501/40.
 DR
 XX
 XX New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 809; 172pp; English.
 XX
 CC The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX . Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
 SQ . Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 150 GTTCTTTGAAAGAAAA 166
 |||||
 DB 1 GTTCTTTGAAAGAAAA 17

RESULT 507
 ADB44767
 ID ADB44767 standard; DNA; 17 BP.
 XX
 AC ADB44767;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #5090.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA

XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-441574/41.
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 627; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ . Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 GATCGCGTCGACAAATC 71
 |||||
 DB 1 GATCGCGTCGACAAAC 17

RESULT 508
 ADB45671
 ID ADB45671 standard; DNA; 17 BP.
 XX
 AC ADB45671;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #5994.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-441574/41.
 DR

XX New nucleic acid encoding human prostate membrane-specific antigen.
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 732; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2898 GTTCCAGGGCCTTTCAA 2914
Db 1 GATCCAGGGCCTTTCAA 17

RESULT 509
ADB45324/C
ID ADB45324 standard; DNA; 17 BP.
XX
AC ADB45324;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #5647.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001PR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 692; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 5 A; 1 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3335 ATTTATCCAAACAGAAC 3351
Db 17 ATTTCTCCAAACAGATC 1

RESULT 510
ADB45499/C
ID ADB45499 standard; DNA; 17 BP.
XX
AC ADB45499;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #5822.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001PR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 712; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,

CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and/or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules.
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX SQ Sequence 17 BP; 1 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1918 GCAGAAACAGCAACTTC 1934
 |||||
 Db 17 GCAGAAACAGCAAGATC 1

RESULT 511
 ADD69451
 ID ADD69451 standard; DNA; 17 BP.
 XX AC ADD69451;
 XX DT 15-JAN-2004 (first entry)
 XX DE 5' anchored (ISSR)-PCR primer - SEQ ID 9.
 XX KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
 XX animal; Basmati rice; ss.
 XX OS Synthetic.
 XX PN WO2003085133-A2.
 XX PD 16-OCT-2003.
 XX PF 09-JAN-2003; 2003WO-IB000041.
 XX PR 08-APR-2002; 2002IN-CH000260.
 XX PA (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 XX PI Nagaraju JG;
 XX DR WPI; 2003-804317/75.
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 PS Claim 1; SEQ ID NO 9; 60pp; English.
 XX The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC 5' anchored (ISSR)-PCR primer of the invention.

XX SQ Sequence 17 BP; 8 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1554 AACAAACAGCAGCAGCAG 1570
 |||||
 Db 1 AAATACAGCAGCAGCAG 17
 RESULT 512
 ADD44223/c
 ID ADD44223 standard; DNA; 17 BP.
 XX AC ADD44223;
 XX DT 15-JAN-2004 (first entry)
 XX DE Carboxypeptidase G2 (CPG2) enzyme mutagenic oligonucleotide OL588.
 XX KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 KW immunogenic; T-cell epitope; MHC class II binding ligand;
 KW immunostimulant; enzyme therapy; immune response;
 KW gene directed enzyme produg strategy; vaccine; enzyme; EC 3.4.17.11;
 KW mutagenic; ss.
 XX OS Synthetic.
 XX OS Pseudomonas sp. RS-16.
 XX PN WO2003045426-A1.
 XX PD 05-JUN-2003.
 XX PF 27-NOV-2002; 2002WO-EP013351.
 XX PR 29-NOV-2001; 2001EP-00128519.
 XX PR 25-JAN-2002; 2002EP-00001778.
 XX PR 13-SEP-2002; 2002EP-00020634.
 XX PA (MERE) MERCK PATENT GMBH.
 XX PI Hellendoorn K, Baker M, Williams S, Carr FJ;
 XX DR WPI; 2003-513617/48.
 XX New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX Example 4; Page 37; 52pp; English.
 CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specific amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme produg strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This polynucleotide sequence represents a mutagenic oligonucleotide used
 CC in the production of a modified CPG2 gene of the invention.
 XX SQ Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX Disclosure; SEQ ID NO 4307; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 XX in the phenomena of tumour suppression, tumour reversion, apoptosis
 XX and/or resistance to viruses. The invention may be useful for the
 XX development of compounds with a cytostatic, virucide, neuroprotective,
 XX neurotropic or neuroleptic activity. The DNA sequences may be useful as
 XX probes and primers for detecting, identifying, quantifying and/or
 XX amplifying nucleic acid, for example as one component of a gene chip, in
 XX vitro as antisense reagents and for production of recombinant
 XX polypeptides. The invention may therefore be useful for preparation of
 XX pharmaceuticals for prevention and/or treatment of viral diseases that
 XX are characterised by development of tumours or cell degeneration. The
 XX specifically cancer but also Alzheimer's disease and schizophrenia. The
 XX present sequence is that of a nucleic acid sequence of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/publishedpct_sequences
 XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1662 GGTCACTTTCACGACTT 1678
 DB 1 GATCACCTTGCACCTT 17
 RESULT 519
 ADI49390
 ID ADI49390 standard; DNA; 17 BP.
 XX AC ADI49390;
 XX DT 15-APR-2004 (first entry)
 XX DE Human tumour suppression/reversion-related DNA sequence SeqID1893.
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 XX primer; PCR; gene chip; antisense; viral disease; tumour;
 XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX Homo sapiens.
 XX WO2003025177-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004523.
 XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX Disclosure; SEQ ID NO 1893; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved

XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX Disclosure; SEQ ID NO 4307; 30pp; French.
 XX This invention relates to novel isolated nucleic acid sequences involved
 XX in the phenomena of tumour suppression, tumour reversion, apoptosis
 XX and/or resistance to viruses. The invention may be useful for the
 XX development of compounds with a cytostatic, virucide, neuroprotective,
 XX neurotropic or neuroleptic activity. The DNA sequences may be useful as
 XX probes and primers for detecting, identifying, quantifying and/or
 XX amplifying nucleic acid, for example as one component of a gene chip, in
 XX vitro as antisense reagents and for production of recombinant
 XX polypeptides. The invention may therefore be useful for preparation of
 XX pharmaceuticals for prevention and/or treatment of viral diseases that
 XX are characterised by development of tumours or cell degeneration.
 XX specifically cancer but also Alzheimer's disease and schizophrenia. The
 XX present sequence is that of a nucleic acid sequence of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/publishedpct_sequences
 XX Sequence 17 BP; 7 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1687 GCTCCTACTTCAGAAA 1703
 DB 1 GATCCTACTTCAGAAA 17
 RESULT 518
 ADI49729
 ID ADI49729 standard; DNA; 17 BP.
 XX AC ADI49729;
 XX DT 15-APR-2004 (first entry)
 XX DE Human tumour suppression/reversion-related DNA sequence SeqID2232.
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 XX primer; PCR; gene chip; antisense; viral disease; tumour;
 XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX Homo sapiens.
 XX WO2003025177-A2.
 XX 27-MAR-2003.
 XX 17-SEP-2002; 2002WO-IB004523.
 XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.

CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 GAGCTCCCCCATGCTG 1124
 |||||
 Db 1 GATCTCTCCCATGCTG 17

RESULT 520
 ADI49542
 ID ADI49542 standard; DNA; 17 BP.
 AC ADI49542;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID2045.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosstatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 PS WPI; 2003-313354/30.
 XX
 DR New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 2045; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX
 SQ Sequence 17 BP; 1 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1339 GATGCTTCTGTTTGC 1355
 |||||
 Db 1 GATCCTTCTGTTTGC 17

RESULT 521
 ADI49656/c
 ID ADI49656 standard; DNA; 17 BP.
 AC ADI49656;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID2159.
 XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosstatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 PS WPI; 2003-313354/30.
 XX
 DR New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 2159; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

Qy 2898 GTTCCAGGGCTTTTCAA 2914

PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX
PS Claim 1; Page 148; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX
SQ Sequence 17 BP; 9 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1982 GATCAGATAACCGACA 1998
Db 1 GATCAGAGAAACAGACA 17
RESULT 527
ADL51684/C
ID ADL51684 standard; RNA; 17 BP.
XX
XX
AC ADL51684;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human PTGDR substrate sequence #803.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PTGDR;
KW substrate; ds.
XX
XX Unidentified.
XX
XX WO200281628-A2.
XX
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX Claim 161; SEQ ID NO 5217; 317pp; English.
PS
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, glomerulonephritis, sepsis, and allergic
CC ischaemia/reperfusion injury, glomerulonephritis or atopic dermatitis). The
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 4 C; 7 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 977 CAGCAGCACCAGCAGCA 993
Db 17 CATCAGCGCCAGCAGCA 1
RESULT 528
ADL48748/C
ID ADL48748 standard; RNA; 17 BP.
XX
XX
AC ADL48748;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human IKK-gamma substrate sequence #1258.
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
KW substrate; ds.
XX
XX Unidentified.
XX
XX WO200281628-A2.
XX
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010512.
XX
XX 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX
XX WPI; 2003-058513/05.
XX
XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX Claim 59; SEQ ID NO 2281; 317pp; English.
PS
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human IKK-gamma substrate sequence.

XX SQ Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 TGGAAATCTGCCTTGTA 2246
||||| ||| |||||
Db 17 TGGAGTCCGCTTGTA 1

RESULT 529

ADL49592/c
ID ADL49592 standard; RNA; 17 BP.

AC ADL49592;

XX 20-MAY-2004 (first entry)

DE Human PKR substrate sequence #706.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fossnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 3125; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.

XX SQ Sequence 17 BP; 1 A; 4 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 672 GCCAGAGGAGCACACCT 688
||||| ||| |||||
Db 17 GCCAGAGAAGCAACCT 1

RESULT 530

ADL46971/c
ID ADL46971 standard; RNA; 17 BP.

AC ADL46971;

XX 20-MAY-2004 (first entry)

DE Human NOGO receptor inozyme substrate sequence #404.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor inozyme; substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fossnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 9; SEQ ID NO 504; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.

XX Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
 SQ

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 70.6%; Pred. No. 2.5e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2508 CACCAACTGGGCTCT 2524

Db 1 CAACAGCGGGCCUCU 17

RESULT 533

ADM54088

ID ADM54088 standard; mRNA; 17 BP.

XX AC ADM54088;

XX DT 03-JUN-2004 (first entry)

XX DE Human GRID mRNA substrate sequence #363.

XX KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
 KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNzyme; Inozyme;
 KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

XX OS Homo sapiens.

XX PN US2003134806-A1.

XX PD 17-JUL-2003.

XX PF 23-FEB-2001; 2001US-00792818.

XX PR 10-FEB-2000; 2000US-0181594P.

XX PA (JARV/) JARVIS T.

XX PA (CARL/) CARLOWITZ I V.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (HAMB/) HAMBLIN P A.

XX PA (ELLI/) ELLIS J H.

XX PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;

XX DR WPI; 2003-829646/77.

XX PT New nucleic acid molecule that down-regulates expression of Grb2-related
 PT with insert domain (GRID) gene, useful for treating a condition
 PT associated with the level of GRID, e.g. tissue/graft rejection and
 PT leukemia.

XX PS Claim 4; SEQ ID NO 363; 74pp; English.

XX CC The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,
 CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 CC including the novel nucleic acid molecule, reducing GRID activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC treating a patient having a condition associated with the level of GRID
 CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel

CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.

XX Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 GCAGCACCAGCAGCAGC 995

Db 1 GCACCACCAGCACCAGC 17

RESULT 534

ADM54297

ID ADM54297 standard; mRNA; 17 BP.

XX AC ADM54297;

XX DT 03-JUN-2004 (first entry)

XX DE Human GRID mRNA substrate sequence #607.

XX KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
 KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNzyme; Inozyme;
 KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

XX OS Homo sapiens.

XX PN US2003134806-A1.

XX PD 17-JUL-2003.

XX PF 23-FEB-2001; 2001US-00792818.

XX PR 10-FEB-2000; 2000US-0181594P.

XX PA (JARV/) JARVIS T.

XX PA (CARL/) CARLOWITZ I V.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (HAMB/) HAMBLIN P A.

XX PA (ELLI/) ELLIS J H.

XX PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;

XX DR WPI; 2003-829646/77.

XX PT New nucleic acid molecule that down-regulates expression of Grb2-related
 PT with insert domain (GRID) gene, useful for treating a condition
 PT associated with the level of GRID, e.g. tissue/graft rejection and
 PT leukemia.

XX PS Claim 4; SEQ ID NO 607; 74pp; English.

XX CC The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,
 CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 CC including the novel nucleic acid molecule, reducing GRID activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC treating a patient having a condition associated with the level of GRID
 CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid

CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.

XX SQ Sequence 17 BP; 4 A; 9 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCACCA 999
Db 1 CCCUGCAGCAGCACCA 17
|||||

RESULT 535

ADM43565

ID ADM43565 standard; cDNA; 17 BP.

XX ADM43565;

AC ADM43565;

DT 03-JUN-2004 (first entry)

XX Signature sequence from human gene suppressed by cholesterol #17.

DE Signature sequence; Human; ss; MPSS;

KW massively parallel signature sequencing; cholesterol homeostasis;

KW atherosclerosis; heart disease.

XX Homo sapiens.

OS US2003170700-A1.

XX 11-SEP-2003.

XX 08-JAN-2003; 2003US-00340192.

XX 09-JAN-2002; 2002US-0347396P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Shang J, Bowen BA;

XX WPI; 2003-811493/76.

XX New polypeptides encoded by polynucleotides suppressed or induced by
PT cholesterol useful for treating responses to alterations in cholesterol
PT levels in cells, tissues or organisms e.g. atherosclerosis or heart
PT disease.
XX Claim 1; SEQ ID NO 17; 45pp; English.

XX The invention relates to isolated or recombinant polypeptides encoded by
XX polynucleotides suppressed or induced by cholesterol. The polypeptides
XX comprise at least one sequence encoded by a polynucleotide as follows:
XX having at least 70% identity to one of ADM43549-ADM43636; having sequence
XX complementary/hybridising under stringent conditions to one of the 88
XX sequences; hybridising to a polynucleotide that is physically linked in
XX human genome to a polynucleotide as in (i) or (ii); or comprising at
XX least 10 contiguous nucleotides of one of the 88 sequences or a
XX complementary sequence. The 88 sequences are signature sequences from
XX cDNAs up- or downregulated in response to cholesterol. Also included are
XX polynucleotide compositions comprising at least one expression vector
XX comprising a polynucleotide as above, cells comprising at least one
XX expression vector as above, labelled probes comprising a polynucleotide
XX as above, an antibody (optionally monoclonal antibody/polyclonal serum)
XX specific for polypeptide, a marker set for evaluating a
XX condition/characteristic associated with altered cholesterol levels and
XX arrays of two or more labelled probes or two or more polypeptides, or
XX comprising marker. The polypeptides can be administered therapeutically
XX to patients to treat responses to alterations of cholesterol levels e.g.
XX atherosclerosis or heart disease. They can be included with a (preferably
XX pharmaceutical) excipient in compositions which can be similarly

CC administered. They can also be used to modulate physiological or
CC pathological responses to alterations in cholesterol levels (especially
CC atherosclerosis or heart disease) in cells (e.g. liver cells), tissues or
CC organisms by modulating polypeptide expression or activity. They are also
CC useful to evaluate conditions/ characteristics associated with
CC alterations in cholesterol levels in subjects e.g. by using marker sets
CC or arrays. Polynucleotide compositions (optionally comprising a
CC pharmaceutical excipient) may be administered therapeutically to treat
CC responses to alterations of cholesterol levels as above. The
CC polynucleotides are also useful to modulate physiological/pathological
CC responses to alterations in cholesterol levels by modulating polypeptide
CC expression/activity as above. They may also be used to detect altered
CC pharmaceuticals administration or diet. The polynucleotides can also be
CC used to evaluate conditions/characteristic associated with alterations in
CC cholesterol levels (especially elevated levels) as above.
CC Polynucleotides, polynucleotide compositions and probes can be used to
CC identify genes capable of altering physiological/pathological responses
CC to alterations in cholesterol level, especially in response to
CC pharmaceuticals administration or diet. The present sequence is a
CC signature sequence from a gene whose expression is suppressed in response
CC to cholesterol.

XX Sequence 17 BP; 3 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3348 GAACGTGGTGTCAATG 3364

Db 1 GATCTGTGTGCAATG 17

|||||

RESULT 536

ADR96182

ID ADR96182 standard; DNA; 17 BP.

XX AC

XX ADK96182;

XX 06-MAY-2004 (first entry)

XX Primer of the invention #1902.

XX human; single nucleotide polymorphism; SNP; ss; primer.

XX Synthetic.

XX JP2003259875-A.

XX 16-SEP-2003.

XX 08-MAR-2002; 2002JP-00064373.

XX 08-MAR-2002; 2002JP-00064373.

XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.

XX WPI; 2004-093977/10.

XX Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX Claim 2; SEQ ID NO 5211; 2627pp; Japanese.

XX The present invention relates to a polynucleotide isolated from a human
XX gene and is useful for detecting a single nucleotide polymorphism in a
XX human gene or for diagnosing of disease. The invention enables the
XX detection of a single nucleotide polymorphism in a human gene. The
XX present sequence represents a primer of the invention.

XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 960 AGCAGCATGCCGGATG 976
|||||
Db 1 AGCAGCATGCTGGAGG 17

RESULT 537
ADM60003/c
ID ADM60003 standard; RNA; 17 BP.
XX
AC ADM60003;
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #2137.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 2137; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 5 A; 2 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1153 AGTAATGCTACTACA 1169
|||||
Db 17 AGTAATGATTACTACA 1

RESULT 538
ADM58484/c
ID ADM58484 standard; RNA; 17 BP.
XX
AC ADM58484;
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #618.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 618; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;

Tue Aug 16 13:09:33 2005

Best Local Similarity 88.2%; Pred. No. 2.5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1154 GTAATGGCTAACTACAT 1170
Db ||||| ||||| ||||| |||||

17 GTAATGATTAACTACAT 1

RESULT 539
ADN45890/c
ID ADN45890 standard; DNA; 17 BP.
XX
AC ADN45890;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2559.
XX
KW cell identification; oligonucleotide-directed sequence alteration;
KW selectable phenotype; transgenic plant; herbicide resistance;
KW sterile plant; abiotic stress tolerance; albino plant;
KW amino acid production; ss.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO2004033708-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031862.
XX
PR 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX
XX (UYDE) UNIV DELAWARE.
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX
PI Kmiec EB, Van Brabant A;
XX
DR WPI; 2004-340941/31.
XX
XX

Identifying a cell with a desired oligonucleotide-directed sequence alteration at a nucleic acid target site within the cell by identifying the desired sequence alteration in cells selected for the presence of a selectable phenotype.
Example 29; SEQ ID NO 2559; 303pp; English.
This invention relates to a novel method of identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cells. The method is useful in identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method may be useful for the production of plants with herbicide resistance, male or female sterile plants, abiotic stress tolerance, albino plants or plants with altered amino acid production as well as for use in mammalian cell lines. The present sequence is that of a mutagenic oligonucleotide which was used in the exemplification of the invention.

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 AGCAGCTCAACAGATA 946
Db ||||| ||||| ||||| |||||

17 AGCAGCTCAACAGCTA 1

RESULT 540
ADN45391
ID ADN45891 standard; DNA; 17 BP.
XX
AC ADN45891;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2560.
XX
KW cell identification; oligonucleotide-directed sequence alteration;
KW selectable phenotype; transgenic plant; herbicide resistance;
KW sterile plant; abiotic stress tolerance; albino plant;
KW amino acid production; ss.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO2004033708-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031862.
XX
PR 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX
XX (UYDE) UNIV DELAWARE.
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX
PI Kmiec EB, Van Brabant A;
XX
DR WPI; 2004-340941/31.
XX
XX

Identifying a cell with a desired oligonucleotide-directed sequence alteration at a nucleic acid target site within the cell by identifying the desired sequence alteration in cells selected for the presence of a selectable phenotype.
Example 29; SEQ ID NO 2560; 303pp; English.
This invention relates to a novel method of identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cells. The method is useful in identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method may be useful for the production of plants with herbicide resistance, male or female sterile plants, abiotic stress tolerance, albino plants or plants with altered amino acid production as well as for use in mammalian cell lines. The present sequence is that of a mutagenic oligonucleotide which was used in the exemplification of the invention.

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 AGCAGCTCAACAGATA 946
Db ||||| ||||| ||||| |||||

1 AGCAGCTCAACAGCTA 17

RESULT 541
ADN44479
ID ADN44479 standard; DNA; 17 BP.
XX

AC ADN44479;
 XX 15-JUL-2004 (first entry)
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1148.
 DE
 XX cell identification; oligonucleotide-directed sequence alteration;
 KW selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX Cucumis sativus.
 OS Synthetic.
 XX WO2004033708-A2.
 XX 22-APR-2004.
 XX 07-OCT-2003; 2003WO-US031862.
 XX 07-OCT-2002; 2002US-0416983P.
 XX 07-MAR-2003; 2003US-0453360P.
 XX (UYDE) UNIV DELAWARE.
 XX (NAPR-) NAPRO BIO THERAPEUTICS INC.
 XX Kmiec EB, Van Brabant A;
 XX WPI; 2004-340941/31.
 XX Identifying a cell with a desired oligonucleotide-directed sequence
 PT alteration at a nucleic acid target site within the cell by identifying
 PT the desired sequence alteration in cells selected for the presence of a
 PT selectable phenotype.
 XX Example 25; SEQ ID NO 1148; 303pp; English.
 XX This invention relates to a novel method of identifying a cell having a
 CC desired oligonucleotide-directed sequence alteration at a first nucleic
 CC acid target site within the cell. The method comprises identifying the
 CC desired sequence alteration in cells that have been selected for the
 CC presence of a selectable phenotype conferred by a concurrent
 CC oligonucleotide-directed sequence alteration at a second nucleic acid
 CC target site within the cells. The method is useful in identifying a cell
 CC having a desired oligonucleotide-directed sequence alteration at a first
 CC nucleic acid target site within the cell. The method may be useful for
 CC the production of plants with herbicide resistance, male or female
 CC sterile plants, abiotic stress tolerance, albino plants or plants with
 CC altered amino acid production as well as for use in mammalian cell lines.
 CC The present sequence is that of a mutagenic oligonucleotide which was
 CC used in the exemplification of the invention.
 XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGA 944
 DB 1 CCAGCTGCTCAACCCGA 17
 RESULT 542
 ADN44498/C
 ID ADN44498 standard; DNA; 17 BP.
 XX AC ADN44498;
 XX 15-JUL-2004 (first entry)
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1167.

KW cell identification; oligonucleotide-directed sequence alteration;
 KW selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX Cucurbita.
 OS Synthetic.
 XX WO2004033708-A2.
 XX 22-APR-2004.
 XX 07-OCT-2003; 2003WO-US031862.
 XX 07-OCT-2002; 2002US-0416983P.
 XX 07-MAR-2003; 2003US-0453360P.
 XX (UYDE) UNIV DELAWARE.
 XX (NAPR-) NAPRO BIO THERAPEUTICS INC.
 XX Kmiec EB, Van Brabant A;
 XX WPI; 2004-340941/31.
 XX Identifying a cell with a desired oligonucleotide-directed sequence
 PT alteration at a nucleic acid target site within the cell by identifying
 PT the desired sequence alteration in cells selected for the presence of a
 PT selectable phenotype.
 XX Example 25; SEQ ID NO 1167; 303pp; English.
 XX This invention relates to a novel method of identifying a cell having a
 CC desired oligonucleotide-directed sequence alteration at a first nucleic
 CC acid target site within the cell. The method comprises identifying the
 CC desired sequence alteration in cells that have been selected for the
 CC presence of a selectable phenotype conferred by a concurrent
 CC oligonucleotide-directed sequence alteration at a second nucleic acid
 CC target site within the cells. The method is useful in identifying a cell
 CC having a desired oligonucleotide-directed sequence alteration at a first
 CC nucleic acid target site within the cell. The method may be useful for
 CC the production of plants with herbicide resistance, male or female
 CC sterile plants, abiotic stress tolerance, albino plants or plants with
 CC altered amino acid production as well as for use in mammalian cell lines.
 CC The present sequence is that of a mutagenic oligonucleotide which was
 CC used in the exemplification of the invention.
 XX SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGA 944
 DB 17 CCAGCTGCTCAACCCGA 1
 RESULT 543
 ADN44478/C
 ID ADN44478 standard; DNA; 17 BP.
 XX AC ADN44478;
 XX 15-JUL-2004 (first entry)
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1147.
 DE
 XX cell identification; oligonucleotide-directed sequence alteration;
 KW selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX Cucumis sativus.

OS Synthetic.
XX WO2004033708-A2.
XX PD 22-APR-2004.
XX PF 07-OCT-2003; 2003WO-US031862.
XX PF 07-OCT-2002; 2002US-0416983P.
XX PR 07-MAR-2003; 2003US-0453360P.
XX XX
XX PA (UYDE) UNIV DELAWARE.
XX PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX PI Kmiec EB, Van Brabant A;
XX DR WPI; 2004-340941/31.
XX XX
XX PT Identifying a cell with a desired oligonucleotide-directed sequence
XX PT alteration at a nucleic acid target site within the cell by identifying
XX PT the desired sequence alteration in cells selected for the presence of a
XX PT selectable phenotype.
XX PS Example 25; SEQ ID NO 1147; 303pp; English.
XX XX
XX CC This invention relates to a novel method of identifying a cell having a
XX CC desired oligonucleotide-directed sequence alteration at a first nucleic
XX CC acid target site within the cell. The method comprises identifying the
XX CC desired sequence alteration in cells that have been selected for the
XX CC presence of a selectable phenotype conferred by a concurrent
XX CC oligonucleotide-directed sequence alteration at a second nucleic acid
XX CC target site within the cells. The method is useful in identifying a cell
XX CC having a desired oligonucleotide-directed sequence alteration at a first
XX CC nucleic acid target site within the cell. The method may be useful for
XX CC the production of plants with herbicide resistance, male or female
XX CC sterile plants, abiotic stress tolerance, albino plants or plants with
XX CC altered amino acid production as well as for use in mammalian cell lines.
XX CC The present sequence is that of a mutagenic oligonucleotide which was
XX CC used in the exemplification of the invention.
XX SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 928 CCAGCAGCTCAACAGCA 944
Db 17 CCAGCTGCTCAACCGA 1
RESULT 544
ADN44499
ID ADN44499 standard; DNA; 17 BP.
XX AC ADN44499;
XX DT 15-JUL-2004 (first entry)
XX DE Mutant cell identification-related mutagenic oligonucleotide SeqID1168.
XX KW cell identification; oligonucleotide-directed sequence alteration;
XX KW selectable phenotype; transgenic plant; herbicide resistance;
XX KW sterile plant; abiotic stress tolerance; albino plant;
XX KW amino acid production; ss.
XX OS Cucurbita.
XX OS Synthetic.
XX XX
XX FN WO2004033708-A2.
XX XX
XX PD 22-APR-2004.
XX XX

PF 07-OCT-2003; 2003WO-US031862.
XX 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX XX
XX PA (UYDE) UNIV DELAWARE.
XX PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX PI Kmiec EB, Van Brabant A;
XX DR WPI; 2004-340941/31.
XX XX
XX PT Identifying a cell with a desired oligonucleotide-directed sequence
XX PT alteration at a nucleic acid target site within the cell by identifying
XX PT the desired sequence alteration in cells selected for the presence of a
XX PT selectable phenotype.
XX PS Example 25; SEQ ID NO 1169; 303pp; English.
XX XX
XX CC This invention relates to a novel method of identifying a cell having a
XX CC desired oligonucleotide-directed sequence alteration at a first nucleic
XX CC acid target site within the cell. The method comprises identifying the
XX CC desired sequence alteration in cells that have been selected for the
XX CC presence of a selectable phenotype conferred by a concurrent
XX CC oligonucleotide-directed sequence alteration at a second nucleic acid
XX CC target site within the cells. The method is useful in identifying a cell
XX CC having a desired oligonucleotide-directed sequence alteration at a first
XX CC nucleic acid target site within the cell. The method may be useful for
XX CC the production of plants with herbicide resistance, male or female
XX CC sterile plants, abiotic stress tolerance, albino plants or plants with
XX CC altered amino acid production as well as for use in mammalian cell lines.
XX CC The present sequence is that of a mutagenic oligonucleotide which was
XX CC used in the exemplification of the invention.
XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 928 CCAGCAGCTCAACAGCA 944
Db 1 CCAGCTGCTCAACCGA 17
RESULT 545
ACN64970
ID ACN64970 standard; DNA; 17 BP.
XX AC ACN64970;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMPLP-1 probe SEQ ID NO:1872.
XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
XX KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.


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PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 1872; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1022 CCCTCCTCTGCTGGACC 1038
Db 1 CCCTCCTGAGCTGGACC 17
RESULT 546
ACN70900
ID ACN70900 standard; DNA; 17 BP.
XX
AC ACN70900;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:7802.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX
XX OS
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX

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PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 7802; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1409 CAGCAGCAGCAGCAGCA 1425.
Db 1 CAGCAGCAGCTGAGCA 17
RESULT 547
ACN65831
ID ACN65831 standard; DNA; 17 BP.
XX
AC ACN65831;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:2733.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW

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KW skeletal muscle function.
 XX Homo sapiens.
 XX US2004137589-A1.
 XX 15-JUL-2004.
 XX 26-NOV-2003; 2003US-00723361.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX (GUYV/) GU Y.
 PA (JIYY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 2733; Opp; English.
 XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 765 CTCCTCAGCTGAGGCC 781
 Db 1 CTACGACGCTGAGGCC 17
 RESULT 548
 ACN63763
 ID ACN63763 standard; DNA; 17 BP.
 XX

AC ACN63763;
 XX 02-DEC-2004 (first entry)
 XX Human GDMPLP-1 probe SEQ ID NO:665.
 XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX Homo sapiens.
 XX US2004137589-A1.
 XX 15-JUL-2004.
 XX 26-NOV-2003; 2003US-00723361.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX (GUYV/) GU Y.
 PA (JIYY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 665; Opp; English.
 XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 665 CAGCAAGCCGAGGAG 681

Db 1 CAGCCAGCGCAGAAG 17

||||| ||||| ||||| ||||| |||||

RESULT 549
ACN70901
ID ACN70901 standard; DNA; 17 BP.
XX AC ACN70901;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMLP-1 probe SEQ ID NO:7803.
XX KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX XX
OS Homo sapiens.
XX US2004137589-AI.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-0004263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 23-MAY-2001; 2001US-0086610B.
XX (GUYY/) GU Y.
PA (JIY/) JI Y.
PA (PENNY) PENN S G.
PA (HANYZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
DR Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX Disclosure; SEQ ID NO 7803; Opp; English.
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103.

[illegible]

CC	(S1), 95% deviation from (S1) which are conservative substitutions, and
CC	65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC	antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A
CC	pharmaceutical composition of the invention is useful for treating or
CC	preventing a disorder associated with decreased expression or activity of
CC	hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.
CC	The present sequence represents a 17-mer nucleotide, used in the
CC	invention for scanning the sequence represented in ACN63102
XX	
SQ	Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
	Query Match 0.4%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	664 TCAGCAAAGCCAGAGGA 680
Db	1 TCAGCCNAGCCAGAGAA 17
RESULT 551	
ACN73845	
ID	ACN73845 standard; DNA; 17 BP.
XX	ACN73845;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Human GDMPL-1 probe SEQ ID NO:10747.
XX	
KW	Human; ss; probe; myosin-like protein-1; hGDMPL-1;
KW	hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
KW	skeletal muscle function.
XX	
OS	Homo sapiens.
XX	
FN	US2004137589-A1.
XX	
PD	15-JUL-2004.
XX	
FF	26-NOV-2003; 2003US-00723361.
XX	
XX	26-MAY-2000; 2000US-0207456P.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
PR	30-JAN-2001; 2001WO-US000661.
PR	30-JAN-2001; 2001WO-US000662.
PR	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000664.
PR	30-JAN-2001; 2001WO-US000665.
PR	30-JAN-2001; 2001WO-US000666.
PR	30-JAN-2001; 2001WO-US000667.
PR	30-JAN-2001; 2001WO-US000668.
PR	30-JAN-2001; 2001WO-US000669.
PR	30-JAN-2001; 2001WO-US000670.
PR	05-FEB-2001; 2001US-0266860P.
PR	25-MAY-2001; 2001US-00866108.
XX	
PA	(GUY/) GU Y.
PA	(JIY/) JI Y.
PA	(PENN/) PENN S G.
PA	(HANZ/) HANZEL D K.
PA	(RANK/) RANK D.
PA	(CHEN/) CHEN W.
PA	(SHAN/) SHANNON M E.
XX	
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX	
DR	WPI; 2004-533378/51.
XX	
PT	Novel myosin-like protein-1, useful for treating or preventing disorder
PT	associated with decreased expression or activity of human genome-derived

PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 XX Disclosure; SEQ ID NO 1873; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
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 SQ Sequence 17 BP; 3-A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1023 CCTCTCTGCTGGACCA 1039
 DB 1 CCTCTGAGTGGACCA 17
 RESULT 553
 ACN73345
 ID ACN73345 standard; DNA; 17 BP.
 AC ACN73345;
 XX
 XX 02-DEC-2004 (first entry)
 DT Human GDMLP-1 probe SEQ ID NO:10247.
 DE
 XX
 XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 XX Homo sapiens.
 OS
 XX US2004137589-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 26-NOV-2003; 2003US-00723361.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.

PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.
 XX (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR

XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX

PS Disclosure; SEQ ID NO 10247; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
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SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1187 TCAGCCCGAGGTGGGCA 1203
 DB 1 TCAGCCAAAGGTGGGCA 17

Search completed: August 16, 2005, 12:54:22
 Job time : 26 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 12:48:29 ; Search time 14 Seconds
(without alignments)
3.358 Million cell updates/sec

Title: US-10-698-070-1
Perfect score: 3763
Sequence: 1 aggtggcgcgagagatgg.....taacacaaatatagagctg 3763

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 337 seqs, 6247 residues

Total number of hits satisfying chosen parameters: 674

Minimum DB seq length: 17
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 346 summaries

Database : fetchrge.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	30.4	0.8	33	1	AR241963
C 3	30	0.8	30	1	AR084541
C 4	30	0.8	30	1	AR165925
C 5	30	0.8	30	1	E34522
C 6	30	0.8	30	1	I84405
C 7	30	0.8	30	1	I84410
C 8	30	0.8	31	1	AR078304
C 9	29	0.8	31	1	AX249451
C 10	24	0.6	24	1	AR084605
C 11	23	0.6	23	1	BD183252
C 12	22	0.6	22	1	BD183253
C 13	22	0.6	25	1	AX754188
C 14	22	0.6	25	1	AX754189
C 15	22	0.6	25	1	AX754190
C 16	22	0.6	25	1	AX754191
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C 18	21.2	0.6	26	1	AX486861
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C 22	21	0.6	21	1	AR084571
C 23	21	0.6	21	1	AR084577
C 24	21	0.6	21	1	AR084580
C 25	21	0.6	21	1	AR084598
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C 29	21	0.6	25	1	AX754187
C 30	21	0.6	25	1	AX754192
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C 33	20.8	0.6	24	1	BD102725

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C 103	16	0.4	20	1	AX167902
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c 173	14.4	0.4	17	1	AX674077	ACCESSION:AX674077	c 246	13.8	0.4	17	1	AR326810	ACCESSION:AR326810
174	14.4	0.4	17	1	AX693263	ACCESSION:AX693263	c 247	13.8	0.4	17	1	AR329035	ACCESSION:AR329035
c 175	14.4	0.4	17	1	AX693264	ACCESSION:AX693264	c 248	13.8	0.4	17	1	AR434101	ACCESSION:AR434101
176	14.4	0.4	17	1	AX723745	ACCESSION:AX723745	c 249	13.8	0.4	17	1	AR456987	ACCESSION:AR456987
c 177	14.4	0.4	17	1	AX728782	ACCESSION:AX728782	c 250	13.8	0.4	17	1	AR458195	ACCESSION:AR458195
178	14.4	0.4	17	1	AX736485	ACCESSION:AX736485	c 251	13.8	0.4	17	1	AR458196	ACCESSION:AR458196
c 179	14.4	0.4	17	1	AX737300	ACCESSION:AX737300	c 252	13.8	0.4	17	1	AR458196	ACCESSION:AR458196

253	13.8	0.4	17	1	AR459056	ACCESSION:AR459056	326	13.8	0.4	17	1	AX738717	ACCESSION:AX738717
254	13.8	0.4	17	1	AR464125	ACCESSION:AR464125	327	13.8	0.4	17	1	AX739573	ACCESSION:AX739573
255	13.8	0.4	17	1	AR464136	ACCESSION:AR464136	328	13.8	0.4	17	1	AX745081	ACCESSION:AX745081
256	13.8	0.4	17	1	AR466570	ACCESSION:AR466570	329	13.8	0.4	17	1	AX754462	ACCESSION:AX754462
257	13.8	0.4	17	1	AR467070	ACCESSION:AR467070	330	13.8	0.4	17	1	AX757210	ACCESSION:AX757210
258	13.8	0.4	17	1	AX037420	ACCESSION:AX037420	331	13.8	0.4	17	1	AX758667	ACCESSION:AX758667
259	13.8	0.4	17	1	AX037426	ACCESSION:AX037426	332	13.8	0.4	17	1	AX758768	ACCESSION:AX758768
260	13.8	0.4	17	1	AX215334	ACCESSION:AX215334	333	13.8	0.4	17	1	AX759017	ACCESSION:AX759017
261	13.8	0.4	17	1	AX215335	ACCESSION:AX215335	334	13.8	0.4	17	1	AX760215	ACCESSION:AX760215
262	13.8	0.4	17	1	AX215661	ACCESSION:AX215661	335	13.8	0.4	17	1	AX760680	ACCESSION:AX760680
263	13.8	0.4	17	1	AX216107	ACCESSION:AX216107	336	13.8	0.4	17	1	AX761769	ACCESSION:AX761769
264	13.8	0.4	17	1	AX216350	ACCESSION:AX216350	337	13.8	0.4	17	1	AX762326	ACCESSION:AX762326
265	13.8	0.4	17	1	AX217014	ACCESSION:AX217014	338	13.8	0.4	17	1	AX762501	ACCESSION:AX762501
266	13.8	0.4	17	1	AX217450	ACCESSION:AX217450	339	13.8	0.4	17	1	AX762673	ACCESSION:AX762673
267	13.8	0.4	17	1	AX217453	ACCESSION:AX217453	340	13.8	0.4	17	1	AX773291	ACCESSION:AX773291
268	13.8	0.4	17	1	AX226753	ACCESSION:AX226753	341	13.8	0.4	17	1	AX773307	ACCESSION:AX773307
269	13.8	0.4	17	1	AX227106	ACCESSION:AX227106	342	13.8	0.4	17	1	AX783646	ACCESSION:AX783646
270	13.8	0.4	17	1	AX227461	ACCESSION:AX227461	343	13.8	0.4	17	1	AX926726	ACCESSION:AX926726
271	13.8	0.4	17	1	AX272889	ACCESSION:AX272889	344	13.8	0.4	17	1	BD075172	ACCESSION:BD075172
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273	13.8	0.4	17	1	AX325009	ACCESSION:AX325009	346	13.8	0.4	17	1	BD132158	ACCESSION:BD132158
274	13.8	0.4	17	1	AX325010	ACCESSION:AX325010							
275	13.8	0.4	17	1	AX325029	ACCESSION:AX325029							
276	13.8	0.4	17	1	AX325030	ACCESSION:AX325030							
277	13.8	0.4	17	1	AX326421	ACCESSION:AX326421							
278	13.8	0.4	17	1	AX326422	ACCESSION:AX326422							
279	13.8	0.4	17	1	AX328593	ACCESSION:AX328593							
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281	13.8	0.4	17	1	AX467582	ACCESSION:AX467582							
282	13.8	0.4	17	1	AX527213	ACCESSION:AX527213							
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287	13.8	0.4	17	1	AX531063	ACCESSION:AX531063							
288	13.8	0.4	17	1	AX531064	ACCESSION:AX531064							
289	13.8	0.4	17	1	AX531472	ACCESSION:AX531472							
290	13.8	0.4	17	1	AX532058	ACCESSION:AX532058							
291	13.8	0.4	17	1	AX578494	ACCESSION:AX578494							
292	13.8	0.4	17	1	AX578973	ACCESSION:AX578973							
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295	13.8	0.4	17	1	AX672024	ACCESSION:AX672024							
296	13.8	0.4	17	1	AX674529	ACCESSION:AX674529							
297	13.8	0.4	17	1	AX687647	ACCESSION:AX687647							
298	13.8	0.4	17	1	AX687651	ACCESSION:AX687651							
299	13.8	0.4	17	1	AX687652	ACCESSION:AX687652							
300	13.8	0.4	17	1	AX688238	ACCESSION:AX688238							
301	13.8	0.4	17	1	AX688403	ACCESSION:AX688403							
302	13.8	0.4	17	1	AX688404	ACCESSION:AX688404							
303	13.8	0.4	17	1	AX688406	ACCESSION:AX688406							
304	13.8	0.4	17	1	AX690658	ACCESSION:AX690658							
305	13.8	0.4	17	1	AX690659	ACCESSION:AX690659							
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307	13.8	0.4	17	1	AX724636	ACCESSION:AX724636							
308	13.8	0.4	17	1	AX724729	ACCESSION:AX724729							
309	13.8	0.4	17	1	AX725477	ACCESSION:AX725477							
310	13.8	0.4	17	1	AX725518	ACCESSION:AX725518							
311	13.8	0.4	17	1	AX725925	ACCESSION:AX725925							
312	13.8	0.4	17	1	AX727570	ACCESSION:AX727570							
313	13.8	0.4	17	1	AX729275	ACCESSION:AX729275							
314	13.8	0.4	17	1	AX731043	ACCESSION:AX731043							
315	13.8	0.4	17	1	AX731511	ACCESSION:AX731511							
316	13.8	0.4	17	1	AX731550	ACCESSION:AX731550							
317	13.8	0.4	17	1	AX731740	ACCESSION:AX731740							
318	13.8	0.4	17	1	AX734784	ACCESSION:AX734784							
319	13.8	0.4	17	1	AX735383	ACCESSION:AX735383							
320	13.8	0.4	17	1	AX735531	ACCESSION:AX735531							
321	13.8	0.4	17	1	AX736303	ACCESSION:AX736303							
322	13.8	0.4	17	1	AX736455	ACCESSION:AX736455							
323	13.8	0.4	17	1	AX736569	ACCESSION:AX736569							
324	13.8	0.4	17	1	AX736585	ACCESSION:AX736585							
325	13.8	0.4	17	1	AX736642	ACCESSION:AX736642							

RESULT 1

AR084540/c

LOCUS Sequence 29 from patent US 5981185.

DEFINITION AR084540

ACCESSION AR084540

VERSION AR084540.1 GI:10011311

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 33)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.

TITLE Oligonucleotide repeat arrays

JOURNAL Patent: US 5981185-A 29 09-NOV-1999;

FEATURES

Location/Qualifiers

source

1..33

/organism="unknown"

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Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440

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Db 33 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 2

RESULT 2

AR241963

LOCUS Sequence 251 from patent US 6472154.

DEFINITION AR241963

ACCESSION AR241963

VERSION AR241963.1 GI:27287775

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 33)

AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes.

JOURNAL Patent: US 6472154-A 251 29-OCT-2002;

FEATURES

Location/Qualifiers

source

1..33

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.8%; Score 30.4; DB 1; Length 33;
Best Local Similarity 96.9%; Pred. No. 11;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGCA 32

RESULT 3
AR084541
LOCUS AR084541 30 bp DNA PAT 01-SEP-2000
DEFINITION Sequence 30 from patent US 5981185.
ACCESSION AR084541
VERSION AR084541.1 GI:10011312
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 30 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 4
AR165925
LOCUS AR165925 30 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6280938.
ACCESSION AR165925
VERSION AR165925.1 GI:16241014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ratum,L.P.W., Koob,M.D., Moseley-Allredge,M.L. and Benzow,K.A.
TITLE SCA7 gene and method of use
JOURNAL Patent: US 6280938-A 4 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 5
E34522
LOCUS E34522 30 bp DNA PAT 18-JUN-2001
DEFINITION SCA7 gene and utilization thereof.
ACCESSION E34522
VERSION E34522.1 GI:13018890
KEYWORDS JP 1999206393-A/4.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Laura,B.W.R. and Michael,D.K.
TITLE SCA7 gene and utilization thereof
JOURNAL Patent: JP 1999206393-A 4 03-AUG-1999;
COMMENT THE REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Homo sapiens (human)
PN JP 1999206393-A/4
PD 03-AUG-1999
PF 19-AUG-1998 JP 1998294732
PR 19-AUG-1997 US 60/056170
PI LAURA B W RANAMU, MICHAEL D KUBU
PC C12N15/09, C07K14/47, C07K16/18, C12Q1/68, G01N33/53, PC
G01N33/566//C12P21/02,
PC C12N15/00
CC
FH
FT
Key Location/Qualifiers
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/db_xref="taxon:9606"

FEATURES
source 1..30
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
|||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 6
I84405
LOCUS I84405 30 bp DNA PAT 04-APR-1998
DEFINITION Sequence 6 from patent US 5695933.
ACCESSION I84405
VERSION I84405.1 GI:3021925
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Housman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 6 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
|||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 7
I84410/c
LOCUS I84410 30 bp DNA PAT 04-APR-1998
DEFINITION Sequence 11 from patent US 5695933.
ACCESSION I84410
VERSION I84410.1 GI:3021930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.


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Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCACAGCAGCAG 1450
Db 2 GCAGCAGCAGCACAGCAGCAG 23

RESULT 16
AX754191
LOCUS AX754191 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 538 from Patent WO03037931.
ACCESSION AX754191
VERSION AX754191.1 GI:32166888
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 538 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCACAGCAGCAG 1450
Db 1 GCAGCAGCAGCACAGCAGCAG 22

RESULT 17
BD174259/c
LOCUS BD174259 Novel physiological active peptide and its use.
DEFINITION BD174259
ACCESSION BD174259
VERSION BD174259.1 GI:28415598
KEYWORDS WO 02062944-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Otaki,T., Masuda,Y., Takatsu,Y., Watanabe,T., Terao,Y., Shintani,Y.
and Hinuma,S.
TITLE Novel physiological active peptide and its use
JOURNAL Patent: WO 02062944-A 6 15-AUG-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA,
YOSHIOHRO TAKATSU,TAKUYA WATANABE,YASUKO TERAU,YASUSHI SHINTANI,
SHUJI HINUMA
COMMENT OS Artificial Sequence
PN WO 02062944-A/6
PD 15-AUG-2002
PF 01-FEB-2002 WO 2002JP000852
PR 02-FEB-2001 JP 01P 026820
PI TETSUYA OTAKI,YASUSHI MASUDA,YOSHIOHRO TAKATSU,TAKUYA
WATANABE,
PI YASUKO TERAU,YASUSHI SHINTANI,SHUJI HINUMA
PC C07K14/47,C07K14/705,C12N15/12,C12P21/02,C07K16/18,A61K67/027,
PC C12N5/10,
PC G01N33/15,G01N33/50,A61P1/00
CC DNA primer, hBv8-F1 primer
FH Key
FT source
1. .26
/organism='Artificial Sequence'.

FEATURES
source
1. .26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 70;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGCAGCAG 1432
Db 26 AACAGCAGCGGCAGCAGCAGAAAGTAG 1

RESULT 18
AX486861/c
LOCUS AX486861 26 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4161 from Patent WO02053728.
ACCESSION AX486861
VERSION AX486861.1 GI:22321009
KEYWORDS Candida albicans
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE 1 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4161 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
1. .26
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match      0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 70;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1568 CAGCAGCAACACACAGCAGCAACA 1593
Db 26 CAACAACAACACACACACACACACA 1

RESULT 19
AR053160/c
LOCUS AR053160 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 66 from patent US 5834183.
ACCESSION AR053160
VERSION AR053160.1 GI:5978022
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for
diagnosis
JOURNAL Patent: US 5834183-A 66 10-NOV-1998;
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/organism="unknown"
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Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAGC 1430
Db 21 AGCAGCAGCAGCAGCAGCAGCAGC 1

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PAT 01-SEP-2000

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ACCESSION AR084598
VERSION AR084598.1 GI:10011369
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 87 09-NOV-1999;
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Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCA 1431
Db 21 GCAGCAGCAGCAGCAGCAGCA 1

RESULT 26
AX104588/c
LOCUS AX104588 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 780 from Patent WO0122972.
ACCESSION AX104588
VERSION AX104588.1 GI:13920785
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 780 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 27
AX355212/c
LOCUS AX355212 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 240 from Patent WO0197843.
ACCESSION AX355212
VERSION AX355212.1 GI:18619879
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 240 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 28
AX547641/c
LOCUS AX547641 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 780 from Patent WO02053141.
ACCESSION AX547641
VERSION AX547641.1 GI:25812785
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 780 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"
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Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 29
AX754187
LOCUS AX754187 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 534 from Patent WO03037931.
ACCESSION AX754187
VERSION AX754187.1 GI:32166884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 534 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
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Query Match 0.6%; Score 21; DB 1; Length 25;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCA 1449

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[illegible]


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13-APR-2001 JP 01P 116000
PI MASAKI MORI, YUKIO SHIMOMURA, MIOKO HARADA, MIKA KURIHARA, CHIEKO
PI KITADA,
PI TAJIJI ASAMI, YOSHIO MATSUMOTO, YUKA ADACHI, TAKUYA WATANABE, PI
TSUKASA SUGO,
PI MICHIO ABE
PC C12N15/12, C07K14/47, C12N1/21, C07K16/18, G01N33/53, G01N33/50, PC
G01N33/15,
PC C12P21/02, C12P21/08, A61K31/711, A61K38/17, A01K67/027, A61P1/14,
PC A61P3/04
CC Primer
FH Key
FT source Location/Qualifiers
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Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1418 CAGCAGCAGCAGCAGCAGCA 1441
Db 1 CAGCGGCAGCAGCAGCAGCA 24
RESULT 34
A27144/c 25 bp DNA linear PAT 22-AUG-1996
LOCUS
DEFINITION synthetic leader.
ACCESSION A27144
VERSION A27144.1 GI:1831892
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1420 GCAGCAGCAGCAGCAGCA 1441
Db 25 GGAGCAGCAGCAGCAGCA 4
RESULT 35
A27143 25 bp DNA linear PAT 22-AUG-1996
LOCUS
DEFINITION synthetic leader.
ACCESSION A27143
VERSION A27143.1 GI:1831891
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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source
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Patent: CA 1306208-A 1 11-AUG-1992;
Location/Qualifiers
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13-APR-2001 JP 01P 116000
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PI KITADA,
PI TAJIJI ASAMI, YOSHIO MATSUMOTO, YUKA ADACHI, TAKUYA WATANABE, PI
TSUKASA SUGO,
PI MICHIO ABE
PC C12N15/12, C07K14/47, C12N1/21, C07K16/18, G01N33/53, G01N33/50, PC
G01N33/15,
PC C12P21/02, C12P21/08, A61K31/711, A61K38/17, A01K67/027, A61P1/14,
PC A61P3/04
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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Best Local Similarity 91.7%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1418 CAGCAGCAGCAGCAGCAGCA 1441
Db 1 CAGCGGCAGCAGCAGCAGCA 24
RESULT 34
A27144/c 25 bp DNA linear PAT 22-AUG-1996
LOCUS
DEFINITION synthetic leader.
ACCESSION A27144
VERSION A27144.1 GI:1831892
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 20.4; DB 1; Length 25;
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1420 GCAGCAGCAGCAGCAGCA 1441
Db 25 GGAGCAGCAGCAGCAGCA 4
RESULT 35
A27143 25 bp DNA linear PAT 22-AUG-1996
LOCUS
DEFINITION synthetic leader.
ACCESSION A27143
VERSION A27143.1 GI:1831891
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ORGANISM
REFERENCE
AUTHORS
JOURNAL
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source
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Patent: CA 1306208-A 1 11-AUG-1992;
Location/Qualifiers
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Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1407 AACAGCAGCAGCAGCAGCAGCA 1431
Db 1 AATTGGAGCAGCAGCAGCAGCA 25
RESULT 36
AX487367/c 20 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 4667 from Patent WO02053728.
ACCESSION AX487367
VERSION AX487367.1 GI:223221515
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
JOURNAL
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/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1553 CAACAACAGCAGCAGCAGCA 1572
Db 20 CAACAACAGCAGCAGCAGCA 1
RESULT 37
AX488408/c 20 bp DNA linear PAT 16-AUG-2002
LOCUS
DEFINITION Sequence 5708 from Patent WO02053728.
ACCESSION AX488408
VERSION AX488408.1 GI:22322488
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1555 ACAACAGCAGCAGCAGCAGC 1574
Db 20 ACAACAGCAGCAGCAGCAGC 1
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ORGANISM	synthetic construct									
REFERENCE	other sequences; artificial sequences.									
AUTHORS	1 (bases 1 to 24)									
TITLE	Conrad,M.J. and Coutts,S.									
JOURNAL	Conjugates of biologically stable polymers and polynucleotides for treating systemic lupus erythematosus									
COMMENT	Patent: JP 2001354569-A 8-25-DEC-2001; LA JOLLA PHARMACEUTICAL CO									
	OS	Artificial Sequence								
	PN	JP 2001354569-A/8								
	PD	25-DEC-2001								
	PF	04-APR-2001								
	PR	16-JAN-1990 US 466138,13-MAR-1990 US 494118 PI								
	PC	MICHAEL J CONRAD,STEPHEN COUTTS								
	CC	A61K31/7088,A61K47/48,A61P37/02,C07K14/00,C12N15/00,C12N15/00								
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	Key	Location/Qualifiers								
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LOCUS	AX088799 22 bp DNA linear PAT 17-MAR-2001									
DEFINITION	Sequence 125 from Patent WO0114416.									
ACCESSION	AX088799									
VERSION	AX088799.1 GI:13397595									
KEYWORDS	synthetic construct									
SOURCE	synthetic construct									
ORGANISM	other sequences; artificial sequences.									
REFERENCE	1									
AUTHORS	Keeper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L. and Wang,X.M.									
TITLE	Synthetic human papillomavirus genes									
JOURNAL	Patent: WO 0114416-A 125 01-MAR-2001;									
	Merck & Co., Inc. (US)									
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DB	2	CGCAACACACAGCAACAGCAGC 22								
RESULT 42										
AR315939/c										
LOCUS	AR315939 20 bp DNA linear PAT 12-JUN-2001									
DEFINITION	Sequence 6476 from patent US 6559294.									
ACCESSION	AR315939									
VERSION	AR315939.1 GI:31709365									
KEYWORDS										

Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoieseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAACAGCAAC 1472
Db 19 CAGCAACAGCAAC 1

RESULT 43
AX088798/c
LOCUS AX088798 23 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 124 from Patent WO0114416.
ACCESSION AX088798
VERSION AX088798.1 GI:13397594
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Neepser, M.P., McClements, W.L., Jansen, K.U., Schultz, L.D., Chen, L. and Wang, X.M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 124 01-MAR-2001;
Merck & Co., Inc. (US)
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/note="Codon-Optimized HPV6 E2 fragment"

Query Match 0.5%; Score 19; DB 1; Length 23;
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Qy 1499 CAACACAGCAACGAGC 1517
Db 22 CAACACAGCAACGAGC 4

RESULT 44
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LOCUS AX360164 22 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 120 from Patent WO0200860.
ACCESSION AX360164
VERSION AX360164.1 GI:18675731
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Plowman, G., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and Charydzak, G.
TITLE Novel proteases
JOURNAL Patent: WO 0200860-A 120 03-JAN-2002;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
source 1..22

Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoieseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAACAGCAAC 1472
Db 19 CAGCAACAGCAAC 1

RESULT 43
AX088798/c
LOCUS AX088798 23 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 124 from Patent WO0114416.
ACCESSION AX088798
VERSION AX088798.1 GI:13397594
KEYWORDS
SOURCE
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synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Neepser, M.P., McClements, W.L., Jansen, K.U., Schultz, L.D., Chen, L. and Wang, X.M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 124 01-MAR-2001;
Merck & Co., Inc. (US)
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Qy 1499 CAACACAGCAACGAGC 1517
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RESULT 44
AX360164/c
LOCUS AX360164 22 bp DNA linear PAT 13-FEB-2002
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ACCESSION AX360164
VERSION AX360164.1 GI:18675731
KEYWORDS
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ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Plowman, G., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and Charydzak, G.
TITLE Novel proteases
JOURNAL Patent: WO 0200860-A 120 03-JAN-2002;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
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ORGANISM
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REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoieseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
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Db 19 CAGCAACAGCAAC 1

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LOCUS AX088798 23 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 124 from Patent WO0114416.
ACCESSION AX088798
VERSION AX088798.1 GI:13397594
KEYWORDS
SOURCE
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synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Neepser, M.P., McClements, W.L., Jansen, K.U., Schultz, L.D., Chen, L. and Wang, X.M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 124 01-MAR-2001;
Merck & Co., Inc. (US)
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1499 CAACACAGCAACGAGC 1517
Db 22 CAACACAGCAACGAGC 4

RESULT 44
AX360164/c
LOCUS AX360164 22 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 120 from Patent WO0200860.
ACCESSION AX360164
VERSION AX360164.1 GI:18675731
KEYWORDS
SOURCE
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Plowman, G., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and Charydzak, G.
TITLE Novel proteases
JOURNAL Patent: WO 0200860-A 120 03-JAN-2002;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
source 1..22

Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoieseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
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RESULT 43
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LOCUS AX088798 23 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 124 from Patent WO0114416.
ACCESSION AX088798
VERSION AX088798.1 GI:13397594
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Neepser, M.P., McClements, W.L., Jansen, K.U., Schultz, L.D., Chen, L. and Wang, X.M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 124 01-MAR-2001;
Merck & Co., Inc. (US)
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Db 22 CAACACAGCAACGAGC 4

RESULT 44
AX360164/c
LOCUS AX360164 22 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 120 from Patent WO0200860.
ACCESSION AX360164
VERSION AX360164.1 GI:18675731
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Plowman, G., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and Charydzak, G.
TITLE Novel proteases
JOURNAL Patent: WO 0200860-A 120 03-JAN-2002;
Sugen, Inc. (US)
FEATURES Location/Qualifiers
source 1..22

Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoieseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
FEATURES Location/Qualifiers
source 1

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AR036870/c
LOCUS          AR036870              20 bp      DNA          linear      PAT 29-SEP-1999
DEFINITION     Sequence 1 from patent US 5800990.
ACCESSION      AR036870
VERSION        AR036870.1  GI:5954726
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Raynolds,M.V. and Perryman,M.Benjamin.
TITLE         Angiotensin-converting enzyme genetic variant screens
JOURNAL       Patent: US 5800990-A 1 01-SEP-1998;
FEATURES       Location/Qualifiers
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                0.5%; Score 18.4; DB 1; Length 20;
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GCAGCAACAGCAGCAGCAGC 1421
Db 20 GCAGCAACAGCAGCAGCAGC 1

RESULT 48
BD244919/c
LOCUS          BD244919              20 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION     Modulation of gene expression by combination therapy.
ACCESSION      BD244919
VERSION        BD244919.1  GI:33054689
KEYWORDS       JP 2002528391-A/47.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE         Modulation of gene expression by combination therapy
JOURNAL       Patent: JP 2002528391-A 47 03-SEP-2002;
COMMENT        METHYLENE INC
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                PN JP 2002528391-A/47
                PD 03-SEP-2002
                PF 19-OCT-1999 JP 2000576885
                PR 19-OCT-1998 US 60/104804
                PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
                A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
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Query Match   Best Local Similarity 95.0%; Score 18.4; DB 1; Length 20;
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Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 49
AR053082/c
LOCUS          AR053082              20 bp      DNA          linear      PAT 12-JAN-2001
DEFINITION     Sequence 6 from Patent WO0071703.
ACCESSION      AR053082
VERSION        AR053082.1  GI:12227139
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 6 30-NOV-2000;
FEATURES       Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="synthetic oligonucleotide"

Query Match   Best Local Similarity 95.0%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 50
AR053091/c
LOCUS          AR053091              20 bp      DNA          linear      PAT 12-JAN-2001
DEFINITION     Sequence 15 from Patent WO0071703.
ACCESSION      AR053091
VERSION        AR053091.1  GI:12227148
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 15 30-NOV-2000;
FEATURES       Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Combined DNA/RNA Molecule: Positions
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                nucleotides; positions 5-16 are deoxyribonucleotides"

Query Match   Best Local Similarity 95.0%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 51
AR317754/c
LOCUS          AR317754              20 bp      DNA          linear      PAT 14-DEC-2001
DEFINITION     Sequence 15 from Patent WO0190313.
ACCESSION      AR317754
VERSION        AR317754.1  GI:17900639
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens

```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE        Methods for assaying gene imprinting and methylated cpg islands
JOURNAL      Patent: WO 0190313-A 15 29-NOV-2001;
              The Johns Hopkins University (US)
FEATURES     Location/Qualifiers
              source
                1..20
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1430 CAGCAGCAGCAGCAGCA 1449
Db 20 CAGTACGACACAGCAGCA 1

RESULT 52
AX546302/c
LOCUS          AX546302
DEFINITION     Sequence 51 from Patent EP1243290.
ACCESSION     AX546302
VERSION       AX546302.1 GI:25811493
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS      Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE        Modulation of gene expression by combination therapy
JOURNAL      Patent: EP 1243290-A 51 25-SEP-2002;
              Methylgene, Inc. (CA)
FEATURES     Location/Qualifiers
              source
                1..20
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="oligonucleotide"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCA 1

RESULT 53
AX546392/c
LOCUS          AX546392
DEFINITION     Sequence 51 from Patent EP1243289.
ACCESSION     AX546392
VERSION       AX546392.1 GI:25811583
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS      Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE        Modulation of gene expression by combination therapy
JOURNAL      Patent: EP 1243289-A 51 25-SEP-2002;
              Methylgene, Inc. (CA)
FEATURES     Location/Qualifiers
              source
                1..20
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
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/note="oligonucleotide"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCA 1

RESULT 54
AR084546
LOCUS          AR084546
DEFINITION     Sequence 35 from patent US 5981185.
ACCESSION     AR084546
VERSION       AR084546.1 GI:10011317
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE        Oligonucleotide repeat arrays
JOURNAL      Patent: US 5981185-A 35 09-NOV-1999;
              Location/Qualifiers
              source
                1..21
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 2 CAACAACAACAACAACA 21

RESULT 55
AR084558
LOCUS          AR084558
DEFINITION     Sequence 47 from patent US 5981185.
ACCESSION     AR084558
VERSION       AR084558.1 GI:10011329
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE        Oligonucleotide repeat arrays
JOURNAL      Patent: US 5981185-A 47 09-NOV-1999;
              Location/Qualifiers
              source
                1..21
                  /organism="unknown"
                  /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAACAACA 1593
Db 1 CAACAACAACAACAACA 20

RESULT 56
AR084600/c
LOCUS          AR084600
DEFINITION     Sequence 89 from patent US 5981185.
ACCESSION     AR084600
VERSION       AR084600.1 GI:10011371
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 20 CAACAACAACAGCAACA 1

RESULT 57
AR084603/c
LOCUS AR084603 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 92 from patent US 5981185.
ACCESSION AR084603
VERSION AR084603.1 GI:10011374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 21 CAACAACAACAGCAACA 2

RESULT 58
AR084528/c
LOCUS AR084528 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 17 from patent US 5981185.
ACCESSION AR084528
VERSION AR084528.1 GI:10011299
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 17 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 59
BD274822/c
LOCUS BD274822 18 bp DNA linear PAT 17-JUL-2003
DEFINITION CANCER CELL VACCINE.
ACCESSION BD274822
VERSION BD274822.1 GI:33084590
KEYWORDS JP 2002531582-A/47.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kusu,M., Qiu,G. and Hunfreese,R.
TITLE CANCER CELL VACCINE
JOURNAL Patent: JP 2002531582-A 47 24-SEP-2002;
COMMENT ANTIGEN EXPRESS INC
OS Artificial Sequence
PN JP 2002531582-A/47
PD 24-SEP-2002 JP 2000586901
PF 24-NOV-1999 JP 2000586901
PR 04-DEC-1998 US 09/205995
PI minzhen kusu,gang qiu,robert hunfreese
CC Description of Artificial Sequence: antisense oligonucleotide
CC corresponding
CC to a specific region of the mouse Ii gene.
FH Key Location/Qualifiers
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 60
AR205288/c
LOCUS AR205288 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 48 from patent US 6368855.
ACCESSION AR205288
VERSION AR205288.1 GI:21502833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Xu,M., Qiu,G. and Humphreys,R.
TITLE MHC class II antigen presenting cells containing oligonucleotides which inhibit Ii protein expression
JOURNAL Patent: US 6368855-A 48 09-APR-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 61
AX598368
LOCUS AX598368 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 642 from Patent WO0244994.
ACCESSION AX598368
VERSION AX598368.1 GI:28398544
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Brower, A., Brow, M.A., Cracauer, R.P., Fors, L., Granske, R., de arruda
Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A., Lyamichev, V.,
Neri, B.P., Reiner, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
Comerford, J., Stump, S. and Vilegut, D.D.
TITLE Systems and method for detection assay production and sale
JOURNAL Patent: WO 0244994-A 642 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1411 GCAGCAGCAGCAGCAGCA 1428
Db 1 GCAGCAGCAGCAGCAGCA 18
RESULT 62
AR271209/c
LOCUS AR271209 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 152 from patent US 6503152.
ACCESSION AR271209
VERSION AR271209.1 GI:29702512
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Pelz, D.T.
TITLE Putting trainer
JOURNAL Patent: US 6503152-A 152 07-JAN-2003;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1602 AGCAGCAGCAGCAACCAT 1619
Db 20 AGCAGCAGCAGCAACCAT 3
RESULT 63
AR084525
LOCUS AR084525 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 14 from patent US 5981185.
ACCESSION AR084525
VERSION AR084525.1 GI:10011296
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Miller, W.L., Lin, D. and Strauss, J.F. III.
TITLE Identification of gene mutations associated with congenital lipoid
adrenal hyperplasia
JOURNAL Patent: US 5981185-A 14 09-NOV-1999;
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1572 AGCAACAACAACAGCAAC 1592
Db 21 AACACAACAACAACAAC 1
RESULT 65
AR038671
LOCUS AR038671 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5807678.
ACCESSION AR038671
VERSION AR038671.1 GI:5958034
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Miller, W.L., Lin, D. and Strauss, J.F. III.
TITLE Identification of gene mutations associated with congenital lipoid
adrenal hyperplasia
JOURNAL Patent: US 5807678-A 5 15-SEP-1998;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCAGCAGCAGCAGCAGCAG 19

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RESULT 66
AR428075
LOCUS AR428075 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6641818.
ACCESSION AR428075
VERSION AR428075.1 GI:40187443
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Unclassified.
AUTHORS Spear, P.G., Warner, M.S., Geraghty, R.J., Martinez, W.M.,
Montgomery, R.I., Cohen, G.H., Eisenberg, R.J., Whitbeck, C.J. and
Krummenacher, C.
TITLE Cellular proteins which mediate herpesvirus entry
JOURNAL Patent: US 6641818-A 5 04-NOV-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 973 GATGAGCGACGACCGAGCAG 991
|||
2 GAAGCAGCAGCAGCAGCAG 20

RESULT 67
AX053083/c
LOCUS AX053083 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 7 from Patent WO0071703.
ACCESSION AX053083
VERSION AX053083.1 GI:12227140
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Macleod, A.R., Li, Z. and Besterman, J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 7 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
|||
20 GCAGCAGCAGCAGCAGCAG 2

RESULT 68
AX053092/c
LOCUS AX053092 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 16 from Patent WO0071703.
ACCESSION AX053092
VERSION AX053092.1 GI:12227149
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 52 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
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AUTHORS Macleod, A.R., Li, Z. and Besterman, J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 16 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions
1-4 and 17-20 are 2'-methoxyribose substituted
nucleotides; positions 5-16 are deoxyribonucleotides"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
|||
20 GCAGCAGCAGCAGCAGCAG 2

RESULT 69
AX149057/c
LOCUS AX149057 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 259 from Patent WO0136625.
ACCESSION AX149057
VERSION AX149057.1 GI:14347581
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 259 25-MAY-2001;
GenSense Technologies Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1456 GCAACAGCAACAGCAACAG 1474
|||
19 GAAACAGCAACAGCAACAG 1

RESULT 70
AX546303/c
LOCUS AX546303 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 52 from Patent EP1243290.
ACCESSION AX546303
VERSION AX546303.1 GI:25811494
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 52 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 71
AX546393/c
LOCUS
DEFINITION Sequence 52 from Patent EP1243289.
ACCESSION AX546393
VERSION AX546393.1 GI:25811584
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 52 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
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        1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 72
BD266062
LOCUS
DEFINITION Universal arrays.
ACCESSION BD266062
VERSION BD266062.1 GI:33075830
KEYWORDS JP 2002539849-A/62.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S.,
TITLE Universal arrays
JOURNAL Lockhart, D.J., Ryder, T. and Sklar, P.
COMMENT Patent: JP 2002539849-A 62 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Homo sapiens (human)
PN JP 2002539849-A/62
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PC DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C1201/68, C12M1/00, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Universal arrays

/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 71
AX546393/c
LOCUS
DEFINITION Sequence 52 from Patent EP1243289.
ACCESSION AX546393
VERSION AX546393.1 GI:25811584
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 52 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
    source
        1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 72
BD266062
LOCUS
DEFINITION Universal arrays.
ACCESSION BD266062
VERSION BD266062.1 GI:33075830
KEYWORDS JP 2002539849-A/62.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S.,
TITLE Universal arrays
JOURNAL Lockhart, D.J., Ryder, T. and Sklar, P.
COMMENT Patent: JP 2002539849-A 62 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Homo sapiens (human)
PN JP 2002539849-A/62
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PC DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C1201/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Universal arrays

/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AGCAACAGCAGCAGCAGCAGC 1424
    |||||
Db 1 AGCAACAGCAGCAGCAGCAGC 21

RESULT 73
CQ821171/c
LOCUS
DEFINITION Sequence 1 from Patent WO2004046377.
ACCESSION CQ821171
VERSION CQ821171.1 GI:48715855
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Casari, G., de Fusco, M. and Marconi, R.
TITLE Diagnostic and therapeutic means for pathologies associated with
JOURNAL alpha 2 subunit of the na, k pump
JOURNAL Patent: WO 2004046377-A 1 03-JUN-2004;
FONDAZIONE CENTRO SAN ROMANELLO DEL MONTE TABOR (IT)
FEATURES
    source
        1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2296 ACAGAGAAACCCCAAGCAA 2314
    |||||
Db 21 ACAGAGAAACCCCAAGCAA 3

RESULT 74
AX146085
LOCUS
DEFINITION Sequence 276 from Patent WO0134840.
ACCESSION AX146085
VERSION AX146085.1 GI:14284603
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Au, K.G., Chen, J.G., Patil, N. and Thomas, D.
TITLE Genetic compositions and methods
JOURNAL Patent: WO 0134840-A 276 17-MAY-2001;
GLAXO GROUP LIMITED (GB); Affymetrix, Inc. (US)
FEATURES
    source
        1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

variation
    /note="n' represents a polymorphic base"

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Query Match	0.5%; Score 17.4; DB 1; Length 21;	
Best Local Similarity	90.0%; Pred. No. 1.1e+02;	
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1440 AACAGCAGCGACGACGCAAA 1459 2 AACAGCAGCGACGACGCA 21 	
Db		
RESULT 75		PAT 02-APR-2003
AX697037/c		
LOCUS	AX697037 21 bp DNA linear	
DEFINITION	Sequence 105 from Patent WO0078961.	
ACCESSION	AX697037	
VERSION	AX697037.1 GI:29498021	
KEYWORDS	. synthetic construct	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1	
AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Deenoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 0078961-A 105 28-DEC-2000;	
Genentech Inc. (US)		
FEATURES	Location/Qualifiers	
source	1..21	
/organism="synthetic construct"		
/mol_type="unassigned DNA"		
/db_xref="taxon:32630"		
Query Match	0.5%; Score 17.4; DB 1; Length 21;	
Best Local Similarity	94.7%; Pred. No. 1.1e+02;	
Matches	18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1400 CAGCAGCACGACGACGC 1418 20 CAGCAGCACGACGACGC 2 	
Db		
RESULT 76		PAT 23-JUN-2003
AX753820		
LOCUS	AX753820 17 bp DNA linear	
DEFINITION	Sequence 167 from Patent WO03037931.	
ACCESSION	AX753820	
VERSION	AX753820.1 GI:32166517	
KEYWORDS	. Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	
AUTHORS	Shannon,M. and Phan,T.	
TITLE	Human angiomotin-like protein 1	
JOURNAL	Patent: WO 03037931-A 167 08-MAY-2003;	
Amersham Biosciences SV Corp. (US)		
FEATURES	Location/Qualifiers	
source	1..17	
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/mol_type="unassigned DNA"		
/db_xref="taxon:9606"		
Query Match	0.5%; Score 17; DB 1; Length 17;	
Best Local Similarity	100.0%; Pred. No. 80;	
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1431 AGCAGCAGCAACAGCAGC 1447 1 AGCAGCAGCAACAGCAGC 17 	
Db		
RESULT 79		PAT 23-JUN-2003
AX753823		
LOCUS	AX753823 17 bp DNA linear	
DEFINITION	Sequence 170 from Patent WO03037931.	
ACCESSION	AX753823	
VERSION	AX753823.1 GI:32166520	
KEYWORDS	. Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		

Query Match	0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity	90.0%; Pred. No. 1.1e+02;
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1440 AACAGCAGCGACGACGACAA 1459 2 AACAGCAGCGACGACGACCA 21
Db	
RESULT 75	
AX697037/c	AX697037 21 bp DNA linear PAT 02-APR-2003
LOCUS	Sequence 105 from Patent WO0078961.
DEFINITION	AX697037 AX697037.1 GI:29498021
ACCESSION	VERSION
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Deenoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0078961-A 105 28-DEC-2000; Genentech Inc. (US)
FEATURES	Location/Qualifiers
source	1..21 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"
Query Match	0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity	94.7%; Pred. No. 1.1e+02;
Matches	18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1400 CAGCAGCACGACGACGC 1418 20 CAGCAGCACGACGACGC 2
Db	
RESULT 76	
AX753820	AX753820 17 bp DNA linear PAT 23-JUN-2003
LOCUS	Sequence 167 from Patent WO03037931.
DEFINITION	AX753820
ACCESSION	VERSION
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Shannon,M. and Phan,T.
TITLE	Human angiomotin-like protein 1
JOURNAL	Patent: WO 03037931-A 167 08-MAY-2003; Amersham Biosciences SV Corp. (US)
FEATURES	Location/Qualifiers
source	1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.5%; Score 17; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 80;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1431 AGCAGCAGCAACAGCAGC 1447 1 AGCAGCAGCAACAGCAGC 17
Db	
RESULT 79	
AX753823	AX753823 17 bp DNA linear PAT 23-JUN-2003
LOCUS	Sequence 170 from Patent WO03037931.
DEFINITION	AX753823
ACCESSION	VERSION
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Shannon,M. and Phan,T.
TITLE	Human angiomotin-like protein 1
JOURNAL	Patent: WO 03037931-A 169 08-MAY-2003; Amersham Biosciences SV Corp. (US)
FEATURES	Location/Qualifiers
source	1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.5%; Score 17; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 80;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1429 GCAGCAGCAACAGCAGC 1445 1 GCAGCAGCAACAGCAGC 17
Db	

Query Match	0.5%; Score 17.4; DB 1; Length 21;	
Best Local Similarity	90.0%; Pred. No. 1.1e+02;	
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1440 AACAGCAGCGACGACGCAAA 1459 2 AACAGCAGCGACGACGCA 21 	
Db		
RESULT 75		PAT 02-APR-2003
AX697037/c		
LOCUS	AX697037 21 bp DNA linear	
DEFINITION	Sequence 105 from Patent WO0078961.	
ACCESSION	AX697037	
VERSION	AX697037.1 GI:29498021	
KEYWORDS	. synthetic construct	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1	
AUTHORS	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Deenoyers,L., Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 0078961-A 105 28-DEC-2000;	
Genentech Inc. (US)		
FEATURES	Location/Qualifiers	
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/db_xref="taxon:32630"		
Query Match	0.5%; Score 17.4; DB 1; Length 21;	
Best Local Similarity	94.7%; Pred. No. 1.1e+02;	
Matches	18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1400 CAGCAGCACGACGACGC 1418 20 CAGCAGCACGACGACGC 2 	
Db		
RESULT 76		PAT 23-JUN-2003
AX753820		
LOCUS	AX753820 17 bp DNA linear	
DEFINITION	Sequence 167 from Patent WO03037931.	
ACCESSION	AX753820	
VERSION	AX753820.1 GI:32166517	
KEYWORDS	. Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	
AUTHORS	Shannon,M. and Phan,T.	
TITLE	Human angiomotin-like protein 1	
JOURNAL	Patent: WO 03037931-A 167 08-MAY-2003;	
Amersham Biosciences SV Corp. (US)		
FEATURES	Location/Qualifiers	
source	1..17	
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/mol_type="unassigned DNA"		
/db_xref="taxon:9606"		
Query Match	0.5%; Score 17; DB 1; Length 17;	
Best Local Similarity	100.0%; Pred. No. 80;	
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1431 AGCAGCAGCAACAGCAGC 1447 1 AGCAGCAGCAACAGCAGC 17 	
Db		
RESULT 79		PAT 23-JUN-2003
AX753823		
LOCUS	AX753823 17 bp DNA linear	
DEFINITION	Sequence 170 from Patent WO03037931.	
ACCESSION	AX753823	
VERSION	AX753823.1 GI:32166520	
KEYWORDS	. Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 GCAGCAGCAACAGCAGC 1448
Db 1 GCAGCAGCAACAGCAGC 17

RESULT 80
AX753824
LOCUS AX753824 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 171 from Patent WO03037931.
ACCESSION AX753824
VERSION AX753824.1 GI:32166521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 171 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCA 1416
Db 1 CAGCAGCAACAGCAGCA 17

RESULT 81
AX753825
LOCUS AX753825 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 172 from Patent WO03037931.
ACCESSION AX753825
VERSION AX753825.1 GI:32166522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 172 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1401 AGCAGCAACAGCAGCAG 1417
Db 1 AGCAGCAACAGCAGCAG 17

RESULT 82
AR083088
LOCUS AR083088 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 2 from patent US 5976803.
ACCESSION AR083088
VERSION AR083088.1 GI:10009878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meek,K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 2 02-NOV-1999;
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GGGAGAATCTCTCTGCA 271
Db 1 GGGAGAATCTCTCTGCA 17

RESULT 83
AR139665/c
LOCUS AR139665/c 21 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 3 from patent US 6207390.
ACCESSION AR139665
VERSION AR139665.1 GI:14482161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cantor,C.R. and Sano,T.
TITLE Methods for the use of reduced affinity streptavidin
JOURNAL Patent: US 6207390-A 3 27-MAR-2001;
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

RESULT 84
AR159548
LOCUS AR159548 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6251589.
ACCESSION AR159548
VERSION AR159548.1 GI:16222233
KEYWORDS
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuchi, S. and Sanpei, K.
TITLE Method for diagnosing spinocerebellar ataxia type 2 and primers therefor
JOURNAL Patent: US 6251589-A 8 26-JUN-2001;
FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1448 CAGCAGCAGCAACAGCAACA 1467
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Db 1 CACCACGACAGCAACA 20
RESULT 85
LOCUS BD177753 20 bp DNA linear PAT 16-APR-2003
DEFINITION A method for snp typing.
ACCESSION BD177753
VERSION BD177753.1 GI:30015016
KEYWORDS JP 2002300894-A/43.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakamura, Y., Tanaka, T., Onishi, Y., Ozaki, K. and Yamada, A.
TITLE A method for snp typing
JOURNAL Patent: JP 2002300894-A 43 15-OCT-2002;
COMMENT THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
OS Artificial Sequence
PN JP 2002300894-A/43
PD 15-OCT-2002
PF 29-JAN-2002 JP 2002019752
PI YUSUKE NAKAMURA, TOSHIHIRO TANAKA, YOZO ONISHI, KOICHI OZAKI, PI AKIRA YAMADA
PC C12N15/09, C12Q1/68, C12N15/00
FH Description of Artificial Sequence: Primer
CC Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1601 CAGCAGCAGCAACCAACATC 1620
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Db 1 CAGCAGCAACCAACCGTC 20
RESULT 86
LOCUS CQ830190/c 20 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 45 from Patent WO2004055049.
ACCESSION CQ830190
VERSION CQ830190.1 GI:50250683
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Morgan, R.G., Pettengell, R., Forraz, N.P. and Mcguckin, C.P.
TITLE Peptides impairing Pbx dependent gene regulation
JOURNAL Patent: WO 2004055049-A 45 01-JUL-2004;
ST. GEORGE'S ENTERPRISES LIMITED (GB)
FEATURES Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 67 CAATCAGAGCAGCGGAGG 86
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Db 20 CAATCAGAGGAGACGGAGG 1
RESULT 87
LOCUS A91543 21 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 70 from Patent WO9824928.
ACCESSION A91543
VERSION A91543.1 GI:6740498
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Pallisgaard, N. and Hokland, P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 70 11-JUN-1998;
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES Location/Qualifiers
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 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 815 TCTGCCCTCTCCACTTCGTC 834
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Db 2 TCTGCCCTCTCCACTTTGTC 21
RESULT 88
LOCUS AX458851 21 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 91 from Patent WO0209295.
ACCESSION AX458851
VERSION AX458851.1 GI:21725463
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Shockey, J.M., Schnurr, J. and Browne, J.A.
TITLE Plant acyl-coa synthetases
JOURNAL Patent: WO 0209295-A 91 31-JAN-2002;
Shockey, Judy M. (US); Schnurr, Judy (US); Browne, John A. (US)
FEATURES Location/Qualifiers
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 /db_xref="taxon:32630"
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Query Match 0.4%; Score 16.8; DB 1; Length 21;

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Best Local Similarity 90.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2;

QY 2902 CAGGGCTTTTCAAGGAAGT 2921
Db 2 CAGGGCTTCTCAGGAATG 21

RESULT 89
BD023325 21 bp DNA linear PAT 27-AUG-2002
LOCUS Method for detecting abnormality in chromosome.
DEFINITION BD023325
ACCESSION BD023325.1 GI:22564548
VERSION JP 2001505428-A/70.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
REFERENCE 1 (bases 1 to 21)
AUTHORS Partsgard,N. and Hukurando,P.
TITLE Method for detecting abnormality in chromosome
JOURNAL Patent: JP 2001505428-A 70 24-APR-2001;
COMMENT NEILLS PARIGARD
PN JP 2001505428-A/70
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLS PARIGARD,PATER HOKURANDO
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)';
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 815 TCTGCCCTTCCACTTGTC 834
Db 2 TCTGCCCTTCCACTTGTC 21

RESULT 90
AR084526 18 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 15 from patent US 5981185.
DEFINITION AR084526
ACCESSION AR084526
VERSION AR084526.1 GI:10011297
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 15 09-NOV-1999;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ACAACACACACACACA 1593
Db 1576 ACAACACACACACACA 1593

RESULT 93
BD266206 18 bp DNA linear PAT 17-JUL-2003
LOCUS Universal arrays.
DEFINITION BD266206
ACCESSION BD266206.1 GI:33075974
VERSION JP 2002539849-A/206.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE Universal arrays
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JOURNAL Patent: JP 2002539849-A 206 26-NOV-2002;
COMMENT WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Artificial Sequence
PN JP 2002539849-A/206
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
JIAN BING PAN, JOEL N HIRSCHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PC DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Primer
FH Key Location/Qualifiers
FT source 1.18
FT Location/Qualifiers
FT source 1.18
FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1395 AGCAACAGCAGCAGCAGC 1412
Db 1 AGCAACAGCAGCAGCAGC 18

RESULT 94
BD230280 20 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Total genome radiation hybrid map of canine genome and its use for
IDENTIFICATION identification of interesting genes.
ACCESSION BD230280
VERSION BD230280.1 GI:33040050
KEYWORDS JP 2002530091-A/149.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE 1 (bases 1 to 20)
JOURNAL Galibert, F. and Andre, C.
COMMENT Total genome radiation hybrid map of canine genome and its use for
IDENTIFICATION identification of interesting genes
OS Canis familiaris (dog)
PN JP 2002530091-A/149
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
CC A0102
FH Key Location/Qualifiers
FT source 1.20
FT /organism="Canis familiaris (dog)".
FT Location/Qualifiers
FT source 1.20
FT /organism="Canis familiaris"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:9615"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Db 1 CAGCAGCAGCAGCAGCAG 18

RESULT 95
AR366677 20 bp DNA linear PAT 12-SEP-2003
LOCUS
DEFINITION Sequence 39 from patent US 6329203.
ACCESSION AR366677
VERSION AR366677.1 GI:34599269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Wyatt, J.
TITLE Antisense modulation of glioma-associated oncogene-1 expression
JOURNAL Patent: US 6329203-A 39 11-DEC-2001;
FEATURES Location/Qualifiers
source 1.20
source /organism="unknown"
source /mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 976 GCAGCAGCAGCAGCAGCA 993
Db 19 GCAGCAGCTCCAGCAGCA 2

RESULT 96
AX149138 20 bp DNA linear PAT 08-JUN-2001
LOCUS
DEFINITION Sequence 340 from Patent WO0136625.
ACCESSION AX149138
VERSION AX149138.1 GI:14347662
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and gross as
JOURNAL inhibitors of microorganisms
COMMENT Patent: WO 0136625-A 340 25-MAY-2001;
GENESENSE Technologies Inc. (CA)
FEATURES Location/Qualifiers
source 1.20
source /organism="synthetic construct"
source /mol_type="unassigned DNA"
source /db_xref="taxon:32630"
source /note="Antisense oligonucleotide"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1466 CAGCAACAGCAGCAGCAG 1483
Db 20 CAGCAACAGCAGCAGCAGCTG 3

RESULT 97
AX764064 20 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION Sequence 9 from Patent WO03040304.
ACCESSION AX764064
VERSION AX764064.1 GI:32258388
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Holmberg, J. and Frisen, J.
TITLE Method of proliferation in neurogenic regions
JOURNAL Patent: WO 03040304-A 9 15-MAY-2003;
Neuronova AB (SE)
FEATURES
source
1. .20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PCR Primer"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGC 1424
|||||
DB 19 AACAGCAGGAGCAGCAGC 2

RESULT 98
AX764066/c
LOCUS 20 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 11 from Patent WO03040304.
ACCESSION AX764066
VERSION AX764066.1 GI:32258390
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE
AUTHORS Holmberg, J. and Frisen, J.
TITLE Method of proliferation in neurogenic regions
JOURNAL Patent: WO 03040304-A 11 15-MAY-2003;
Neuronova AB (SE)
FEATURES
source
1. .20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PCR Primer"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGC 1424
|||||
DB 19 AACAGCAGGAGCAGCAGC 2

RESULT 99
AX273039
LOCUS 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 608 from Patent WO0162911.
ACCESSION AX273039
VERSION AX273039.1 GI:16545776
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 608 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
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/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 975 TGCAGCAGCAGCAGCA 990
|||||
DB 2 TGCAGCAGCAGCAGCA 17

RESULT 100
AX753819
LOCUS 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 166 from Patent WO03037931.
ACCESSION AX753819
VERSION AX753819.1 GI:32166516
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiomin-like protein 1
JOURNAL Patent: WO 03037931-A 166 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAG 1444
|||||
DB 2 GCAGCAGCAGCAACAG 17

RESULT 101
AX753826
LOCUS 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 173 from Patent WO03037931.
ACCESSION AX753826
VERSION AX753826.1 GI:32166523
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiomin-like protein 1
JOURNAL Patent: WO 03037931-A 173 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1402 GCAGCAACAGCAGCAG 1417
|||||
DB 1 GCAGCAACAGCAGCAG 16
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Query Match	Score	Pred. No.	Indels	Gaps
Best Local Similarity	0.48;	1.2e+02;	0;	0;
Conservative matches	15;		1;	

[illegible]

Query Match		0.4%; Score 15.4; DB 1; Length 17;	
Best Local Similarity		94.1%; Pred. No. 1.2e+02;	
Matches		16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	978 AGCAGCACCAGCAGC 994		
Db	1 AGCAGCACCAGCAGC 17		
/mol_type="unassigned RNA"			
/db_xref="taxon:9606"			
RESULT 112			
AX272794			
LOCUS		17 bp	RNA
DEFINITION		Sequence 363 from Patent WO0162911.	PAT 29-OCT-2001
ACCESSION		AX272794	
VERSION		AX272794.1	GI:16545531
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.	
AUTHORS		Method and reagent for the inhibition of grid	
TITLE		Patent: WO 0162911-A 363 30-AUG-2001;	
JOURNAL		RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)	
FEATURES		Location/Qualifiers	
source		1..17	
		/organism="Homo sapiens"	
		/mol_type="unassigned RNA"	
		/db_xref="taxon:9606"	
Query Match			
Best Local Similarity		0.4%; Score 15.4; DB 1; Length 17;	
Matches		16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	979 GCAGCACCAGCAGCAGC 995		
Db	1 GCAGCACCAGCAGCAGC 17		
RESULT 113			
AX273040			
LOCUS		17 bp	RNA
DEFINITION		Sequence 609 from Patent WO0162911.	PAT 29-OCT-2001
ACCESSION		AX273040	
VERSION		AX273040.1	GI:16545777
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.	
AUTHORS		Method and reagent for the inhibition of grid	
TITLE		Patent: WO 0162911-A 609 30-AUG-2001;	
JOURNAL		RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)	
FEATURES		Location/Qualifiers	
source		1..17	
		/organism="Homo sapiens"	
		/mol_type="unassigned RNA"	
		/db_xref="taxon:9606"	
Query Match			
Best Local Similarity		0.4%; Score 15.4; DB 1; Length 17;	
Matches		16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	986 CAGCAGCACCAGCAGC 1002		
Db	1 CAGCAGCACCAGCAGC 17		
RESULT 114			
AX272713/c			
LOCUS		17 bp	DNA
DEFINITION		Sequence 4900 from Patent WO03025176.	PAT 08-MAY-2003
ACCESSION		AX272713	
VERSION		AX272713.1	GI:30506556
KEYWORDS		Mus musculus (house mouse)	
SOURCE		Mus musculus	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE		Telerman,A., Anson,R. and Tuijnder,M.	
AUTHORS		Sequences involved in phenomena of tumour suppression, tumour	
TITLE		reversion, apoptosis and/or virus resistance and their use as	
JOURNAL		medicines	
FEATURES		Patent: WO 03025176-A 4900 27-MAR-2003;	
source		Molecular Engines Laboratories (FR)	
		Location/Qualifiers	
		1..17	
		/organism="Mus musculus"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:10090"	
Query Match			
Best Local Similarity		0.4%; Score 15.4; DB 1; Length 17;	
Matches		16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	705 TGCAGAAATAGTGATC 721		
Db	17 TAGAGAAATAGTGATC 1		
RESULT 115			
AX732594			
LOCUS		17 bp	DNA
DEFINITION		Sequence 4228 from Patent WO03025175.	PAT 08-MAY-2003
ACCESSION		AX732594	
VERSION		AX732594.1	GI:30511937
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		Telerman,A., Anson,R. and Tuijnder,M.	
AUTHORS		Sequences involved in phenomena of tumour suppression, tumour	
TITLE		reversion, apoptosis and/or virus resistance and their use as	
JOURNAL		medicines	
FEATURES		Patent: WO 03025175-A 4228 27-MAR-2003;	
source		Molecular Engines Laboratories (FR)	
		Location/Qualifiers	
		1..17	
		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:9606"	
Query Match			
Best Local Similarity		0.4%; Score 15.4; DB 1; Length 17;	
Matches		16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1909 GATCATGAGCAGAAAC 1925		
Db	1 GATCATGTAGCAGAAAC 17		
RESULT 116			
AX753827			
LOCUS		17 bp	DNA
DEFINITION		Sequence 174 from Patent WO03037931.	PAT 23-JUN-2003

ACCESSION AX753827
VERSION AX753827.1 GI:32166524
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 174 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1505 CAGCAACAGCAGCAGAG 1521
Db 1 CAGCAACAGCAGCAGGG 17

RESULT 117
AX757672/c
LOCUS 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 993 from Patent WO03040369.
ACCESSION AX757672
VERSION AX757672.1 GI:32252288
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Telerman,A., Anson,R. and Tuijnder,M.
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
Molecular Engines Laboratories (FR)
JOURNAL Patent: WO 03040369-A 993 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1222 GCAAAAGCCTCAGGATC 1238
Db 17 GCCAAAGCCTCAGGATC 1

RESULT 118
AX761771
LOCUS 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5092 from Patent WO03040369.
ACCESSION AX761771
VERSION AX761771.1 GI:32256387
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Telerman,A., Anson,R. and Tuijnder,M.

ACCESSION AX753827
VERSION AX753827.1 GI:32166524
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Shannon,M. and Phan,T.
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
Molecular Engines Laboratories (FR)
JOURNAL Patent: WO 03040369-A 5092 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1909 GATCATGGAGCAGAAAC 1925
Db 1 GATCATGTAGCAGAAAC 17

RESULT 119
BD067335
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067335
VERSION BD067335.1 GI:22612938
KEYWORDS JP 2001511003-A/175.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 175 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/175
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1. .17
/organism="Unidentified".
/organism="Unidentified".
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3633 GAGAACCTAGAAACAT 3649
Db 1 GAGAACCTAGAAATCAT 17

RESULT 120
AR028606/c
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5858728.
ACCESSION AR028606
VERSION AR028606.1 GI:5940579

FEATURES

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source      1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 AACAAACAACAGCAACAA 1591
Db 19 AACAAACAACAGCAACAA 3

RESULT 125
LOCUS AX129105 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 323 from Patent WO0130362.
ACCESSION AX129105
VERSION AX129105.1 GI:14135410
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 323 03-MAY-2001; IMMUSOL, INC. (US)
FEATURES
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk3 ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2942 TTGTGACTTCCTCAGCCA 2958
Db 3 TTGTGACTTCCTCAGCCA 19

RESULT 126
LOCUS AX129106 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 324 from Patent WO0130362.
ACCESSION AX129106
VERSION AX129106.1 GI:14135411
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 324 03-MAY-2001; IMMUSOL, INC. (US)
FEATURES
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk3 ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;

source      1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GGTTCCTTCAAAAGA 163
Db 17 GGTTCCTTCAAAAGA 3

RESULT 128
LOCUS AX753818 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 165 from Patent WO03037931.
ACCESSION AX753818
VERSION AX753818.1 GI:32166515
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 165 08-MAY-2003; Amersham Biosciences SV Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACA 1443
Db 3 GCAGCAGCAGCAACA 17

RESULT 129
AR078304/c

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2942 TTGTGACTTCCTCAGCCA 2958
Db 2 TTGTGACTTCCTCAGCCA 18

RESULT 127
LOCUS AX737070/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2660 from Patent WO03025177.
ACCESSION AX737070
VERSION AX737070.1 GI:30516358
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 2660 27-MAR-2003; Molecular Engines Laboratories (FR)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GGTTCCTTCAAAAGA 163
Db 17 GGTTCCTTCAAAAGA 3

RESULT 128
LOCUS AX753818 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 165 from Patent WO03037931.
ACCESSION AX753818
VERSION AX753818.1 GI:32166515
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 165 08-MAY-2003; Amersham Biosciences SV Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACA 1443
Db 3 GCAGCAGCAGCAACA 17

RESULT 129
AR078304/c

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Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 CAACAGCAGCAGCAGCAG 1423
 DB 1 CACGAGCGGAGCAGCAG 18

RESULT 132
 AR096354 18 bp DNA linear PAT 08-SEP-2000
 LOCUS
 DEFINITION Sequence 25 from patent US 6007995.
 ACCESSION AR096354
 VERSION AR096354.1 GI:10025089
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Baker,B.P. and Cowsert,L.M.
 TITLE Antisense inhibition of TNFR1 expression
 JOURNAL Patent: US 6007995-A 25 28-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 977 CAGCAGCACCAGCAGCAG 994
 DB 1 CAGGAGCCAGCGGCGAG 18

RESULT 133
 AR122214 18 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 60 from patent US 6165713.
 ACCESSION AR122214
 VERSION AR122214.1 GI:14106531
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Liskay,R.M., Bronner,C.Eric., Baker,S.M., Bollag,R.J. and Kolodner,R.D.
 TITLE Composition and methods relating to DNA mismatch repair genes
 JOURNAL Patent: US 6165713-A 60 26-DEC-2000;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAGCCTCAGGATCTC 1240
 DB 1 CAAAGCTTCAGAAATCTC 18

RESULT 134
 AR131188 18 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 60 from patent US 6191268.
 ACCESSION AR131188
 VERSION AR131188.1 GI:14119513
 KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Liskay,R.M., Bronner,C.Eric., Baker,S.M., Bollag,R.J. and
              Kolodner,R.D.
TITLE        Compositions and methods relating to DNA mismatch repair genes
JOURNAL      Patent: US 6191268-A 60 20-FEB-2001;
FEATURES     Location/Qualifiers
source       1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAGCCTCAGGATCTC 1240
Db 1 CAAAGCCTCAGGATCTC 18

RESULT 135
LOCUS      AR142758          18 bp      DNA          linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6204008.
ACCESSION  AR142758
VERSION     AR142758.1 GI:15104044
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Borneman,W.Scott., Goyal,A., Conder,M.J. and Vinci,V.A.
TITLE        Bioprocess for production of dipeptide based compounds
JOURNAL      Patent: US 6204008-A 3 20-MAR-2001;
FEATURES     Location/Qualifiers
source       1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCAGCAGC 1000
Db 1 CACCAGCCTCAGCAGCAGC 18

RESULT 136
LOCUS      BD217401          18 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION  BD217401
VERSION     BD217401.1 GI:33027171
KEYWORDS    JP 2002519015-A/24.
SOURCE      unidentified
ORGANISM     unidentified
              unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Baker,B.F. and Cowsewrt,L.M.
TITLE        Antisense modulation of TNFR1 expression
JOURNAL      Patent: JP 2002519015-A 24 02-JUL-2002;
FEATURES     Location/Qualifiers
source       1..18
              /organism="unidentified"
              /db_xref="taxon:32644"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCAGCAGC 994
Db 1 CAGGAGCAGCAGCAGCAGC 18

RESULT 137
LOCUS      BD217402          18 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION  BD217402
VERSION     BD217402.1 GI:33027172
KEYWORDS    JP 2002519015-A/25.
SOURCE      unidentified
ORGANISM     unidentified
              unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Baker,B.F. and Cowsewrt,L.M.
TITLE        Antisense modulation of TNFR1 expression
JOURNAL      Patent: JP 2002519015-A 25 02-JUL-2002;
COMMENT      ISIS PHARMACEUTICALS INC
              OS Unidentified
              PN JP 2002519015-A/25
              PD 02-JUL-2002
              PF 17-JUN-1999 JP 2000557265
              PR 26-JUN-1998 US 09/106038
              PI BRENDA F BAKER,LEX M COWSBERT
              PC
              Cl2N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P43/00, PC
              Cl2Q1/68,
              PC Cl2N15/00
              CC Strandedness: Single;
              CC Topology: Linear;
              CC Antisense modulation of TNFR1 expression
              FH Key Location/Qualifiers
              FT source 1..18
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              /organism="Unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1406 CAACAGCAGCAGCAGCAG 1423
Db 1 CACCAGCGCAGCAGCAG 18

RESULT 138
LOCUS      E39177/c          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION DNA encoding novel fused protein and process for producing useful
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RESULT 140

/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCACGACGACGACGACGA 1428
Db 18 GCACGACGACGACGACGA 1

RESULT 143
LOCUS AR301003 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 60 from patent US 6538108.
ACCESSION AR301003
VERSION AR301003.1 GI:31688693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Liskay,R.M., Bronner,C.E., Baker,S.M., Bolleg,R.J. and Kolodner,R.D.
TITLE Compositions and methods relating to DNA mismatch repair genes
JOURNAL Patent: US 6538108-A 60 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAGCCTCAGGATCTC 1240
Db 1 CAAAGCTTCAGGATCTC 18

RESULT 144
LOCUS AR324782 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2184 from patent US 6566127.
ACCESSION AR324782
VERSION AR324782.1 GI:33710590
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2184 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1094 ACATGAGCCGACGAGC 1111
Db 1 ACATGAGCCGACGAGC 18

RESULT 145
AX317750 18 bp DNA linear PAT 14-DEC-2001
LOCUS

Sequence 11 from Patent WO0190313.
ACCESSION AX317750
VERSION AX317750.1 GI:17900635
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE Methods for assaying gene imprinting and methylated cpG islands
JOURNAL Patent: WO 0190313-A 11 29-NOV-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1024 CTCCTCTGCTGCACCATC 1041
Db 1 CTCCTCTGCGGGCCATC 18

RESULT 146
AX796108 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 451 from Patent WO03052135.
ACCESSION AX796108
VERSION AX796108.1 GI:37516774
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Lilloglou,T., Lipscher,E., Maier,S. and Nimrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell proliferative disorder
JOURNAL Patent: WO 03052135-A 451 26-JUN-2003;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for CACNA1G"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3583 TATAGTTTGTGGAGT 3600
Db 1 TTTAGTTTGTAGAGT 18

RESULT 147
AS2143/c 17 bp DNA linear PAT 11-MAR-1997
LOCUS
DEFINITION Sequence 9 from Patent WO9619579.
ACCESSION AS2143
VERSION AS2143.1 GI:2304748
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hemmings,B.A. and Millward,T.A.

TITLE JOURNAL COMMENT FEATURES source	NUCLEAR PROTEIN SERINE/THREONINE KINASES									
	Patent: WO 9619579-A 9 27-JUN-1996;									
	CIBA GEIGY AG (CH)									
	Other publication AU 4388296 960710.									
	Db	16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 16-MAY-2001								
		Sequence 1659 from patent US 6132967.								
		AR115213								
		Accession AR115213								
		Version AR115213.1 GI:14095535								
		Keywords Location/Qualifiers								
		Source Unknown.								
		Organism Unknown.								
		Reference 1 (bases 1 to 17)								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
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		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
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		Source Unknown.								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
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		Source Unknown.								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
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		Version AR057455.1 GI:5983032								
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		Source Unknown.								
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		Source Unknown.								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Keywords Unknown.								
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		17 bp DNA linear PAT 29-SEP-1999								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Accession AR057455								
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		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
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		17 bp DNA linear PAT 29-SEP-1999								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	3209 AAATGGAAAGCAGAAA 3224								
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		17 bp DNA linear PAT 29-SEP-1999								
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		AR057455								
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		Version AR057455.1 GI:5983032								
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		Reference 1 (bases 1 to 17)								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Accession AR057455								
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		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	3209 AAATGGAAAGCAGAAA 3224								
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		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
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Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	3209 AAATGGAAAGCAGAAA 3224								
		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
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		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
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Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	3209 AAATGGAAAGCAGAAA 3224								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
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		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	3209 AAATGGAAAGCAGAAA 3224								
		16 AAAGGAAAGCAGAAA 1								
		17 bp DNA linear PAT 29-SEP-1999								
		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
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		Keywords Unknown.								
		Source Unknown.								
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Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	3209 AAATGGAAAGCAGAAA 3224								
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		Version AR057455.1 GI:5983032								
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		Source Unknown.								
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		17 bp DNA linear PAT 29-SEP-1999								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
		Reference 1 (bases 1 to 17)								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
		Source Unknown.								
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		16 AAAGGAAAGCAGAAA 1								
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		AR057455								
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		Sequence 1659 from patent US 5837542.								
		AR057455								
		Accession AR057455								
		Version AR057455.1 GI:5983032								
		Keywords Unknown.								
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		Reference 1 (bases 1 to 17)								
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		Sequence 1659 from patent US 5837542.								
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		Accession AR057455								
		Version AR057455.1 GI:5983032								
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Query Match Best Local Similarity 93.8%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	3209 AAATGGAAAGCAGAAA 3224								
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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS     Soncin,F. and Mattot,V.
TITLE       Soluble factor secreted by endothelial cells in blood vessels
JOURNAL     Patent: WO 2004076482-A 13 10-SEP-2004;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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    /db_xref="taxon:32630"
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1084 TGGTCAGCAGACATTC 1099
Db 1 TGGGACGACAGACATTC 16

RESULT 157
LOCUS      AR188500              17 bp      DNA              linear      PAT 20-APR-2002
DEFINITION Sequence 3988 from patent US 6346398.
ACCESSION  AR188500
VERSION    AR188500.1 GI:20234465
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6346398-A 1988 12-FEB-2002;
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
Db 1 AATTGCTCTAATGA 16

RESULT 158
LOCUS      AR324353              17 bp      RNA              linear      PAT 17-AUG-2003
DEFINITION Sequence 1785 from patent US 6566127.
ACCESSION  AR324353
VERSION    AR324353.1 GI:33710161
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1755 20-MAY-2003;
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
Db 1 AATTGCTCTAATGA 16

RESULT 159
LOCUS      AR329005              17 bp      RNA              linear      PAT 17-AUG-2003
DEFINITION Sequence 6407 from patent US 6566127.
ACCESSION  AR329005
VERSION    AR329005.1 GI:33714813
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 6407 20-MAY-2003;
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
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Qy 3494 AATTGCTCTAATAGA 3509
Db 1 AATTGCTCTAATGA 16

RESULT 160
LOCUS      AR463524              17 bp      DNA              linear      PAT 20-FEB-2004
DEFINITION Sequence 7201 from patent US 6866188.
ACCESSION  AR463524
VERSION    AR463524.1 GI:42698581
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
           Shannon,M.E.
TITLE      Polynucleotide encoding a human myosin-like polypeptide expressed
           predominantly in heart and muscle
JOURNAL    Patent: US 6866188-A 7201 03-FEB-2004;
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCTATGAGC 337
Db 2 GACCTTCCGATGAGC 17

RESULT 161
LOCUS      AR463525              17 bp      DNA              linear      PAT 20-FEB-2004
DEFINITION Sequence 7202 from patent US 6866188.
ACCESSION  AR463525
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VERSION AR463525.1 GI:42698582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7202 03-FEB-2004;
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCCCTATGAGC 337
Db 1 GACCTTGCCGATGAGC 16

RESULT 162
AR464790
LOCUS AR464790 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8467 from patent US 6686188.
ACCESSION AR464790
VERSION AR464790.1 GI:42699847
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8467 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACTGGAGAACATGA 617
Db 2 GAGCTGGAGAACATGA 17

RESULT 163
AR464791
LOCUS AR464791 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8468 from patent US 6686188.
ACCESSION AR464791
VERSION AR464791.1 GI:42699848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8468 03-FEB-2004;
FEATURES
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        Location/Qualifiers
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QY 1689 TCCTACTTCAGCAAAAT 1704
Db 1 TCCTACTTCAGCAAAAT 1704

VERSION AR463525.1 GI:42698582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7202 03-FEB-2004;
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Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACTGGAGAACATGA 617
Db 1 GAGCTGGAGAACATGA 16

RESULT 164
AX088231/c
LOCUS AX088231 17 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 15 from Patent WO0114520.
ACCESSION AX088231
VERSION AX088231.1 GI:13397142
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wadskov-Hansen, S.L., Hammer, K. and Martinussen, J.
TITLE Phage resistant lactic acid bacterial mutants
JOURNAL Patent: WO 0114520-A 15 01-MAR-2001;
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                /note="Oligonucleotide pyG8b used for PCR"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1570 GCAGCAACAAACACAG 1585
Db 17 GCAGCAACAAACACTG 2

RESULT 165
AX214792
LOCUS AX214792 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 234 from Patent WO0159103.
ACCESSION AX214792
VERSION AX214792.1 GI:15524835
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., Mcswiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 234 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Mcswiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1689 TCCTACTTCAGCAAAAT 1704
Db 1 TCCTACTTCAGCAAAAT 1704
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Db	2 TCCTACTTCAGAAAAT 17		AX272955.1 GI:16545692		Homo sapiens (human)	
	AX214793		Homo sapiens		Homo sapiens	
	LOCUS		Sequence 235 from Patent WO0159103.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	DEFINITION		AX214793		1	
	ACCESSION		AX214793.1 GI:15524836		Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.	
	KEYWORDS		synthetic construct		Method and reagent for the inhibition of grid	
	SOURCE		synthetic construct		Patent: WO 0162911-A 524 30-AUG-2001; GLAXO GROUP LIMITED (GB)	
	ORGANISM		other sequences; artificial sequences.		RIBOZYME PHARMACEUTICALS, INC. (US) ;	
	REFERENCE		1		Location/Qualifiers	
	AUTHORS		Blatt, L., Mcswiggen, J. and Chowrira, B.M.		1..17	
Db	TITLE		Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression		/organism="Homo sapiens"	
	JOURNAL		Patent: WO 0159103-A 235 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Mcswiggen, James (US) ; Chowrira, Bharat M. (US)		/mol_type="unassigned RNA"	
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	Db		1 TCCTACTTCAGAAAAT 16			
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Db	AX272814		AX531065		Sequence 574 from Patent EPI239051.	
	LOCUS		AX531065		17 bp DNA	
	DEFINITION		AX531065		linear	
	ACCESSION		AX531065		PAT 22-NOV-2002	
	VERSION		AX272814.1 GI:16545551			
	KEYWORDS		Homo sapiens (human)			
	SOURCE		Homo sapiens			
	ORGANISM		Homo sapiens			
	REFERENCE		1			
	AUTHORS		Shannon, M.			
Db	TITLE		Human posh-like protein 1			
	JOURNAL		Patent: EP 1239051-A 574 11-SEP-2002;			
	KEYWORDS		Aeomica, Inc. (US)			
	SOURCE		Location/Qualifiers			
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	Query Match		0.4%; Score 14.4; DB 1; Length 17;			
	Best Local Similarity		93.8%; Pred. No. 1.5e+02;			
	Matches		15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
	QY		2553 CCCTGACGCTCTGCAGG 2568			
	Db		2 CCCAGACGCTCTGCAGG 17			
Db	RESULT 170					
	AX531066		AX531066		Sequence 575 from Patent EPI239051.	
	LOCUS		AX531066		17 bp DNA	
	DEFINITION		AX531066		linear	
	ACCESSION		AX531066		PAT 22-NOV-2002	
	VERSION		AX531066.1 GI:25253914			
	KEYWORDS		Homo sapiens (human)			
	SOURCE		Homo sapiens			
	ORGANISM		Homo sapiens			
	REFERENCE		1			
Db	AUTHORS		Shannon, M.			
	TITLE		Human posh-like protein 1			
	JOURNAL		Patent: EP 1239051-A 575 11-SEP-2002;			
	KEYWORDS		Human posh-like protein 1			
	SOURCE		Human posh-like protein 1			
	ORGANISM		Human posh-like protein 1			
	REFERENCE		1			
	AUTHORS		Shannon, M.			
	TITLE		Human posh-like protein 1			
	JOURNAL		Patent: EP 1239051-A 575 11-SEP-2002;			


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Db      17 AGGCTTCTCCTTACA 2

RESULT 175
AX693264/c
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5996 from Patent EPI281758.
ACCESSION AX693264
VERSION   AX693264.1 GI:29416228
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
           mdz12
JOURNAL   Patent: EP 1281758-A 5996 05-FEB-2003;
           Aesomica, Inc. (US)
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1368 AGCCTTCTCCTTACA 1383
Db      16 AGGCTTCTCCTTACA 1

RESULT 176
AX723745
LOCUS      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1432 from Patent WO03025176.
ACCESSION AX723745
VERSION   AX723745.1 GI:30503088
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
           reversion, apoptosis and/or virus resistance and their use as
           medicines
JOURNAL   Patent: WO 03025176-A 1432 27-MAR-2003;
           Molecular Engines Laboratories (FR)
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source    1..17
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3255 ATTCTTGTTTAAATC 3270
Db      2 ATCTTGTTTAAATC 17

RESULT 177
AX728782/c
LOCUS      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 416 from Patent WO03025175.
ACCESSION AX728782

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VERSION   AX728782.1 GI:30508125
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
           reversion, apoptosis and/or virus resistance and their use as
           medicines
JOURNAL   Patent: WO 03025175-A 416 27-MAR-2003;
           Molecular Engines Laboratories (FR)
FEATURES
source    1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2778 AGCTAAGCACACAGAT 2793
Db      17 AGCTAAGCAACACAGAT 2

RESULT 178
AX736485
LOCUS      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2075 from Patent WO03025177.
ACCESSION AX736485
VERSION   AX736485.1 GI:30515773
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
           reversion, apoptosis and/or resistance to viruses and the use
           thereof as medicaments
JOURNAL   Patent: WO 03025177-A 2075 27-MAR-2003;
           Molecular Engines Laboratories (FR)
FEATURES
source    1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      718 GATCAAAAGTGAATAC 733
Db      1 GATCAAAAGTGAACAC 16

RESULT 179
AX737300
LOCUS      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2890 from Patent WO03025177.
ACCESSION AX737300
VERSION   AX737300.1 GI:30516588
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE

```



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AUTHORS
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL
Patent: WO 03025177-A 2890 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 233 GATATCAAAAGAAATTC 248
Db 1 GATCTCAAAAGAAATTC 16

RESULT 180
AX738735
LOCUS
AX738735 17 bp DNA linear PAT 08-MAY-2003
DEFINITION
Sequence 4325 from Patent WO03025177.
ACCESSION
AX738735
VERSION
AX738735.1 GI:30518025
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Telerman,A., Anson,R. and Tuijnder,M.
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL
Patent: WO 03025177-A 4325 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3330 ATCCAAATTTATCCAAA 3345
Db 2 ATCCCAATTTATCCAAA 17

RESULT 181
AX753828
LOCUS
AX753828 17 bp DNA linear PAT 23-JUN-2003
DEFINITION
Sequence 175 from Patent WO03037931.
ACCESSION
AX753828
VERSION
AX753828.1 GI:32166525
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shannon,M. and Phan,T.
TITLE
Human angiotensin-like protein 1
JOURNAL
Patent: WO 03037931-A 175 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"

AUTHORS
Telerman,A., Anson,R. and Tuijnder,M.
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL
Patent: WO 03040369-A 6091 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3182 TGGACTACATGAAGAT 3197
Db 17 TGGACTACATGAAGAT 2

RESULT 183
AR076398/c
LOCUS
AR076398 18 bp DNA linear PAT 30-AUG-2000
DEFINITION
Sequence 18 from patent US 5958773.
ACCESSION
AR076398
VERSION
AR076398.1 GI:10003144
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Monia,B.P. and Cowseert,L.M.
TITLE
Antisense modulation of AKT-1 expression
JOURNAL
Patent: US 5958773-A 18 28-SEP-1999;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .18
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 GAAGCAGCGCAGGAG 88
Db 18 GAAGCAGCGCAGGAG 3
```

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RESULT 184
ARI06771
LOCUS          ARI06771          18 bp      DNA          linear          PAT 14-FEB-2001
DEFINITION     Sequence 19 from patent US 6107091.
ACCESSION      ARI06771
VERSION        ARI06771.1 GI:12821301
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Cowser,L.M.
TITLE          Antisense inhibition of G-alpha-16 expression
JOURNAL        Patent: US 6107091-A 19 22-AUG-2000;
FEATURES       Location/Qualifiers
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"
                0.4%; Score 14.4; DB 1; Length 18;
Query Match    Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1532 GCCCAACAGCAGCAGC 1547
Db 3 GCCCAAAAGCAGCAGC 18

RESULT 185
BD250786/C
LOCUS          BD250786          18 bp      DNA          linear          PAT 17-JUL-2003
DEFINITION     Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation.
ACCESSION      BD250786
VERSION        BD250786.1 GI:33060556
KEYWORDS       JP 2002511276-A/340.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Cowser,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M., Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE          Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation
JOURNAL        Patent: JP 2002511276-A 340 16-APR-2002;
COMMENT        ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002511276-A/340
                PD 16-APR-2002
                PF 13-APR-1999 JP 2000543647
                PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
                LEX M COWSER,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
                M SASNOR,
                PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
                BORCHERS,
                PI TIMOTHY A VIKKARS
                PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
                C12N15/00
                CC Antisense Oligonucleotide
                FH Key
                FT source
                FT source
                FT Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match    0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

```

Qy 73 GAAGCAGCGGAGGAG 88
Db 18 GAAGCAGCGGAGGAG 3

RESULT 186
CQ808040
LOCUS          CQ808040          18 bp      DNA          linear          PAT 10-MAY-2004
DEFINITION     Sequence 1490 from Patent WO2004035803.
ACCESSION      CQ808040
VERSION        CQ808040.1 GI:47113434
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.
TITLE          Method and nucleic acids for the improved treatment of breast cell proliferative disorders
JOURNAL        Patent: WO 2004035803-A 1490 29-APR-2004;
FEATURES       Epigenomics AG (DE)
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Detection oligonucleotide for CACNA1G"

Query Match    0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3585 TAGGTTTGTGGAGT 3600
Db 1 TAGGTTTGTGGAGT 16

RESULT 187
AX111519
LOCUS          AX111519          18 bp      DNA          linear          PAT 29-MAY-2002
DEFINITION     Sequence 2252 from Patent WO0123604.
ACCESSION      AX111519
VERSION        AX111519.1 GI:13927811
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.
TITLE          Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL        Patent: WO 0123604-A 2252 05-APR-2001;
FEATURES       Infectio Diagnostic (I.D.I.) INC. (CA)
                Location/Qualifiers
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"

Query Match    0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2257 CACATACAGTGTCTCT 2272
Db 2 CACATACAGTGTCTCT 17

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RESULT 188
LOCUS      BD174259                26 bp    DNA    linear    PAT 18-FEB-2003
DEFINITION Novel physiological active peptide and its use.
ACCESSION  BD174259
VERSION     BD174259.1 GI:28415598
KEYWORDS    WO 02062944-A/6.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 26)
AUTHORS     Otaki,T., Masuda,Y., Takatsu,Y., Watanabe,T., Terao,Y., Shintani,Y.
            and Hinuma,S.
TITLE       Novel physiological active peptide and its use
JOURNAL     Patent: WO 02062944-A 6 15-AUG-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA,
            YOSHITIRO TAKATSU,TAKUYA WATANABE,YASUKO TERAO,YASUSHI SHINTANI,
            SHUJI HINUMA
COMMENT     OS Artificial Sequence
            PN WO 02062944-A/6
            PD 15-AUG-2002
            PF 01-FEB-2002 WO 2002JP000852
            PR 02-FEB-2001 JP OIP 026820
            PT TETSUYA OTAKI,YASUSHI MASUDA,YOSHITIRO TAKATSU,TAKUYA
            WATANABE,
            PI YASUKO TERAO,YASUSHI SHINTANI,SHUJI HINUMA
            PC C07K14/47,C07K14/705,C12N15/12,C12P21/02,C07K16/18,A61K67/027,
            C12N5/10,
            PC G01N33/15 G01N33/50,A61P1/00
            CC DNA primer, HBV-F1 primer
            FH key      Location/Qualifiers
            FT source   1..26
                        /organism="Artificial Sequence".

FEATURES
source      1..26
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1931 CTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCGCTGCTG 24

RESULT 189
LOCUS      AX734811/c              17 bp    DNA    linear    PAT 08-MAY-2003
DEFINITION Sequence 401 from Patent WO03025177.
ACCESSION  AX734811
VERSION     AX734811.1 GI:30514088
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 401 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES
source      1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1931 CTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCGCTGCTG 24

RESULT 190
LOCUS      AX737775              17 bp    DNA    linear    PAT 08-MAY-2003
DEFINITION Sequence 3365 from Patent WO03025177.
ACCESSION  AX737775
VERSION     AX737775.1 GI:30517063
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 3365 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES
source      1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 GATCTCTGAGCTGCA 549
Db 1 GATCTCTGAGCTGCA 14

RESULT 191
LOCUS      AX744267/c              17 bp    DNA    linear    PAT 14-MAY-2003
DEFINITION Sequence 232 from Patent WO03031621.
ACCESSION  AX744267
VERSION     AX744267.1 GI:30722934
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhang,J.
TITLE       A human G protein coupled receptor
JOURNAL     Patent: WO 03031621-A 232 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES
source      1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 GTGGCTCTCTCTAA 2673
Db 1 GTGGCTCTCTCTAA 4

RESULT 192

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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1042 ACCAGGTCCATTGT 1055
Db 17 ACCAGGTCCATTGT 4

RESULT 190
LOCUS      AX737775              17 bp    DNA    linear    PAT 08-MAY-2003
DEFINITION Sequence 3365 from Patent WO03025177.
ACCESSION  AX737775
VERSION     AX737775.1 GI:30517063
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 3365 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES
source      1..17
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            /mol_type="unassigned DNA"
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Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 GATCTCTGAGCTGCA 549
Db 1 GATCTCTGAGCTGCA 14

RESULT 191
LOCUS      AX744267/c              17 bp    DNA    linear    PAT 14-MAY-2003
DEFINITION Sequence 232 from Patent WO03031621.
ACCESSION  AX744267
VERSION     AX744267.1 GI:30722934
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhang,J.
TITLE       A human G protein coupled receptor
JOURNAL     Patent: WO 03031621-A 232 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES
source      1..17
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 GTGGCTCTCTCTAA 2673
Db 1 GTGGCTCTCTCTAA 4

RESULT 192

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AX744268/c
LOCUS AX744268 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 233 from Patent WO03031621.
ACCESSION AX744268
VERSION AX744268.1 GI:30722935
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 233 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCTCTCTAA 2673
Db 16 GTGGCTCTCTCTAA 3
RESULT 193
AX744269/c
LOCUS AX744269 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 234 from Patent WO03031621.
ACCESSION AX744269
VERSION AX744269.1 GI:30722936
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 234 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCTCTCTAA 2673
Db 16 GTGGCTCTCTCTAA 3
RESULT 194
AX744270/c
LOCUS AX744270 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 235 from Patent WO03031621.
ACCESSION AX744270
VERSION AX744270.1 GI:30722937
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 235 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCTCTCTAA 2673
Db 15 GTGGCTCTCTCTAA 2
RESULT 195
AX753817
LOCUS AX753817 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 164 from Patent WO03037931.
ACCESSION AX753817
VERSION AX753817.1 GI:32166514
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 164 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
Db 4 GCAGCAGCAGCAAC 17
RESULT 196
AR084541/c
LOCUS AR084541 30 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 30 from patent US 5981185.
ACCESSION AR084541
VERSION AR084541.1 GI:10011312
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 30 09-NOV-1999;
FEATURES
source
1. .30
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 235 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCTCTCTAA 2673
Db 14 GTGGCTCTCTCTAA 1
RESULT 195
AX753817
LOCUS AX753817 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 164 from Patent WO03037931.
ACCESSION AX753817
VERSION AX753817.1 GI:32166514
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 164 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
Db 4 GCAGCAGCAGCAAC 17
RESULT 196
AR084541/c
LOCUS AR084541 30 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 30 from patent US 5981185.
ACCESSION AR084541
VERSION AR084541.1 GI:10011312
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 30 09-NOV-1999;
FEATURES
source
1. .30
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 197
AR165925/c
LOCUS I84405 30 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6280938.
ACCESSION AR165925
VERSION AR165925.1 GI:16241014
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Rannum,L.P.W., Koob,M.D., Moseley-Allidredge,M.L. and Benzow,K.A.
TITLE SCA7 gene and method of use
JOURNAL Patent: US 6280938-A 4 28-AUG-2001;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 198
E34522/c
LOCUS E34522 30 bp DNA linear PAT 18-JUN-2001
DEFINITION SCA7 gene and utilization thereof.
ACCESSION E34522
VERSION E34522.1 GI:13018890
KEYWORDS JP 1999206393-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Laura,B.W.R. and Michael,D.K.
TITLE SCA7 gene and utilization thereof
JOURNAL Patent: JP 1999206393-A 4 03-AUG-1999;
COMMENT THE REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Homo sapiens (human)
PN JP 1999206393-A/4
PD 03-AUG-1999
PF 19-AUG-1998 JP 1998294732
PR 19-AUG-1997 US 60/056170
PI LAURA B W RANAMU,MICHAEL D KUBU
PC C12N15/09,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
G01N33/566//C12P21/02,
PC C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..30
FT /organism="Homo sapiens (human)".

FEATURES
source 1..30
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||

Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 199
I84405/c
LOCUS I84405 30 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 6 from patent US 5695933.
ACCESSION I84405
VERSION I84405.1 GI:3021925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Houseman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 6 09-DEC-1997;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 200
I84410
LOCUS I84410 30 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 11 from patent US 5695933.
ACCESSION I84410
VERSION I84410.1 GI:3021930
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Houseman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 11 09-DEC-1997;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 201
AR040055/c
LOCUS AR040055 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 903 from patent US 5807743.
ACCESSION AR040055
VERSION AR040055.1 GI:5959418
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes

Query Match 0.4%; Score 13.8; DB 1; Length 17;

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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 938 AAACAGATAGCTGCTAA 954
Db 1 AAACAGATAGATGATAA 17

RESULT 206
BD202795/c
LOCUS BD202795 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD202795
VERSION BD202795.1 GI:33012565
KEYWORDS JP 2002509721-A/5821.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 5821 02-APR-2002;
COMMENT RiBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/5821
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism="Homo sapiens (human)".
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3090 AAAGAAGAAGGAAGA 3106
Db 17 AAAGAAAAAAGGAAGA 1

RESULT 207
BD231281
LOCUS BD231281 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Genes for assessing cardiovascular status and compositions for use
thereof.
ACCESSION BD231281
VERSION BD231281.1 GI:33041051
KEYWORDS JP 2002527079-A/45.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
TITLE Genes for assessing cardiovascular status and compositions for use
thereof.
JOURNAL Patent: JP 2002527079-A 45 27-AUG-2002;
COMMENT PAIROSEAKENSINGU AB
PN JP 2002527079-A/51
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576056
PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM,
PI LENA JONSSON
PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
for assessing cardiovascular status
and compositions for
CC Key Location/Qualifiers
FH Key use thereof
FT source 1..17
FT /organism="Artificial Sequence".
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source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;

thereof
Patent: JP 2002527079-A 45 27-AUG-2002;
COMMENT PAIROSEAKENSINGU AB
PN JP 2002527079-A/45
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576056
PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM,
PI LENA JONSSON
PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
for assessing cardiovascular status
and compositions for
CC Key Location/Qualifiers
FH Key use thereof
FT source 1..17
FT /organism="Artificial Sequence".
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source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGCGCGCAGCAGCAACA 17

RESULT 208
BD231287
LOCUS BD231287 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Genes for assessing cardiovascular status and compositions for use
thereof.
ACCESSION BD231287
VERSION BD231287.1 GI:33041057
KEYWORDS JP 2002527079-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
TITLE Genes for assessing cardiovascular status and compositions for use
thereof.
JOURNAL Patent: JP 2002527079-A 51 27-AUG-2002;
COMMENT PAIROSEAKENSINGU AB
PN JP 2002527079-A/51
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576056
PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM,
PI LENA JONSSON
PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
for assessing cardiovascular status
and compositions for
CC Key Location/Qualifiers
FH Key use thereof
FT source 1..17
FT /organism="Artificial Sequence".
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGCGCGCAGCAGCAACA 17

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCA 1443
Db 1 CGGCGCAGCAGCA 17

RESULT 209
BD256637/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 17)
AUTHORS
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE
Regulation of repressor genes using nucleic acid molecules
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/4430
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
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source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3100 GGGAGACAAATTACAA 3116
Db 17 GTGAAGACAATTGACAA 1

RESULT 211
BD257658
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 17)
AUTHORS
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE
Regulation of repressor genes using nucleic acid molecules
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/5451
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
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source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3100 GGGAGACAAATTACAA 3116
Db 17 GTGAAGACAATTGACAA 1

RESULT 210
BD257085/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 17)
AUTHORS
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE
Regulation of repressor genes using nucleic acid molecules
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/4878
PD 10-DEC-2002

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PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3100 GGGAGACAAATTACAA 3116
Db 17 GTGAAGACAATTGACAA 1

RESULT 211
BD257658
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 17)
AUTHORS
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE
Regulation of repressor genes using nucleic acid molecules
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Eukaryote
PN JP 2002541795-A/5451
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
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source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3369 ATTAATTGCTAAATA 3385
Db 1 ATTCATTTCGTAATA 17

RESULT 212
BD259675/c
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD259675
VERSION BD259675.1 GI:33069445
KEYWORDS JP 2002541795-A/7468.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 7468 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/7468
PD 10-DEC-2002
PE 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02/A61K31/711, (C12N5/10, C12R1/91), (C12P21/02, PC
C12R1/91),
PC (C12P21/02, C12R1/91), (C12P21/02, C12R1/91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1/91)
CC Regulation of repressor genes using nucleic acid molecules PH
Key source Location/Qualifiers
FT 1..17
FT Location/Qualifiers
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3351 CTGTGTGTCATGTGT 3367
Db 17 CTGTGGAGTAAATGTGT 1

RESULT 213
BD266197
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Universal arrays.
ACCESSION BD266197
VERSION BD266197.1 GI:33075965
KEYWORDS JP 2002539849-A/197.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE Universal arrays
JOURNAL Patent: JP 2002539849-A 197 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Artificial Sequence
PN JP 2002539849-A/197
PD 26-NOV-2002
PF 27-NOV-2000 JP 2000608794

PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Primer
FT Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 815 TCTGCCCTCTCCACTTC 831
Db 1 TCTGCCCTCTGCACCTC 17

RESULT 214
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 664 from Patent WO0192524.
ACCESSION CQ615924
VERSION CQ615924.1 GI:41666142
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 664 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAGCCAGAGGA 680
Db 1 TCAGCAAGCCAGAGAA 17

RESULT 215
LOCUS 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 665 from Patent WO0192524.
ACCESSION CQ615925
VERSION CQ615925.1 GI:41666143
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.

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TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 665 06-DEC-2001;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 665 CAGCAAGCCAGAGAG 681
 Db 1 CAGCAAGCCAGAGAG 17

RESULT 216
 CQ617132
 LOCUS CQ617132 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 1872 from Patent WO0192524.
 ACCESSION CQ617132
 VERSION CQ617132.1 GI:41667350
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 1872 06-DEC-2001;
 Aeomica, Inc. (US)

FEATURES Location/Qualifiers
 source 1..17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1022 CCCTCCTGCTGGACC 1038
 Db 1 CCCTCCTGCTGGACC 17

RESULT 217
 CQ617133
 LOCUS CQ617133 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 1873 from Patent WO0192524.
 ACCESSION CQ617133
 VERSION CQ617133.1 GI:41667351
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 1873 06-DEC-2001;
 Aeomica, Inc. (US)

FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 CCTCCTCTGCTGGACCA 1039
 Db 1 CCTCCTGAGCTGGACCA 17

RESULT 218
 CQ617993
 LOCUS CQ617993 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 2733 from Patent WO0192524.
 ACCESSION CQ617993
 VERSION CQ617993.1 GI:41668211
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 2733 06-DEC-2001;
 Aeomica, Inc. (US)

FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
 Db 1 CTCAGCAGCTGAGGCC 17

RESULT 219
 CQ623062
 LOCUS CQ623062 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 7802 from Patent WO0192524.
 ACCESSION CQ623062
 VERSION CQ623062.1 GI:41673280
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 7802 06-DEC-2001;
 Aeomica, Inc. (US)

FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCA 1425
 Db 1 CAGCAGCAGCTGAAGCA 17

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RESULT 220
LOCUS       CQ623063              17 bp    DNA          linear    PAT 02-FEB-2004
DEFINITION   Sequence 7803 from Patent WO0192524.
ACCESSION    CQ623063
VERSION      CQ623063.1  GI:41673281
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE        Myosin-like gene expressed in human heart and muscle
JOURNAL      Patent: WO 0192524-A 7803 06-DEC-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
             source             1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
Db 1 AGCAGCAGCAGCAGCAA 17

RESULT 221
LOCUS       CQ625507              17 bp    DNA          linear    PAT 02-FEB-2004
DEFINITION   Sequence 10247 from Patent WO0192524.
ACCESSION    CQ625507
VERSION      CQ625507.1  GI:41675725
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE        Myosin-like gene expressed in human heart and muscle
JOURNAL      Patent: WO 0192524-A 10247 06-DEC-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
             source             1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1187 TCAGCCCGAGGTGGCA 1203
Db 1 TCAGCCCAAGGTGGCA 17

RESULT 222
LOCUS       CQ626007              17 bp    DNA          linear    PAT 02-FEB-2004
DEFINITION   Sequence 10747 from Patent WO0192524.
ACCESSION    CQ626007
VERSION      CQ626007.1  GI:41676225
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens

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REFERENCE    1
AUTHORS      Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE        Myosin-like gene expressed in human heart and muscle
JOURNAL      Patent: WO 0192524-A 10747 06-DEC-2001;
              Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
             source             1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1771 TGTGTAGCCGAGAAC 1787
Db 1 TGTGTGTGGCTGAACA 17

RESULT 223
LOCUS       I37425/c              17 bp    DNA          linear    PAT 13-MAY-1997
DEFINITION   Sequence 438 from patent US 5612215.
ACCESSION    I37425
VERSION      I37425.1  GI:2085385
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
              Stinchcomb,D.T.
TITLE        Stromelysin targeted ribozymes
JOURNAL      Patent: US 5612215-A 438 18-MAR-1997;
              Location/Qualifiers
FEATURES     Location/Qualifiers
             source             1..17
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 560 AATGAACCTGACCAACAT 576
Db 17 ACTGAAGTGACCAACAT 1

RESULT 224
LOCUS       I37439/c              17 bp    DNA          linear    PAT 13-MAY-1997
DEFINITION   Sequence 452 from patent US 5612215.
ACCESSION    I37439
VERSION      I37439.1  GI:2085399
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
              Stinchcomb,D.T.
TITLE        Stromelysin targeted ribozymes
JOURNAL      Patent: US 5612215-A 452 18-MAR-1997;
              Location/Qualifiers
FEATURES     Location/Qualifiers
             source             1..17
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 17;

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QY 2166 TGCTACTTCTCAGGG 2182
Db 1 TGCTGCTTCTCAGG 17

RESULT 230
LOCUS AR185993 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1481 from patent US 6346398.
ACCESSION AR185993
VERSION AR185993.1 GI:20231958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1481 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGGGA 2183
Db 1 GTCTGCTTCTCAGGA 17

RESULT 231
LOCUS AR186381 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1869 from patent US 6346398.
ACCESSION AR186381
VERSION AR186381.1 GI:20232346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1869 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGGGA 2183
Db 1 GTCTGCTTCTCAGGA 17

RESULT 231
LOCUS AR186381 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1869 from patent US 6346398.
ACCESSION AR186381
VERSION AR186381.1 GI:20232346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1869 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
Db 17 GGAGCCAGAGAGATC 1

RESULT 232
LOCUS AR186382 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1870 from patent US 6346398.
ACCESSION AR186382
VERSION AR186382.1 GI:20232347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
Db 17 GGAGCCAGAGAGATC 1

RESULT 232
LOCUS AR186382 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1870 from patent US 6346398.
ACCESSION AR186382
VERSION AR186382.1 GI:20232347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
Db 17 GGAGCCAGAGAGATC 1

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 AGGAGCCAGGAGACT 445
Db 17 AGGAGCCAGAGAGACT 1

RESULT 233
LOCUS AR187083 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2571 from patent US 6346398.
ACCESSION AR187083
VERSION AR187083.1 GI:20233048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2571 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCTTGATATCAA 240
Db 1 TCATGCTTGTGATTTCAA 17

RESULT 234
LOCUS AR188877 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4365 from patent US 6346398.
ACCESSION AR188877
VERSION AR188877.1 GI:20234842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4365 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCTTGATATCAA 240
Db 1 TCATGCTTGTGATTTCAA 17

RESULT 234
LOCUS AR188877/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4365 from patent US 6346398.
ACCESSION AR188877
VERSION AR188877.1 GI:20234842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4365 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1509 AACAGCAGCAGACTCA 1525

AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7450 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2757 GTCTGAATCTCAGACC 2773
Db 1 GGCTGACTCTCAGACC 17
RESULT 238
LOCUS AR283934/c 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6528257.
ACCESSION AR283934
VERSION AR283934.1 GI:29720834
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sharma,V.M. and Ganesan,K.
TITLE Method for the simultaneous monitoring of individual mutants in mixed populations
JOURNAL Patent: US 6528257-A 13 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2753 AGGGTCTGAATCTCAG 2769
Db 17 AGGGTCTGACGCTCAG 1
RESULT 239
LOCUS AR322623 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 25 from patent US 6566127.
ACCESSION AR322623
VERSION AR322623.1 GI:33708431
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 25 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2166 TGCTACTTCTCAGGG 2182
Db 1 TGCTGCTTCTCAGGG 17

Db 17 AACAGGAGGAGAGCTCA 1
RESULT 235
LOCUS AR191745 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7233 from patent US 6346398.
ACCESSION AR191745
VERSION AR191745.1 GI:20237710
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7233 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2166 TGCTACTTCTCAGGG 2182
Db 1 TGCTGCTTCTCAGGG 17
RESULT 236
LOCUS AR191746 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7234 from patent US 6346398.
ACCESSION AR191746
VERSION AR191746.1 GI:20237711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7234 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2167 GTCTACTTCTCAGGGA 2183
Db 1 GTCTGCTTCTCAGGGA 17
RESULT 237
LOCUS AR191962 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7450 from patent US 6346398.
ACCESSION AR191962
VERSION AR191962.1 GI:20237927
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)

Db 1 TGCTGCTTCTCAGG 17
RESULT 240
AR322624
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 26 from patent US 6566127.
ACCESSION AR322624
VERSION AR322624.1 GI:33708432
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 26 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2167 GTCTACTTCTCAGGGA 2183
Db 1 GTCTGCTTCTCAGGA 17
RESULT 241
AR323012/c
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 414 from patent US 6566127.
ACCESSION AR323012
VERSION AR323012.1 GI:33708820
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 414 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 430 GGAGCCGAGAGACTC 446
Db 17 GGAGCCGAGAGAGATC 1
RESULT 242
AR323013/c
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 415 from patent US 6566127.
ACCESSION AR323013
VERSION AR323013.1 GI:33708821
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 415 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 429 AGGAGCCGAGAGACT 445
Db 17 AGGAGCCGAGAGAGT 1
RESULT 243
AR323693
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1095 from patent US 6566127.
ACCESSION AR323693
VERSION AR323693.1 GI:33709501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1095 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 224 TCATTTCTTGATATCAA 240
Db 1 TCATGCTTTGATTTCAA 17
RESULT 244
AR324730/c
LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2132 from patent US 6566127.
ACCESSION AR324730
VERSION AR324730.1 GI:33710538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2132 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGGAGGAGAGCTCA 1

related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6437 20-MAY-2003;

JOURNAL
FEATURES
source

RESULT 245
AR325854 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 3256 from patent US 6566127.
DEFINITION
ACCESSION AR325854
VERSION AR325854.1 GI:33711662
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 3256 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCTGATCTCAGACCC 2773
Db 1 GGCTGACTCTCAGACCC 17

RESULT 246
AR326810 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 4212 from patent US 6566127.
DEFINITION
ACCESSION AR326810
VERSION AR326810.1 GI:33712618
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 4212 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGCTCTCTCTCAGG 2181
Db 1 CTGCTCTCTCTCAGG 17

RESULT 247
AR329035 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 6437 from patent US 6566127.
DEFINITION
ACCESSION AR329035
VERSION AR329035.1 GI:33714843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions

JOURNAL Patent: US 6566127-A 6437 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGCTCTCTCTCAGG 2181
Db 1 CTGCTCTCTCTCAGG 17

RESULT 248
AR434101 17 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 524 from patent US 6656700.
DEFINITION
ACCESSION AR434101
VERSION AR434101.1 GI:40196944
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E

JOURNAL Patent: US 6656700-A 524 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

JOURNAL
FEATURES
source

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGAGC 1111
Db 1 CATGAGCCCACTGAGC 17

RESULT 248
AR434101 17 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 524 from patent US 6656700.
DEFINITION
ACCESSION AR434101
VERSION AR434101.1 GI:40196944
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E

JOURNAL Patent: US 6656700-A 524 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAAATGACCAAGAGAA 489
Db 1 CAAAGGAACCAAGAGAA 17

RESULT 249
AR456987 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 664 from patent US 6686188.
DEFINITION
ACCESSION AR456987
VERSION AR456987.1 GI:42692044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle

JOURNAL Patent: US 6686188-A 664 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAGCCAGAGAA 680
Db 1 TCAGCAAGCCAGAGAA 17

RESULT 250
AR456988
LOCUS AR456988 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 665 from patent US 6686188.
ACCESSION AR456988
VERSION AR456988.1 GI:42692045
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 665 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 665 CAGCAAGCCAGAGGAG 681
|||||
Db 1 CAGCAAGCCAGAGGAG 17
RESULT 251
AR458195
LOCUS AR458195 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1872 from patent US 6686188.
ACCESSION AR458195
VERSION AR458195.1 GI:42693252
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1872 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1022 CCTCTCTGCTGGACC 1038
|||||
Db 1 CCTCTCTGCTGGACC 17
RESULT 252
AR458196
LOCUS AR458196 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1873 from patent US 6686188.
ACCESSION AR458196
VERSION AR458196.1 GI:42693253
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1873 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Shannon, M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
Patent: US 6686188-A 1873 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1023 CCTCTCTGCTGGACCA 1039
|||||
Db 1 CCTCTCTGCTGGACCA 17
RESULT 253
AR459056
LOCUS AR459056 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2733 from patent US 6686188.
ACCESSION AR459056
VERSION AR459056.1 GI:42694113
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2733 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCCTCAGCTGAGGCC 781
|||||
Db 1 CTCCTCAGCTGAGGCC 17
RESULT 254
AR464125
LOCUS AR464125 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7802 from patent US 6686188.
ACCESSION AR464125
VERSION AR464125.1 GI:42699182
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7802 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCCTCAGCTGAGGCC 781
|||||
Db 1 CTCCTCAGCTGAGGCC 17
RESULT 254
AR464125
LOCUS AR464125 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7802 from patent US 6686188.
ACCESSION AR464125
VERSION AR464125.1 GI:42699182
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7802 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCA 1425
 Db 1 CAGCAGCAGCTGAAGCA 17
 RESULT 255
 LOCUS AR464126 linear PAT 20-FEB-2004
 DEFINITION Sequence 7803 from patent US 6686188.
 ACCESSION AR464126
 VERSION AR464126.1 GI:42699183
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 7803 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1425 ACCAGCAGCAGCA 1441
 Db 1 AGCAGCAGCTGAAGCA 17
 RESULT 256
 LOCUS AR466570 linear PAT 20-FEB-2004
 DEFINITION Sequence 10247 from patent US 6686188.
 ACCESSION AR466570
 VERSION AR466570.1 GI:42701627
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 10247 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
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 /mol_type="genomic DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1187 TCAGCCAGGTGGCA 1203
 Db 1 TCAGCCAAAGGTGGCA 17
 RESULT 257
 LOCUS AR467070 linear PAT 20-FEB-2004
 DEFINITION Sequence 10747 from patent US 6686188.
 ACCESSION AR467070
 VERSION AR467070.1 GI:42702127
 KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 10747 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1771 TGTGTAGCCAGCA 1787
 Db 1 TGTGTGTGGCTGAACA 17
 RESULT 258
 LOCUS AX037420 linear PAT 16-NOV-2000
 DEFINITION Sequence 45 from Patent WO0056922.
 ACCESSION AX037420
 VERSION AX037420.1 GI:11226845
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Norberg, L.T., Olafsson, E., Jonsson, L., Lindstrom, P.H. and Sanders, R.
 TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
 JOURNAL Patent: WO 0056922-A 45 28-SEP-2000;
 NORBERG LEIF TORBJORN (SE) ; OLAFSSON ERIK (SE) ; JONSSON LENA (SE) ; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ; SANDERS RHIANON (SE)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide primer"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1427 CAGCAGCAGCAGCA 1443
 Db 1 CGCGCGCAGCAGCA 17
 RESULT 259
 LOCUS AX037426 linear PAT 16-NOV-2000
 DEFINITION Sequence 51 from Patent WO0056922.
 ACCESSION AX037426
 VERSION AX037426.1 GI:11226851
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Norberg, L.T., Olafsson, E., Jonsson, L., Lindstrom, P.H. and Sanders, R.
 TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
 JOURNAL Patent: WO 0056922-A 51 28-SEP-2000;

NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
SANDERS RHIANON (SE)

FEATURES

source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGCGGCAGCAGCAACA 17
|||||

RESULT 260

AX215324
LOCUS AX215324 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 766 from Patent WO0159103.
ACCESSION AX215324
VERSION AX215324.1 GI:15525367

KEYWORDS

SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 766 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGC 1427
Db 1 CGCGGCAGCAGCAGC 17
|||||

RESULT 261

AX215325
LOCUS AX215325 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 767 from Patent WO0159103.
ACCESSION AX215325
VERSION AX215325.1 GI:15525368

KEYWORDS

SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 767 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"

/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGC 1427
Db 1 GCAGCAGCTGCAGCATC 17
|||||

RESULT 262

AX215661
LOCUS AX215661 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1103 from Patent WO0159103.
ACCESSION AX215661
VERSION AX215661.1 GI:15525704

KEYWORDS

SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 1103 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1687 GCTCCTACTTCAGCAA 1703
Db 1 GATCCTACTTCAGAAA 17
|||||

RESULT 263

AX216107
LOCUS AX216107 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1549 from Patent WO0159103.
ACCESSION AX216107
VERSION AX216107.1 GI:15526150

KEYWORDS

SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 1549 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

```
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 125 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 666 AGCAAGCCAGGAGC 682
Db 17 AGCAGAGCTAGAGGAGC 1

RESULT 269
AX227106/c
LOCUS AX227106 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 478 from Patent WO0157206.
ACCESSION AX227106
VERSION AX227106.1 GI:15556247
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 478 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 667 GCAAGCCAGGAGCA 683
Db 17 GCAGAGCTAGAGGAGCA 1

RESULT 270
AX227461/c
LOCUS AX227461 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 833 from Patent WO0157206.
ACCESSION AX227461
VERSION AX227461.1 GI:15556602
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 833 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 125 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CACGAAGCCAGGAGC 681
Db 17 CAGCAGAGCTAGAGGAGC 1

RESULT 271
AX272889
LOCUS AX272889 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 458 from Patent WO0162911.
ACCESSION AX272889
VERSION AX272889.1 GI:16545626
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 458 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2508 CACCAAACTGGGCTCT 2524
Db 1 CAACAAGCTGGGCTCT 17

RESULT 272
AX273038
LOCUS AX273038 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 607 from Patent WO0162911.
ACCESSION AX273038
VERSION AX273038.1 GI:16545775
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 607 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 CACCAGCAGCAGCACCA 999
Db 1 CCCCTGCAGCAGCACCA 17
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REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 2559 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Brassica napus"
/mol_type="unassigned DNA"
/db_xref="taxon:3708"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATA 946
|||||
Db 17 AGCAGCTCAACAGCTA 1

RESULT 278
AX326422 17 bp DNA linear PAT 02-SEP-2002
LOCUS
DEFINITION Sequence 2560 from Patent WO0192512.
ACCESSION AX326422
VERSION AX326422.1 GI:18097186
KEYWORDS
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 2560 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..17
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/mol_type="unassigned DNA"
/db_xref="taxon:3708"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATA 946
|||||
Db 1 AGCAGCTCAACAGCTA 17

RESULT 279
AX328593 17 bp DNA linear PAT 08-JAN-2002
LOCUS
DEFINITION Sequence 90 from Patent EP1164203.
ACCESSION AX328593
VERSION AX328593.1 GI:18101792
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hallenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 90 19-DEC-2001;
SEQUENOM, INC. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1399 ACAGCAGCAACAGCAGC 1415
|||||
Db 1 ACAGCAGCAACAGCATC 17

RESULT 280
AX429297/c 17 bp DNA linear PAT 21-JUN-2002
LOCUS
DEFINITION Sequence 2 from Patent EP1201676.
ACCESSION AX429297
VERSION AX429297.1 GI:21540603
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Cook,P.D.
TITLE Pna-dna-pna chimeric macromolecules
JOURNAL Patent: EP 1201676-A 2 02-MAY-2002;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PNA analogue"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 CGGAAATTCAGCGAGAA 54
|||||
Db 17 CTGAAATGCGAGCGAGAA 1

RESULT 281
AX467582 17 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 18 from Patent WO224889.
ACCESSION AX467582
VERSION AX467582.1 GI:21900774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Epstein,N.D., Haseanzadeh,S., Winitzky,S. and Davis,J.S.
TITLE Optimized cardiac contraction through differential phosphorylation
JOURNAL Patent: WO 0224889-A 18 28-MAR-2002;
The Secretary of the Department of Health and Human Services (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 845 TCAGTCCCTCAGAGCCA 861
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Db 1 TCAGACCCCGCAGAGCCA 17

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RESULT 282
AX527213
LOCUS AX527213 17 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 243 from Patent WO0226818.
ACCESSION AX527213
VERSION AX527213.1 GI:25171828
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y. and Corrigan, A.
TITLE Human nedd-1
JOURNAL Patent: WO 0226818-A 243 04-APR-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2673 ACCAGTTAACACGACGCA 2689
Db 1 ACCAGTTAAGACCATCA 17
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2673 ACCAGTTAACACGACGCA 2689
Db 1 ACCAGTTAAGACCATCA 17
RESULT 283
AX527214
LOCUS AX527214 17 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 244 from Patent WO0226818.
ACCESSION AX527214
VERSION AX527214.1 GI:25171829
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y. and Corrigan, A.
TITLE Human nedd-1
JOURNAL Patent: WO 0226818-A 244 04-APR-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2674 CCAGTTAACACGACGAG 2690
Db 1 CCAGTTAAGACCATCAG 17
RESULT 284
AX527215
LOCUS AX527215 17 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 245 from Patent WO0226818.
ACCESSION AX527215
VERSION AX527215.1 GI:25171830
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y. and Corrigan, A.
TITLE Human nedd-1
JOURNAL Patent: WO 0226818-A 247 04-APR-2002;
Aeomica, Inc. (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2676 AGTTAACACGACGAGTG 2692
Db 1 AGTTAAGACCATCAGTG 17
RESULT 286
AX527217
LOCUS AX527217 17 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 247 from Patent WO0226818.
ACCESSION AX527217
VERSION AX527217.1 GI:25171832
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y. and Corrigan, A.
TITLE Human nedd-1
JOURNAL Patent: WO 0226818-A 247 04-APR-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2676 AGTTAACACGACGAGTG 2692
Db 1 AGTTAAGACCATCAGTG 17

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/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2677 GTTAACACCGACGCTGC 2693
Db 1 GTTAAGACCATCAGTGC 17

RESULT 287
AX531063
LOCUS AX531063 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 572 from Patent EP1239051.
ACCESSION AX531063
VERSION AX531063.1 GI:25253908
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 572 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2550 AAGCCCTGACGCTCTGCA 2566
Db 1 AACCCAGACGCTCTGCA 17

RESULT 288
AX531064
LOCUS AX531064 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 573 from Patent EP1239051.
ACCESSION AX531064
VERSION AX531064.1 GI:25253910
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 573 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
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            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2551 AGCCCTGACGCTCTGCA 2567
Db 1 ACCCCAGACGCTCTGCA 17

RESULT 289
AX531472/c
LOCUS AX531472 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 981 from Patent EP1239051.
ACCESSION AX531472
VERSION AX531472.1 GI:25254721
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 981 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3090 AAAGAAGAAAGGGAAGA 3106
Db 17 AAACAAGATAGGGAAGA 1

RESULT 290
AX532058/c
LOCUS AX532058 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1567 from Patent EP1239051.
ACCESSION AX532058
VERSION AX532058.1 GI:25255879
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1567 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
        1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2211 TTCAGAAATATGGGGATG 2227
Db 17 TTCTGAAATGGGGATG 1

RESULT 291
AX578494
LOCUS AX578494 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 332 from Patent WO0211674.
ACCESSION AX578494
VERSION AX578494.1 GI:27647696
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 332 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2211 TTCAGAAATATGGGGATG 2227
Db 17 TTCTGAAATGGGGATG 1
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Qy 1982 GATCAGATAAACCCAGCA 1998
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 Db 1 GATCAGAGAAACAGACA 17

RESULT 296
 AX674529
 LOCUS AX674529 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 2974 from Patent WO03004526.
 ACCESSION AX674529
 VERSION AX674529.1 GI:29332877
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or resistance to viruses and their use as
 medicines
 JOURNAL Patent: WO 03004526-A 2974 16-JAN-2003;
 Molecular Engines Laboratories (FR)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3348 GAACGTGGTGTCATG 3364
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 Db 1 GATCTGGTGGCAATG 17

RESULT 297
 AX687647/c
 LOCUS AX687647 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 379 from Patent EPI281758.
 ACCESSION AX687647
 VERSION AX687647.1 GI:29410343
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 mdz12
 JOURNAL Patent: EP 1281758-A 379 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 980 CAGCACCAGCAGCAGCA 996
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 Db 17 CAGCACCAGCAGCTCCA 1

RESULT 298
 AX687651/c

LOCUS AX687651 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 383 from Patent EPI281758.
 ACCESSION AX687651
 VERSION AX687651.1 GI:29410347
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 mdz12
 JOURNAL Patent: EP 1281758-A 383 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 976 GCACGACGACCCAGCAGC 992
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 Db 17 GCTCCAGCACCAGCAGC 1

RESULT 299
 AX687652/c
 LOCUS AX687652 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 384 from Patent EPI281758.
 ACCESSION AX687652
 VERSION AX687652.1 GI:29410348
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 mdz12
 JOURNAL Patent: EP 1281758-A 384 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCAGCAGCAGCAG 991
 ||||| ||||| |||||
 Db 17 TGCTCCAGCACCAGCAGCAG 1

RESULT 300
 AX688238
 LOCUS AX688238 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 970 from Patent EPI281758.
 ACCESSION AX688238
 VERSION AX688238.1 GI:29410938
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 970 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2941 TTTTGACTTCTCAGCC 2957
|||||
Db 17 TTTTGACTTCTCAGCC 1

RESULT 303
AX688406/c
LOCUS AX688406 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1138 from Patent EP1281758.
ACCESSION AX688406
VERSION AX688406.1 GI:29411108
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1138 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2939 GCTTTTGACTTCTCAG 2955
|||||
Db 17 GCTTTTGACTTCTCAG 1

RESULT 304
AX690658/c
LOCUS AX690658 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3390 from Patent EP1281758.
ACCESSION AX690658
VERSION AX690658.1 GI:29413539
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3390 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 976 GCAGCAGCAGCAGCAGC 992
|||||

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 970 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 CCCACAGGTACACCTG 2594
|||||
Db 1 CCCACAGGAGACCTG 17

RESULT 301
AX688403/c
LOCUS AX688403 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1135 from Patent EP1281758.
ACCESSION AX688403
VERSION AX688403.1 GI:29411105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1135 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2942 TTTTGACTTCTCAGCCA 2958
|||||
Db 17 TTTTGACTTCTCAGCCA 1

RESULT 302
AX688404/c
LOCUS AX688404 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1136 from Patent EP1281758.
ACCESSION AX688404
VERSION AX688404.1 GI:29411106
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1136 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"

Db 17 GCTCCAGCACCAGCAGC 1

RESULT 305
AX690659/c
LOCUS AX690659 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3391 from Patent EP1281758.
ACCESSION AX690659
VERSION AX690659.1 GI:29413540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3391 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCACCAGCAGC 991
Db 17 TGCTCCAGCACCAGCAGC 1

RESULT 306
AX694226
LOCUS AX694226 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 6958 from Patent EP1281758.
ACCESSION AX694226
VERSION AX694226.1 GI:29417356
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 6958 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1664 TCACCTTTGCCACTTCA 1680
Db 1 TCACCTTGCACCTTA 17

RESULT 307
AX724636
LOCUS AX724636 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2323 from Patent WO03025176.
ACCESSION AX724636
VERSION AX724636.1 GI:30503979

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2323 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2756 GGTCGAATCTCAGACC 2772
Db 1 GATCTGAATCTCAGAAC 17

RESULT 308
AX724729
LOCUS AX724729 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2416 from Patent WO03025176.
ACCESSION AX724729
VERSION AX724729.1 GI:30504072
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2416 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1982 GATCAGATAAACCCACA 1998
Db 1 GATCAGATAAACCCATCA 17

RESULT 309
AX725477/c
LOCUS AX725477 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3164 from Patent WO03025176.
ACCESSION AX725477
VERSION AX725477.1 GI:30504820
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025176-A 3164 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 998 CAGCCTACCACTGGTC 1014
Db 17 CAGCCACCACTGATC 1

RESULT 310
AX725518/c
LOCUS AX725518 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3205 from Patent WO03025176.
ACCESSION AX725518
VERSION AX725518.1 GI:30504861
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 3205 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1222 GCATAAGCCTCAGGATC 1238
Db 17 GGATAAGCCCGAGATC 1

RESULT 311
AX725925/c
LOCUS AX725925 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3612 from Patent WO03025176.
ACCESSION AX725925
VERSION AX725925.1 GI:30505268
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 3612 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025176-A 3164 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3013 TTTATTGAAGTCAGATC 3029
Db 17 TTTATTGAAGTCAGATC 1

RESULT 312
AX727570
LOCUS AX727570 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5257 from Patent WO03025176.
ACCESSION AX727570
VERSION AX727570.1 GI:30506913
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5257 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1909 GATCATGCAGCAGAAC 1925
Db 1 GATCATGCAGCAGAAC 17

RESULT 313
AX729275/c
LOCUS AX729275 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 909 from Patent WO03025175.
ACCESSION AX729275
VERSION AX729275.1 GI:30508618
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 909 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1747 ACAACAGACAGCAGGATC 1763
Db 17 ACAACAGACATAGGATC 1

RESULT 314
AX731043
LOCUS AX731043 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2677 from Patent WO03025175.
ACCESSION AX731043
VERSION AX731043.1 GI:30510386
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 2677 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 536 GATCCTGAGCTGCAGGA 552
Db 1 GATCCTGAGCTGCCGAA 17

RESULT 315
AX731511
LOCUS AX731511 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3145 from Patent WO03025175.
ACCESSION AX731511
VERSION AX731511.1 GI:30510854
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3145 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1909 GATCATGACGAGAAAC 1925
Db 1 GATCCTGGAACAGAAAC 17

RESULT 316

AX731550/c
LOCUS AX731550 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3184 from Patent WO03025175.
ACCESSION AX731550
VERSION AX731550.1 GI:30510893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3184 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3417 AAAAAGGTAAAGAAC 3433
Db 17 AAAAAGGTAAAGATC 1

RESULT 317
AX731740/c
LOCUS AX731740 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3374 from Patent WO03025175.
ACCESSION AX731740
VERSION AX731740.1 GI:30511083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3374 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2186 AGAATGCCATCATATC 2202
Db 17 AGAAGGCCATCATGATC 1

RESULT 318
AX734784/c
LOCUS AX734784 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 374 from Patent WO03025177.
ACCESSION AX734784
VERSION AX734784.1 GI:30514061
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
source	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	523 AGACAACTGATGGATC 539
Db	17 AGCACAACGTGTGGATC 1
LOCUS	AX735383 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 973 from Patent WO03025177.
ACCESSION	AX735383
VERSION	AX735383.1 GI:30514660
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 973 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
source	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	523 AGACAACTGATGGATC 539
Db	17 AGCACAACGTGTGGATC 1
LOCUS	AX735531 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1121 from Patent WO03025177.
ACCESSION	AX735531
VERSION	AX735531.1 GI:30514808
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 973 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
source	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	523 AGACAACTGATGGATC 539
Db	17 AGCACAACGTGTGGATC 1
LOCUS	AX735531 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1121 from Patent WO03025177.
ACCESSION	AX735531
VERSION	AX735531.1 GI:30514808
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 973 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
source	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	523 AGACAACTGATGGATC 539
Db	17 AGCACAACGTGTGGATC 1
LOCUS	AX735531 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1121 from Patent WO03025177.
ACCESSION	AX735531
VERSION	AX735531.1 GI:30514808
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 973 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
source	1. .17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Qy	523 AGACAACTGATGGATC 539
Db	17 AGCACAACGTGTGGATC 1
LOCUS	AX735531 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1121 from Patent WO03025177.
ACCESSION	AX735531
VERSION	AX735531.1 GI:30514808
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1
TITLE	Telerman, A., Amson, R. and Tuijinder, M.
JOURNAL	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 973 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR) Location/Qualifiers
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Query Match	0.4%; Score 13.8; DB 1; Length 17;
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Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	523 AGACAACTGATGGATC 539
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LOCUS	AX735531 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1121 from Patent WO03025177.
ACCESSION	AX735531
VERSION	AX735531.1 GI:30514808
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homin


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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1339 GATCCCTTCTGTTTGC 1355
Db 1 GATCCTTTCTGTTTGC 17

RESULT 323
AX736569/c
LOCUS AX736569 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2159 from Patent WO03025177.
ACCESSION AX736569
VERSION AX736569.1 GI:30515857
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2159 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3066 ATGAATCTTGGGGAAC 3082
Db 17 ATGATACTTGGGGATC 1

RESULT 324
AX736585
LOCUS AX736585 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2175 from Patent WO03025177.
ACCESSION AX736585
VERSION AX736585.1 GI:30515873
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2175 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2898 GTTCCAGGCTTTTCAA 2914
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Db 1 GATCCAGGCTTTTCAA 17

RESULT 325
AX736642
LOCUS AX736642 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2232 from Patent WO03025177.
ACCESSION AX736642
VERSION AX736642.1 GI:30515930
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2232 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1662 GGTCACTTTGCCACTT 1678
Db 1 GATCACCTTGCCACTT 17

RESULT 326
AX738717
LOCUS AX738717 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4307 from Patent WO03025177.
ACCESSION AX738717
VERSION AX738717.1 GI:30518007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4307 27-MAR-2003;
Molecular Engines Laboratories (FR)
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source Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1687 GCTCTACTTCAGCAAA 1703
Db 1 GATCCTACTTCAGAAAA 17

RESULT 327
AX739573/c
LOCUS AX739573 17 bp DNA linear PAT 08-MAY-2003
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DEFINITION Sequence 5163 from Patent WO03025177.
ACCESSION AX739573
VERSION AX739573.1 GI:30518870
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5163 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1918 GCAGAACAGCAGCACTTC 1934
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Db 17 GCAGAACAGCAGCAATC 1

RESULT 328
AX745081/c
LOCUS AX745081 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1046 from Patent WO03031621.
ACCESSION AX745081
VERSION AX745081.1 GI:30723748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang,J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 1046 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2367 CAAGTAATAATAACAAT 2383
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Db 17 CAATCATATAACAAT 1

RESULT 329
AX754462
LOCUS AX754462 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 809 from Patent WO03037931.
ACCESSION AX754462
VERSION AX754462.1 GI:32167159
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumour suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 809 15-MAY-2003;
Molecular Engines Laboratories (FR)
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/organism="Homo sapiens"
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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QY 2756 GGTCTGAATCTCAGACC 2772
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Db 17 GTTCTGAATCTCAGATC 1

RESULT 331
AX758667/c
LOCUS AX758667 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1988 from Patent WO03040369.
ACCESSION AX758667
VERSION AX758667.1 GI:32253283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1988 15-MAY-2003;
Molecular Engines Laboratories (FR)
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QY 2756 GGTCTGAATCTCAGACC 2772
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Db 17 GTTCTGAATCTCAGATC 1
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

LOCUS AX761769 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 5090 from Patent WO03040369.
ACCESSION AX761769
VERSION AX761769.1 GI:32256385
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5090 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
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Qy 55 GATCGCGTGCACAAATC 71
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Db 1 GATCGTGTGCACAAACC 17
RESULT 337
LOCUS AX762326/c 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 5647 from Patent WO03040369.
ACCESSION AX762326
VERSION AX762326.1 GI:32256942
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5647 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
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Qy 335 ATTTATCCAAACAGAAC 3351
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Db 17 ATTTCTCCAACAGATC 1
RESULT 338
LOCUS AX762501/c 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 5822 from Patent WO03040369.
ACCESSION AX762501
VERSION AX762501.1 GI:32257117
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5822 15-MAY-2003;
Molecular Engines Laboratories (FR)
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Qy 1918 GCAGAAACAGCAACTTC 1934
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Db 17 GCAGAAACAGCAAGATC 1
RESULT 339
LOCUS AX762673 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 5994 from Patent WO03040369.
ACCESSION AX762673
VERSION AX762673.1 GI:32257289
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5994 15-MAY-2003;
Molecular Engines Laboratories (FR)
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Qy 2898 GTTCCAGGGCTTTTCAA 2914
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Db 1 GATCCAGGGCTTTTCAA 17
RESULT 340
LOCUS AX773291/c 17 bp DNA PAT 09-JUL-2003
DEFINITION Sequence 265 from Patent WO03045426.
ACCESSION AX773291
VERSION AX773291.1 GI:32485234
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
AUTHORS T-cell epitopes in carboxypeptidase g2
TITLE Patent: WO 03045426-A 265 05-JUN-2003;
JOURNAL MERCK PATENT GmbH (DE)
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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Qy 3590 TTGTTGGAGTAACCAA 3606
Db 17 TTCTTTGGAGTAACCAA 1

RESULT 341
AX773307
LOCUS AX773307 17 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 281 from Patent WO03045426.
ACCESSION AX773307
VERSION AX773307.1 GI:32485250
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
TITLE T-cell epitopes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 281 05-JUN-2003;
MERCK PATENT GmbH (DE)
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3590 TTGTTGGAGTAACCAA 3606
Db 1 TTCTTTGGAGTAACCAA 17

RESULT 342
AX783646/c
LOCUS AX783646 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 1977 from Patent WO03050284.
ACCESSION AX783646
VERSION AX783646.1 GI:32951495
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 1977 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
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AX926726
LOCUS AX926726 17 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 9 from Patent WO03085133.
ACCESSION AX926726
VERSION AX926726.1 GI:40247023
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Nagaraju,J.G.
TITLE Novel f1ssr-pcr primers and method of identifying genotyping
diverse genomes of plant and animal systems including rice
varieties, a kit thereof
JOURNAL Patent: WO 03085133-A 9 16-OCT-2003;
Centre for DNA Fingerprinting and Diagnostics, Centre for; the
Department of Biotechnology, Ministry of Science & Technology (IN)
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source Location/Qualifiers
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Qy 1554 AACACAGCAGCAGCAG 1570
Db 1 AATACAGCAGCAGCAG 17

RESULT 344
BD075172
LOCUS BD075172 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for assessing cardiovascular status and compositions for
use thereof.
ACCESSION BD075172
VERSION BD075172.1 GI:22620775
KEYWORDS JP 2001519660-A/45.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
TITLE Methods for assessing cardiovascular status and compositions for
use thereof
JOURNAL Patent: JP 2001519660-A 45 23-OCT-2001;
EURONA MEDICAL AB
COMMENT OS Artificial Sequence
PN JP 2001519660-A/45
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PR 04-APR-1997 US 60/042930
PI LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM
PC C12Q1/68,C07K14/72,C07K14/575,C12N9/48
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QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGGCGGCAGCAGCAACA 17

RESULT 345
BD075178 17 bp DNA linear PAT 27-AUG-2002
LOCUS Methods for assessing cardiovascular status and compositions for
DEFINITION use thereof.
ACCESSION BD075178
VERSION BD075178.1 GI:22620781
KEYWORDS JP 2001519660-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND COMPOSITIONS FOR
USE THEREOF
Patent: JP 2001519660-A 51 23-OCT-2001;
EUROPA MEDICAL AB
OS Artificial Sequence
PN JP 2001519660-A/51
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PI 04-APR-1997 US 60/042930
PI LEIF TOREBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM
PC C12Q1/68,C07K14/72,C07K14/575,C12N9/48
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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QY 1399 ACAGCAGCAGCAGCAGC 1415
DB 1 ACAGCAGCAGCAGCAGC 17

Search completed: August 16, 2005, 12:48:45
Job time : 15 secs

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QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGGCGGCAGCAGCAACA 17

RESULT 346
BD132158 17 bp DNA linear PAT 18-SEP-2002
LOCUS DNA diagnosis method based on mass spectrometry.
DEFINITION
ACCESSION BD132158
VERSION BD132158.1 GI:23227103
KEYWORDS JP 2002507883-A/90.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Room,D.V.D., Jurinke,C. and Rupert,A.
DNA diagnosis method based on mass spectrometry
Patent: JP 2002507883-A 90 12-MAR-2002;
SEQUENOM INC
PN JP 2002507883-A/90
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR

FEATURES
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1. .17
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Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
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 High quality sequence stop: 27.

FEATURES

Location/Qualifiers
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 /clone="UUGC1M0172120"
 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: K column: 09
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

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 Db 27 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1

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ACCESSION AZ779573
 VERSION AZ779573.1 GI:12910362
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Query Match 0.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.4; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GCAGCAGCAGCAGCAGCAGCAGCA 24

RESULT 4

AZ831993
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 DEFINITION 2M0112M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112M01 F, genomic survey sequence.

ACCESSION AZ831993
 VERSION AZ831993.1 GI:13001901
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0112 row: M column: 01
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0112M01"
 /sex="Male"

source

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
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Query Match 0.5%; Score 17; DB 1; Length 21;
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 Db 5 CAGCAACAGCAGCAGCA 21

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 Job time : 0.001 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 19:24:35 ; Search time 130 Seconds
(without alignments)
918.832 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22.6	31.0	601	4	US-09-949-016-135532	Sequence 135532, A
22.6	31.0	1506	4	US-09-949-016-2284	Sequence 2284, Ap
22.6	31.0	1893	1	US-08-271-667B-5	Sequence 5, Appl
22.6	31.0	1893	3	US-08-165-889C-18	Sequence 18, Appl
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ALIGNMENTS

RESULT 1

US-09-949-016-17375
; Sequence 17375, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17375
; LENGTH: 84296
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(84296)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17375

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Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 11530 AGGTTAACTACTGTTAACTTTGACGAGGTGGTTAACT 11569

RESULT 2

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; Sequence 130, Application US/08311731A
; Patent No. 6863286
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: C0044/7125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 130:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36941 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: MYCOBACTERIUM LEPRAE

US-08-311-731A-130

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Best Local Similarity 65.0%; Pred. No. 16;

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US-09-949-016-82614

; Sequence 82614, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 82614

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-82614

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Db 123 AATCAGCTGTTGAAGCTTGTGATGTGTACGTAGTTCTCGTGCCATGATTTT 175

RESULT 4

US-09-949-016-82615

; Sequence 82615, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20


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US-09-949-016-12822

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; LENGTH: 256176
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; NAME/KEY: misc feature
; LOCATION: (1)_(256176)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15524

Query Match      35.1%; Score 25.6; DB 4; Length 256176;
Best Local Similarity 77.5%; Pred. No. 56;
Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 14 GGTAACTACTCTGTGAAGCTTGACGAGTGGTTAACTTA 53
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Db 230491 GGGTAGGAACCTGTTGTAGCTAAAGCAGGTGGTAAATGTA 230452

RESULT 10
US-09-949-016-58/c
; Sequence 58, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 5798
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (698)..(1468)
; OTHER INFORMATION: unknown D2
US-09-809-016-58673

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCGAGGAGATAGGTTAACTACTCTGTTGAAGCTTGACGAGTGGTTAACTTCTCT 59
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Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCT 3119

RESULT 11
US-09-809-665A-60/c
; Sequence 60, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5798
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (698)..(1468)
; OTHER INFORMATION: unknown D2
US-09-809-665A-60

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCGAGGAGATAGGTTAACTACTCTGTTGAAGCTTGACGAGTGGTTAACTTCTCT 59
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCT 3119

RESULT 12
US-09-949-016-58673
; Sequence 58673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 5798
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; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2886)..(4446)
; OTHER INFORMATION: unknown D1
US-09-809-665A-58

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCGAGGAGATAGGTTAACTACTCTGTTGAAGCTTGACGAGTGGTTAACTTCTCT 59
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Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCT 3119

RESULT 11
US-09-809-665A-60/c
; Sequence 60, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5798
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (698)..(1468)
; OTHER INFORMATION: unknown D2
US-09-809-665A-60

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCGAGGAGATAGGTTAACTACTCTGTTGAAGCTTGACGAGTGGTTAACTTCTCT 59
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Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCT 3119

RESULT 12
US-09-949-016-58673
; Sequence 58673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 5798
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; SEQ ID NO 58673
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58673

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 9 AGATAGTTAACTACCTGTTGAAGCTTGACAGCTGTTAATCTATCTCTGCTAACAGT 68
Db 524 AGCTAGATGATGAGCCTGGTGAAGCGCAGGCTGTTGCTAATATTTCTCTTTTCACAGT 583
Qy 69 TT 70
Db 584 CT 585

RESULT 13

US-09-949-016-58674
; Sequence 58674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58674
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58674

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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Qy 69 TT 70
Db 278 CT 279

RESULT 14

US-09-949-016-58675
; Sequence 58675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58675
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58675

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 9 AGATAGTTAACTACCTGTTGAAGCTTGACAGCTGTTAATCTATCTCTGCTAACAGT 68
Db 46 AGCTAGATGATGAGCCTGGTGAAGCGCAGGCTGTTGCTAATATTTCTCTTTTCACAGT 105
Qy 69 TT 70
Db 106 CT 107

RESULT 15

US-09-949-016-153205
; Sequence 153205, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153205
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-153205

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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Db 160 TTTCAGGTGATTTGTAATACTACTGAAAGTGGCTGGTGGTCTCATCCCTGTAATC 219
Qy 61 CTAACAGTTT 70
Db 220 CCAACACTTT 229

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Job time : 135 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
744.708 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	29	39.7	101507	20	US-10-698-070-2
C 4	28.2	38.6	600	22	US-10-719-993-6772
C 5	28	38.4	28	21	Sequence 41910, A
C 6	28	38.4	3763	21	US-10-698-070-5
C 7	28	38.4	5419	19	US-10-698-070-1
					Sequence 3, Appli

Sequence 4710, Ap	US-10-956-157-4710	5458	38.4	28	C 8
Sequence 5783, Ap	US-10-425-114-5783	1240	36.7	26.8	C 9
Sequence 3768, A	US-10-425-114-3768	18	36.7	26.8	C 10
Sequence 2243, A	US-10-425-115-2243	20	36.7	26.8	C 11
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Sequence 3, Appli	US-10-479-546-3	19	36.4	26.6	C 13
Sequence 4710, Ap	US-10-956-157-4710	21	36.4	26.6	C 14
Sequence 655, App	US-10-087-192-655	15	36.4	26.6	C 15
Sequence 146, App	US-10-322-281-146	19	36.4	26.6	C 16
Sequence 163609,	US-10-425-115-163609	17	36.2	26.4	C 17
Sequence 392, App	US-09-764-864-392	9	35.3	25.8	C 18
Sequence 1915, Ap	US-10-104-047-1915	17	35.3	25.8	C 19
Sequence 1416, Ap	US-10-108-260A-1416	17	35.3	25.8	C 20
Sequence 739, App	US-10-723-860-739	20	34.8	25.4	C 21
Sequence 58, App	US-09-809-665A-58	11	34.8	25.4	C 22
Sequence 60, Appl	US-09-809-665A-60	11	34.8	25.4	C 23
Sequence 58, Appl	US-10-854-299-58	11	34.8	25.4	C 24
Sequence 60, Appl	US-10-854-299-60	21	34.8	25.4	C 25
Sequence 32, Appl	US-10-336-091-32	17	34.8	25.4	C 26
Sequence 27658, A	US-10-242-535A-27658	17	34.8	25.4	C 27
Sequence 16484, A	US-10-085-783A-27658	18	34.5	25.2	C 28
Sequence 5727, Ap	US-10-741-601-5727	19	34.5	25.2	C 29
Sequence 201892,	US-10-027-632-201892	13	34.2	25.2	C 30
Sequence 201893,	US-10-027-632-201893	13	34.2	25.2	C 31
Sequence 201894,	US-10-027-632-201894	13	34.2	25.2	C 32
Sequence 201892,	US-10-027-632-201892	13	34.2	25.2	C 33
Sequence 201893,	US-10-027-632-201893	13	34.2	25.2	C 34
Sequence 201894,	US-10-027-632-201894	13	34.2	25.2	C 35
Sequence 201894,	US-10-027-632-201894	17	34.2	25.2	C 36
Sequence 155258,	US-10-425-115-155258	20	34.0	24.8	C 37
Sequence 622, App	US-10-723-860-622	321	33.7	24.6	C 38
Sequence 9, Appli	US-10-813-805-9	1201	33.7	24.6	C 39
Sequence 5, Appli	US-10-432-985-5	21	33.7	24.6	C 40
Sequence 5231, Ap	US-10-956-157-5231	18	33.7	24.6	C 41
Sequence 3708, Ap	US-09-880-107-3708	9	33.7	24.6	C 42
Sequence 586, App	US-10-505-680-586	21	33.7	24.6	C 43
Sequence 5264, Ap	US-10-723-860-5264	20	33.7	24.6	C 44
Sequence 122, App	US-10-732-620-122	21	33.7	24.6	C 45
Sequence 70, Appl	US-10-331-053-70	19	33.7	24.6	C 46
Sequence 1, Appli	US-09-363-959-1	9	33.7	24.6	C 47
Sequence 139896,	US-10-425-115-139896	20	33.4	24.4	C 48
Sequence 14160, A	US-09-864-761-14160	9	33.4	24.4	C 49
Sequence 226524,	US-10-027-632-226524	13	33.4	24.4	C 50
Sequence 13761, A	US-10-027-632-226524	591	33.4	24.4	C 51
Sequence 4741, Ap	US-10-767-701-13761	19	33.4	24.4	C 52
Sequence 96175, A	US-10-425-115-4741	1985	33.4	24.4	C 53
Sequence 11, Appl	US-10-437-963-96175	4344	33.4	24.4	C 54
Sequence 11, Appl	US-10-072-977-11	5402	33.4	24.4	C 55
Sequence 11, Appl	US-10-027-983-11	392000	33.4	24.4	C 56
Sequence 1, Appli	US-10-448-753-11	17	33.4	24.4	C 57
Sequence 15735, A	US-09-933-267A-1	9	33.4	24.4	C 58
Sequence 15735, A	US-10-027-632-15735	728	33.2	24.2	C 59
Sequence 3183, Ap	US-10-027-632-15735	728	33.2	24.2	C 60
Sequence 57350, A	US-10-260-238-3183	862	33.2	24.2	C 61
Sequence 29562, A	US-10-437-963-57350	971	33.2	24.2	C 62
Sequence 129082,	US-10-369-493-29562	1118	33.2	24.2	C 63
Sequence 91601, A	US-10-424-599-129082	1188	33.2	24.2	C 64
Sequence 459, App	US-10-424-599-91601	2169	33.2	24.2	C 65
Sequence 9, Appli	US-10-437-963-459	2934	33.2	24.2	C 66
Sequence 59, Appl	US-10-024-623-9	3357	33.2	24.2	C 67
Sequence 54, Appl	US-10-154-419-59	3357	33.2	24.2	C 68
Sequence 3, Appli	US-10-146-733-54	3357	33.2	24.2	C 69
Sequence 39, Appl	US-09-921-159-3	3408	33.2	24.2	C 70
Sequence 7, Appli	US-10-467-685-39	3760	33.2	24.2	C 71
Sequence 57, Appl	US-10-024-623-7	4632	33.2	24.2	C 72
Sequence 23, Appl	US-10-154-419-57	4632	33.2	24.2	C 73
Sequence 52, Appl	US-10-146-733-52	4632	33.2	24.2	C 74
Sequence 34, Appl	US-10-352-684A-23	4632	33.2	24.2	C 75
Sequence 7351, Ap	US-10-336-091-34	9144	33.2	24.2	C 76
Sequence 78, Appl	US-09-764-891-7351	22073	33.2	24.2	C 77
Sequence 78, Appl	US-10-737-082-78	64275	33.2	24.2	C 78
Sequence 1, Appli	US-10-765-790-78	64275	33.2	24.2	C 79
Sequence 1, Appli	US-09-847-513A-1	105184	33.2	24.2	C 80

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C 83	24	32.9	579	20	US-10-357-930-24625	Sequence	24625, A	
C 84	24	32.9	579	20	US-10-357-930-28421	Sequence	28421, A	
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C 86	24	32.9	632	20	US-10-357-930-37168	Sequence	37168, A	
C 87	24	32.9	663	13	US-10-027-633-211618	Sequence	211618, A	
C 88	24	32.9	663	13	US-10-027-633-211619	Sequence	211619, A	
C 89	24	32.9	663	17	US-10-027-633-211618	Sequence	211618, A	
C 90	24	32.9	763	17	US-10-027-633-211619	Sequence	211619, A	
C 91	24	32.9	763	13	US-10-027-633-151369	Sequence	151369, A	
C 92	24	32.9	763	17	US-10-027-633-151369	Sequence	151369, A	
C 93	24	32.9	800	13	US-10-027-633-152922	Sequence	152922, A	
C 94	24	32.9	850	17	US-10-027-633-152922	Sequence	152922, A	
C 95	24	32.9	1431	17	US-10-282-122A-16477	Sequence	16477, A	
C 96	24	32.9	2046	15	US-10-282-122A-1783	Sequence	1783, Ap	
C 97	24	32.9	2516	17	US-10-282-122A-37397	Sequence	37397, A	
C 98	24	32.9	2550	18	US-10-424-599-52068	Sequence	52068, A	
C 99	24	32.9	2622	17	US-10-282-122A-38751	Sequence	38751, A	
C 100	24	32.9	5136	19	US-10-437-963-45475	Sequence	45475, A	

ALIGNMENTS

```

RESULT 1
US-10-698-070-2
; Sequence 2, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kave, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RNAi clone
US-10-698-070-2

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RESULT 2
US-10-698-070-2/c
; Sequence 2, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RNAi clone
US-10-698-070-2

Query Match          65.8%; Score 48; DB 21; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.1e-07;
Matches 54; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTGCGAGGATAGGTTAACTACTCTCTGAAGCTTCAGCAGTGGTAACTATCTATCTCCTG 60
Db 64 TTACGAGGATAGATTAACCACTCTCAAGCTTCACAGGTAGTTAACCTATCTCTG 5

Qy 61 CTA 64
Db 4 CCAA 1

RESULT 3
US-10-719-993-6772/c
; Sequence 6772, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6772
; LENGTH: 101507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6772

Query Match          39.7%; Score 29; DB 20; Length 101507;
Best Local Similarity 67.2%; Pred. No. 13;
Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 10 GATAGGTTAACTACCTGTTGAAGCTTTGAGCAGTGGTAACTATCTATCTCTGCTAAACAGTT 69
Db 92204 GATAGCTTTATACACTGGTACAGCCTGGCAGGTGCTATTCTACCTATTGCTGACTGTG 92145

Qy 70 T 70
Db 92144 T 92144

RESULT 4
US-10-972-079-41910/c
; Sequence 41910, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41910
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894278239_1
US-10-972-079-41910

Query Match 38.6%; Score 28.2; DB 22; Length 600;
Best Local Similarity 61.6%; Pred. No. 4.7;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTACTCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCCTG 60
Db 267 TTGGCTGCAGCTTGATGGAGCTTTGTGGAAATCCAGCAGATGGTTTATTTCTGCTG 208

Qy 61 CTAAACGTTTTTT 73
Db 207 CAAACGTTGTTTT 195

RESULT 5
US-10-698-070-5
; Sequence 5, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiva, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mect1-MAML2 sequence
US-10-698-070-5

Query Match 38.4%; Score 28; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTACTCTGTT 28
Db 1 TTGCAGGAGATAGGTTAACTACTCTGTT 28

RESULT 6
US-10-698-070-1/c
; Sequence 1, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiva, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 3763
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-698-070-1

Query Match 38.4%; Score 28; DB 21; Length 3763;
Best Local Similarity 100.0%; Pred. No. 10;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGCAGGAGATAGGTTAACTACTCTGTT 28
Db 192 TTGCAGGAGATAGGTTAACTACTCTGTT 165

RESULT 7
US-10-479-546-3/c
; Sequence 3, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 5419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-546-3

Query Match 38.4%; Score 28; DB 19; Length 5419;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTACTCTGTT 28
Db 1848 TTGCAGGAGATAGGTTAACTACTCTGTT 1821

RESULT 8
US-10-956-157-4710/c
; Sequence 4710, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4710
; LENGTH: 5458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4710

Query Match 38.4%; Score 28; DB 21; Length 5458;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTACTCTGTT 28
Db 1878 TTGCAGGAGATAGGTTAACTACTCTGTT 1851

RESULT 9
US-10-425-114-5783/c
; Sequence 5783, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

```
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5783
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700472565_FLI
US-10-425-114-5783

Query Match          36.7%; Score 26.8; DB 18; Length 1240;
Best Local Similarity 68.5%; Pred. No. 20;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 12 TAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCGCTTAAC 65
Db 1142 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTGCTCTTAACGCCTCTTTAC 1089

RESULT 10
US-10-425-114-33768/c
; Sequence 33768, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33768
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17168H09_FLI
US-10-425-114-33768

Query Match          36.7%; Score 26.8; DB 18; Length 1984;
Best Local Similarity 68.5%; Pred. No. 23;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 12 TAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCGCTTAAC 65
Db 1854 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTGCTCTTAACGCCTCTTTAC 1801

RESULT 11
US-10-425-115-22243/c
; Sequence 22243, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22243
; LENGTH: 2381
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120288C.1
US-10-425-115-22243

Query Match          36.7%; Score 26.8; DB 20; Length 2381;
Best Local Similarity 68.5%; Pred. No. 25;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 12 TAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCGCTTAAC 65
Db 1994 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTGCTCTTAACGCCTCTTTAC 1941

RESULT 12
US-10-698-070-1
; Sequence 1, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyu, Taketumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 3763
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-698-070-1

Query Match          36.4%; Score 26.6; DB 21; Length 3763;
Best Local Similarity 78.0%; Pred. No. 34;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 27 TTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTTAACAG 67
Db 155 TTGAAAAGAAACAGAGGTAGTTAACTATCTCTGCTCAACAG 195

RESULT 13
US-10-479-546-3
; Sequence 3, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 5419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-546-3
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Query Match 36.4%; Score 26.6; DB 19; Length 5419;
Best Local Similarity 78.0%; Pred. No. 38;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGGTTAACTATCTCTCTCTAACAG 67
|||||
DB 1811 TTGAAGAAGAAACAGGTAGTTACCTATCTCTGCCAACAG 1851

RESULT 14

US-10-956-157-4710
; Sequence 4710, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4710
; LENGTH: 5458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4710

Query Match 36.4%; Score 26.6; DB 21; Length 5458;
Best Local Similarity 78.0%; Pred. No. 38;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGGTTAACTATCTCTCTCTAACAG 67
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DB 1841 TTGAAGAAGAAACAGGTAGTTACCTATCTCTGCCAACAG 1881

RESULT 15

US-10-087-192-655
; Sequence 655, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 655
; LENGTH: 71678
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71678)
; OTHER INFORMATION: n = A, T, C or G
US-10-087-192-655

Query Match 36.4%; Score 26.6; DB 13; Length 71678;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 15 GTTAACTACCTGTGAAGCTTGAGCAGGTGGTTAACTATCTCTCTAACAGTTTT 71
|||||

Db 44626 GTGAACCTTTGTGTGTAGCTGGATCAGGTGGTAGATCTATTTCTAGCACATTGATTT 44682

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Job time : 639 secs

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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 06:55:40 ; Search time 438 Seconds
(without alignments)

986.624 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73
Sequence: 1 ttggcaggagataggtaaac.....tctctgctaacagttttt 73

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
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7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28	38.4	3459	10	Adc59309 DNA encod
C 2	28	38.4	5419	8	Aba00947 MAML2 cod
C 3	26.6	36.4	633	4	Aah32177 Human olf
C 4	26.6	36.4	3459	10	Adc59309 DNA encod
C 5	26.6	36.4	5419	8	Aba00947 MAML2 cod
C 6	26.6	36.4	60747	4	Abli16128 Drosophil
C 7	26.6	36.4	71678	11	Acn44284 Mouse gen
C 8	26.6	36.4	138837	13	Abd33163 Human can
C 9	26.4	36.2	36941	10	Adb74381 Mycobacte
C 10	25.8	35.3	805	4	Aas26213 Human cdn
C 11	25.8	35.3	805	8	Abx73554 Human nov
C 12	25.8	35.3	2874	10	Adb63761 Human the
C 13	25.8	35.3	3352	13	Adc509779 Human th
C 14	25.8	35.3	3363	10	Adc29954 Human nov
C 15	25.8	35.3	3597	13	Adr08359 Full leng
C 16	25.8	35.3	3818	11	Adm02731 Human cdn
C 17	25.8	35.3	3828	10	Adc31891 Human nov
C 18	25.8	35.3	3828	13	Adc11143 Human the
C 19	25.8	35.3	4078	13	Adr06863 Full leng
C 20	25.6	35.1	110000	6	Continuation (8 of

C 94 24.2 33.2 3519 10 ADC10059 Human NOV
 C 95 24.2 33.2 3583 10 ADC10053 Human NOV
 C 96 24.2 33.2 3760 8 RAD47366 Human tra
 C 97 24.2 33.2 4632 6 ABQ74264 Human 544
 C 98 24.2 33.2 4632 10 ADD37480 Human tra
 C 99 24.2 33.2 4632 10 ADK52565 Hematolog
 C 100 24.2 33.2 4632 12 ADI27959 Human 544

ALIGNMENTS

RESULT 1

ID ADC59309/c standard; DNA; 3459 BP.

XX AC ADC59309;

XX DT 18-DEC-2003 (first entry)

XX DE DNA encoding human polypeptide #1.

XX KW Human; ds; polyglutamine disease; gene;
 XX KW genealogical polyglutamine disease; nootropic; anticonvulsant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..3459

XX FT /*tag= a

XX FT /product= "Polypeptide #1"

XX PN JP2002360268-A.

XX PD 17-DEC-2002.

XX PF 03-AUG-2001; 2001JP-00236788.

XX PR 04-AUG-2000; 2000JP-00236839.

XX PR 06-APR-2001; 2001JP-00108723.

XX XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX PA (DAUC) DAIICHI PHARM CO LTD.

XX DR WPI; 2003-516153/49.

XX DR P-PSDB; ADC59310.

XX PT A genealogical line diagnostic marker for polyglutamine disease, useful
 PT in the diagnosis, prevention and/or treatment, comprises a polyglutamine
 PT related gene and its encoded polypeptide.

XX PS Claim 1; SEQ ID NO 1; 72pp; Japanese.

XX CC The invention discloses polyglutamine disease related genes and their
 CC encoded polypeptides. Also claimed is a recombinant vector,
 CC transformants, preparation of the polynucleotides and resultant
 CC polypeptides, diagnostic methods and a kit. The genes and encoded
 CC polypeptides are useful in the diagnosis, prevention and treatment of
 CC genealogical polyglutamine disease. The sequence presented is a DNA
 CC encoding one of the polypeptides of the invention.

XX SQ Sequence 3459 BP; 1023 A; 1031 C; 767 G; 638 T; 0 U; 0 Other;

Query Match 38.4%; Score 28; DB 10; Length 3459;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACCTGTT 28

Db 563 TTGGCAGGAGATAGGTTAACTACCTGTT 536

RESULT 2

ABA00947/c
 ID ABA00947 standard; cDNA; 5419 BP.

XX AC ABA00947;

XX DT 28-APR-2003 (first entry)

XX DE MAML2 coding sequence.

XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
 KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
 KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour;
 KW chromosome 11q21; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1286..4747

XX FT /*tag= a

XX FT /product= "MAML2"

XX PN WC2003004645-A1.

XX PD 16-JAN-2003.

XX PF 03-JUL-2002; 2002WO-US021344.

XX PR 03-JUL-2001; 2001US-0302788P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kaye FJ, Tonon G;

XX DR WPI; 2003-210364/20.

XX DR P-PSDB; AAG79910.

XX PT Screening a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 PT translocation, useful for treating mucoepidermoid carcinoma comprises
 PT detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
 PT a tissue sample.

XX PS Disclosure; Page 57-58; 65pp; English.

XX CC This sequence encodes human MAML2. The MAML2 gene contains 5 exons and
 CC spans 340 kb at human 11q21. MAML2 exon 1 is contained within the BAC
 CC RP11-16K5, while exon 2 was separated by a 270 kb intron 1, confirming
 CC the MAML2 was disrupted by a chromosomal breakpoint near the 3' end of
 CC the large MAML2 intron 1. The method of the invention allows for
 CC screening of a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 CC translocation and comprises detecting the presence of MECT1-MAML2
 CC chimeric nucleic acid or protein in a tissue sample. Direct sequencing
 CC demonstrated a chimeric RNA species representing exon 1 of MECT1 fused in
 CC frame to MAML2 exons 2-5. The method of the invention is useful for
 CC diagnosing and treating cancer, including cancer that involves the NOTCH
 CC pathway, particularly cancer of mucoepidermoid carcinoma, the most common
 CC malignant salivary gland tumour

XX SQ Sequence 5419 BP; 1627 A; 1438 C; 1163 G; 1191 T; 0 U; 0 Other;

Query Match 38.4%; Score 28; DB 8; Length 5419;

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACCTGTT 28

Db 1848 TTGGCAGGAGATAGGTTAACTACCTGTT 1821

RESULT 3

AAH32177/c

ID AAH32177 standard; DNA; 633 BP.

XX AC AAH32177;


```

XX DT 30-JUL-2001 (first entry)
XX DE Human olfactory receptor polynucleotide, SEQ ID NO: 750.
XX KW Human; olfactory receptor; OR; primary scent determination;
XX KW secondary scent determination; polypeptide library; odour receptor;
XX KW scent profile; scent fingerprint; scent representation; ds.
XX OS Homo sapiens.
XX PN WO200127158-A2.
XX PD 19-APR-2001.
XX PF 06-OCT-2000; 2000WO-US027582.
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX PT New polynucleotides which encode polypeptides involved in olfactory
XX PT sensation for identifying olfactory agonists and antagonists.
XX PS Claim 8; Page 481-482; 1857pp; English.
XX CC The present sequence is one of a number of isolated polynucleotides which
XX CC encode polypeptides involved in olfactory sensation. The polynucleotides
XX CC can be used in screening for olfactory agonists and antagonists. The
XX CC methods allow for the determination of primary scents and the
XX CC identification of the odour receptors used to detect these primary
XX CC scents. The methods also enable determination of secondary scents and the
XX CC identification of combinations of odour receptors that are involved in
XX CC detecting such secondary scents. This enables the construction of a scent
XX CC representation (also called a scent fingerprint or scent profile), which
XX CC may be used to re-create and edit scents. Libraries of olfactory
XX CC receptors are useful for determining the interaction pattern of a
XX CC composition with the receptors, and can be used for determining
XX CC differences in the olfactory faculties of different individuals
XX SQ Sequence 633 BP; 138 A; 157 C; 135 G; 203 T; 0 U; 0 Other;

Query Match 36.4%; Score 26.6; DB 4; Length 633;
Best Local Similarity 63.1%; Pred. No. 11;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 8 GAGATAGTTAACTACCTGTGAAGCTTGAGCTTGAGCAGGTGTTAATCTATCTCTCTTAACAG 67
DB 111 GACAAAGATAACTGATGCTGATCTCTGTGAAGGAGATAGTTCTATCTTCGCAACCAA 52

QY 68 TTTT 72
DB 51 GTTCT 47

RESULT 4
ADCS9309
ID ADCS9309 standard; DNA; 3459 BP.
XX AC ADCS9309;
XX DT 18-DEC-2003 (first entry)
XX DE DNA encoding human polypeptide #1.
XX KW Human; ds; polyglutamine disease; gene;
XX KW genealogical polyglutamine disease; nootropic; anticonvulsant.

XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1286..4747
XX FT /*tag= a
XX FT /product= "MAML2"
XX PN WO2003004645-A1.
XX PD 16-JAN-2003.

XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1..3459
XX FT /*tag= a
XX FT /product= "Polypeptide #1"
XX PN JP2002360268-A.
XX PD 17-DEC-2002.
XX PF 03-AUG-2001; 2001JP-00236788.
XX PR 04-AUG-2000; 2000JP-00236839.
XX PR 06-APR-2001; 2001JP-00108723.
XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX PA (DAUC ) DAICHI PHARM CO LTD.
XX WPI; 2003-516153/49.
XX DR P-PSDB; ADCS9310.
XX PT A genealogical line diagnostic marker for polyglutamine disease, useful
XX PT in the diagnosis, prevention and/or treatment, comprises a polyglutamine
XX PT related gene and its encoded polypeptide.
XX PS Claim 1; SEQ ID NO 1; 72pp; Japanese.
XX CC The invention discloses polyglutamine disease related genes and their
XX CC encoded polypeptides. Also claimed is a recombinant vector,
XX CC transformants, preparation of the polynucleotides and resultant
XX CC polypeptides, diagnostic methods and a kit. The genes and encoded
XX CC polypeptides are useful in the diagnosis, prevention and treatment of
XX CC genealogical polyglutamine disease. The sequence presented is a DNA
XX CC encoding one of the polypeptides of the invention.
XX SQ Sequence 3459 BP; 1023 A; 1031 C; 767 G; 638 T; 0 U; 0 Other;

Query Match 36.4%; Score 26.6; DB 10; Length 3459;
Best Local Similarity 78.0%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGTTAATCTATCTCTCTTAACAG 67
DB 526 TTGAAAGAAACAGGTAGTTAACTATCTCTCTTAACAG 566

RESULT 5
ABA00947
ID ABA00947 standard; cDNA; 5419 BP.
XX AC ABA00947;
XX DT 28-APR-2003 (first entry)
XX DE MAML2 coding sequence.
XX KW Consensus sequence: NOTCH; Mastermind-like; gene family; screening; t(11;
XX KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
XX KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour;
XX KW chromosome 11q21; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1286..4747
XX FT /*tag= a
XX FT /product= "MAML2"
XX PN WO2003004645-A1.
XX PD 16-JAN-2003.

```

XX 03-JUL-2002; 2002WO-US021344.
XX
XX
XX 03-JUL-2001; 2001US-0302788P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kaye FJ, Tonon G;
XX WPI; 2003-210364/20.
XX P-PSDB; AAG79910.
XX
XX Screening a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
XX translocation, useful for treating mucoepidermoid carcinoma comprises
XX PT detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
XX a tissue sample.
XX
XX Disclosure; Page 57-58; 65pp; English.
XX
XX This sequence encodes human MAML2. The MAML2 gene contains 5 exons and
XX spans 340 kb at human 11q21. MAML2 exon 1 is contained within the BAC
XX RP11-16K5, while exon 2 was separated by a 270 kb intron 1, confirming
XX the MAML2 was disrupted by a chromosomal breakpoint near the 3' end of
XX the large MAML2 intron 1. The method of the invention allows for
XX screening of a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
XX translocation and comprises detecting the presence of MECT1-MAML2
XX chimeric nucleic acid or protein in a tissue sample. Direct sequencing
XX demonstrated a chimeric RNA species representing exon 1 of MECT1 fused in
XX -frame to MAML2 exons 2-5. The method of the invention is useful for
XX diagnosing and treating cancer, including cancer that involves the NOTCH
XX pathway, particularly cancer of mucoepidermoid carcinoma, the most common
XX malignant salivary gland tumour
XX
XX Sequence 5419 BP; 1627 A; 1438 C; 1163 G; 1191 T; 0 U; 0 Other;
SQ
Query Match 36.4%; Score 26.6; DB 8; Length 5419;
Best Local Similarity 78.0%; Pred. No. 19;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 27 TTGAAGCTTGACGAGTGGTTAACTATCTCTCTGCTACAG 67
DB 1811 TTGAAAGAAACACGGTAGTTAACTATCTCTCTGCAACAG 1851
RESULT 6
ABL16128/c
ID ABL16128 standard; cDNA; 60747 BP.
XX
XX ABL16128;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 42866.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX

DR P-PSDB; ABB72025.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX
XX Claim 1; SEQ ID NO 42866; 2ipp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60747 BP; 18756 A; 12091 C; 12746 G; 17154 T; 0 U; 0 Other;
SQ
Query Match 36.4%; Score 26.6; DB 4; Length 60747;
Best Local Similarity 60.3%; Pred. No. 38;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 TTGCGAGGAGTAGGTTAACTACCTGTTCAGGCTTGACGAGGTGGTTAACTATCTCTG 60
DB 49416 TTGGTAACAGATAGATTAGTGTTAATCTGATCAGGATTTTTTTTAAATTTTG 49357
QY 61 CTACAGTTTTTT 73
DB 49356 CGTAGCTTTCTTT 49344
RESULT 7
ACN44284
ID ACN44284 standard; DNA; 71678 BP.
XX
XX ACN44284;
XX
XX 18-NOV-2004 (first entry)
XX
XX Mouse genomic sequence MCG16994.
XX
XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
XX
XX Mus musculus.
XX
XX WO2003073826-A2.
XX
XX 12-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WPI; 2003-328604/31.
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX
XX Claim 1; SEQ ID NO 655; Opp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
XX are associated with carcinomas. The sequences are useful for: (i) for
XX screening drug candidates; (ii) for screening of bioactive agent capable
XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX a bioactive agent capable of modulating the activity of CAP; (iv) for
XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX

CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US200218586A1, for which no sequence data was published
XX
SQ Sequence 71678 BP; 20309 A; 14954 C; 15127 G; 20103 T; 0 U; 1185 Other;
Query Match 36.4%; Score 26.6; DB 11; Length 71678;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 15 GTTAACCTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTCTCTCAACAGTTT 71
DB 44626 GTGACCTTGTGGTGTAGCTGATCAGTGTGATCTATTTCTAGCACATTGATT 44682
RESULT 8
ABD33163
ID ABD33163 standard; DNA; 138837 BP.
XX
AC ABD33163;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated (CA) gene HD07-022.
XX
KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW db; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN W02004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PS (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-499109/47.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Claim 16; SEQ ID NO 146; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 138837 BP; 34853 A; 26094 C; 29642 G; 41293 T; 0 U; 6955 Other;

Query Match 36.4%; Score 26.6; DB 13; Length 138837;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 17 TAACTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTCTCTCAACAGTTT 73
DB 58591 TTAGTACTATCTCAAGCTTGTCTAGCTGGTAACTGTAATGCCCTGTAAAAATTTT 58647
RESULT 9
ADB74381
ID ADB74381 standard; DNA; 36941 BP.
XX
AC ADB74381;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mycobacterium leprae DNA #15.
XX
KW Non-naturally occurring peptide; anion pump protein; tuberculosis;
KW hypersensitivity reaction; tuberculostatic; gene; ds.
XX
OS Mycobacterium leprae.
XX
PN US6583266-B1.
XX
PD 24-JUN-2003.
XX
PF 16-SEP-1994; 94US-00311731.
XX
PR 19-AUG-1993; 93US-00109181.
PR 22-OCT-1993; 93US-00142558.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Smith DR, Mao J;
XX
DR WPI; 2003-656441/62.
XX
PT New Mycobacterium tuberculosis anion pump peptide useful for as
PT tuberculosis vaccine and diagnosis of tuberculosis infection.
XX
PS Disclosure; SEQ ID NO 130; 26pp; English.
XX
CC The invention relates to a non-naturally occurring peptide of
CC Mycobacterium tuberculosis comprising an amino acid sequence
CC corresponding to an anion pump protein. The invention also relates to a
CC non-naturally occurring nucleic acid corresponding to a DNA sequence of
CC Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
CC useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
CC leprae or for screening for new tuberculosis drugs. Purified proteins
CC derived from the sequences of the invention may elicit a specific immune
CC response. The peptide may also be used to detect hypersensitivity
CC reactions of individuals exposed to Mycobacterium tuberculosis or
CC Mycobacterium leprae. The proteins and peptides may be affixed to solid
CC supports to detect antibodies typical of hypersensitivity reactions, from
CC a patient's sera. This sequence represents Mycobacterium leprae DNA of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 36941 BP; 8242 A; 11465 C; 10255 G; 6979 T; 0 U; 0 Other;
Query Match 36.2%; Score 26.4; DB 10; Length 36941;
Best Local Similarity 65.0%; Pred. No. 40;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 2 TGCGAGGAGATAGGTTAACTACTGTTGAAGTTTGAGCGGTGGTAACTATCTCTCTGC 61
DB 25498 TGGATGGAGATTGGTAAACCAACCAACCACTCAACATGAGCGAGTGGCTTCACGC 25557
RESULT 10


```

PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251088P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488783/53.
XX P-PSDB; AAU16226.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 1; SEQ ID NO 392; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodysplasia,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
Query Match 35.3%; Score 25.8; DB 4; Length 805;
Best Local Similarity 63.9%; Pred. No. 23;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 13 AGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTCTCGTAAACAGTTTTT 72
Db 407 ACGGTACCTTCTCTGAACTTGAGGAAGTCTTTTGTCTTCCAGCTGCTCAGGGTTCTC 466
QY 73 T 73
Db 467 T 467
RESULT 11
ABX73554
ID ABX73554 standard; DNA; 805 BP.
XX

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AC ABX73554;
XX
XX 18-MAR-2003 (first entry)
XX
XX Human novel polynucleotide #382.
XX
XX Human; gene; ds; neural disorder; immune system disorder; renal disorder;
XX muscular disorder; respiratory disease; reproductive disorder;
XX gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
XX hyperproliferative disorder; inflammatory disease; allergic reaction;
XX blood related disorder; cancer; immunosuppressive; antiinflammatory;
XX cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
XX haemostatic; antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX US2002132753-A1.
XX
XX 19-SEP-2002.
XX
XX 17-JAN-2001; 2001US-00764864.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0226686P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 08-SEP-2000; 2000US-0229513P.
XX 21-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0234223P.
XX 25-SEP-2000; 2000US-0234274P.
XX 27-SEP-2000; 2000US-0234997P.
XX 29-SEP-2000; 2000US-0235834P.
XX 29-SEP-2000; 2000US-0236327P.
XX 29-SEP-2000; 2000US-0236367P.
XX 29-SEP-2000; 2000US-0236368P.
XX 29-SEP-2000; 2000US-0236369P.
XX 29-SEP-2000; 2000US-0236370P.
XX 02-OCT-2000; 2000US-0236802P.
XX 02-OCT-2000; 2000US-0237037P.
XX 02-OCT-2000; 2000US-0237038P.
XX 02-OCT-2000; 2000US-0237039P.
XX 13-OCT-2000; 2000US-0237040P.
XX 20-OCT-2000; 2000US-0239355P.
XX 20-OCT-2000; 2000US-0240960P.
XX 20-OCT-2000; 2000US-0241785P.
XX 01-NOV-2000; 2000US-0241809P.
XX 17-NOV-2000; 2000US-0244617P.
XX 08-DEC-2000; 2000US-0249299P.
XX 08-DEC-2000; 2000US-0251856P.
XX 08-DEC-2000; 2000US-0251868P.
XX 08-DEC-2000; 2000US-0251869P.
XX

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Search completed: August 14, 2005, 20:21:40
Job time : 449 secs

AD R08359 standard; cDNA; 3597 BP.
AD R08359;
04-NOV-2004 (first entry)
Full length human cDNA useful for treating neurological disease Seq 1865.
gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
osteoporosis; neurological disease; Alzheimer's disease;
Parkinson's disease; dementia; short memory; cancer;
sense or motor function; emotional reaction; fear response; panic;
osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
tranquilliser.
XX Homo sapiens.
XX
XX EP14747413-A2.
XX
XX 18-AUG-2004.
XX
XX 12-FEB-2004; 2004EP-00003145.
XX
XX 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
XX WPI; 2004-583265/57.
DR P-PSDB; ADR10315.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 1865; 2686pp; English.
XX
XX This invention relates to novel, isolated full length human cDNA
molecules and the encoded proteins thereof. Specifically, it refers to
cDNA clones obtained by an oligo-capping method, where none of these
clones are identical to any known human mRNAs. The present invention
describes an immunoassay to identify agonists and antagonists, as well as
antibodies, antisense molecules and siRNAs that can all be used to bind
to and modulate expression of the cDNA molecules. As such, these
molecules are useful for diagnostic markers or therapeutic targets for
the various diseases or morbid states. In particular, they are useful in
the gene therapy for treating osteoporosis, neurological disease, Alzheimer's
disease, Parkinson's disease, dementia, short memory and various cancers,
as well as for maintaining equilibrium of sense or motor function, and
for treating emotional reaction, fear response and panic. Accordingly,
they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
cytostatic and tranquilliser activities. This polynucleotide is a full
length human cDNA sequence of the invention. NOTE: This sequence is not
given in the sequence listing of the specification but can be obtained on
CD-ROM from the European Patent Office, Vienna Sub-office.
XX
XX Sequence 3597 BP; 793 A; 943 C; 920 G; 941 T; 0 U; 0 Other;
SQ
Query Match 35.3%; Score 25.8; DB 13; Length 3597;
Best Local Similarity 60.9%; Pred. No. 35;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGTAACTACCTGTTGACGCTTGACGAGTGGTTAATCTATCTCTG 60
DB 803 TTGGAATAGTTCCTTTAAATCTGCTTGAATAATGGAACAGTTCCTCTCTCTC 862
QY 61 CTACAGTT 69
DB 863 CCATGTGT 871

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 14:09:25 ; Search time 1916 Seconds
(without alignments)
1846.154 Million cell updates/sec

Title: US-10-698-070-2
Perfect score: 73
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*
1: gb_da.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	31.8	43.6	178468	10	AL845354
c 2	31.8	43.6	233378	8	AL122277 Mus muscu
c 3	30.2	41.4	178468	10	AL845354
c 4	30.2	41.4	233378	2	AL122277 Mus muscu
c 5	29.6	40.5	107660	8	AL151668
c 6	29.6	40.5	116983	8	AL139709
c 7	29.6	40.5	120033	2	AL141364
c 8	29.6	40.5	123355	2	AL137835
c 9	29.6	40.5	124033	8	AC093544
c 10	29.6	40.5	124158	2	AL142142
c 11	29.6	40.5	124977	2	AL126018
c 12	29.6	40.5	320731	2	AL149573
c 13	29.4	40.3	147552	2	AC019298
c 14	29.4	40.3	151329	9	AC025623
c 15	29.4	40.3	154866	2	AC079965
c 16	29.4	40.3	211445	9	AC103794
c 17	29.2	40.0	152884	9	AC138625
c 18	29.2	40.0	158420	9	AC137788
c 19	29	39.7	157610	9	AC087235

C	93	26.6	36.4	179009	9	AL355543	Human DNA
	94	26.6	36.4	179060	2	AC074382	Homo sapi
	95	26.6	36.4	179310	9	AC006160	Homo sapi
C	96	26.6	36.4	189631	2	AC011842	Homo sapi
C	97	26.6	36.4	196606	9	AP000779	Homo sapi
	98	26.6	36.4	199230	2	AC048360	Homo sapi
	99	26.6	36.4	216800	10	AL599744	Mouse DNA
C	100	26.6	36.4	239237	2	AC094621	Rattus no

ALIGNMENTS

RESULT 1
AL845354/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL845354 178468 bp DNA linear ROD 24-JUN-2003
Mouse DNA sequence from clone RP23-318L10 on chromosome 2, complete sequence.

AL845354
AL845354.13 GI:32187955
HTG.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178468)
Tracey.A.
Direct Submission
Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 24 2003 this sequence version replaced gi:32131063.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TrEMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-318L10 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6.
Location/Qualifiers
1. .178468
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosomes="2"
/clone="RP23-318L10"
/clone_lib="RPCI-23"

FEATURES
source

ORIGIN
Query Match 43.6%; Score 31.8; DB 10; Length 178468;
Best Local Similarity 67.2%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGGTTAACTCTTGAAGCTTGACGAGTGTTAATCTATCTCTG 60
DB 48646 TTGGCAGGAGACACAGTAACCTACTTATTAAAGTTCAACAGGAGGTTCTCTTACCTG 48587
QY 61 CTAACAG 67
DB 48586 CAAAGAG 48580
RESULT 2
AC122277 233378 bp DNA linear HTG 30-JUL-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC122277 233378 bp DNA linear HTG 30-JUL-2002
Mus musculus chromosome UNK clone RP23-231N7, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
AC122277
AC122277.2 GI:22004622
HTG; HTG PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 233378)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 233378)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (23-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 233378)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Jul 30, 2002 this sequence version replaced gi:21105133.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:<http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M BA0231N07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 229423 bases at least Q40
Consensus quality: 230099 bases at least Q30
Consensus quality: 230466 bases at least Q20
Insert size: 170000; agarose-gel
Insert size: 232778; sum-of-contigs
Quality coverage: 13.22 in Q20 bases; agarose-gel
Quality coverage: 10.03 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

* 1 71720: contig of 71720 bp in length
* 71721 71820: gap of unknown length
* 71821 134774: contig of 62954 bp in length
* 134775 134874: gap of unknown length
* 134875 136238: contig of 1364 bp in length
* 136239 136339: gap of unknown length
* 136339 138393: contig of 2055 bp in length
* 138393 138493: gap of unknown length
* 138494 140771: contig of 2278 bp in length
* 140771 140871: gap of unknown length
* 140872 182344: contig of 41473 bp in length
* 182345 182445: gap of unknown length
* 182445 233378: contig of 50934 bp in length.

```

FEATURES

source

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1. .233378
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-231N7"

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misc_feature

```

1. .71720
/notes="assembly_name:Contig10"

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misc_feature

```

71821..134774
/notes="assembly_name:Contig11"

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misc_feature

```

134875..136238
/notes="assembly_name:Contig5"

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misc_feature

```

136339..138393
/notes="assembly_name:Contig6"

```

misc_feature

```

138494..140771
/notes="assembly_name:Contig7"

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misc_feature

```

140872..182344
/notes="assembly_name:Contig8"

```

misc_feature

```

182445..233378
/notes="assembly_name:Contig9"

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ORIGIN

```

Query Match 43.6%; Score 31.8; DB 2; Length 233378;
Best Local Similarity 67.2%; Pred. No. 2.9;
Matches 45; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TTGGCAGGATAGGTAACTACTGTTGAAGCTTGAGCTTGAGCAGGTTGTTAATCTATCTCTCTG 60
Db 218932 TTGGCAGAACCAACAGTAACACTTTTATTAAGTTCAACAGAGGTTCTCTTACCCCTG 218991
QY 61 CTAACAG 67
Db 218992 CAAAGAG 218998

```

RESULT 3

AL845354

```

LOCUS Mouse DNA sequence from clone RP23-318L10 on chromosome 2, complete
DEFINITION

```

ACCESSION

AL845354

VERSION

AL845354.13

KEYWORDS

HTG

SOURCE

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Jun 24, 2003 this sequence version replaced gi:32131063.
Sequence may have been used to confirm this sequence. Sequence data
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
-----

```

Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-318L10 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBac3.6.

FEATURES

source

```

1. .178468
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-318L10"
/clone_lib="RPCI-23"

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ORIGIN

```

Query Match 41.4%; Score 30.2; DB 10; Length 178468;
Best Local Similarity 65.7%; Pred. No. 10;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TTGGCAGGATAGGTAACTACTGTTGAAGCTTGAGCTTGAGCAGGTTGTTAATCTATCTCTG 60
Db 48583 TTGGCAGGATAGGTAACTACTGTTGAAGCTTGAGCTTGAGCAGGTTGTTAATCTATCTCTG 48642
QY 61 CTAACAG 67
Db 48643 CCAAAAG 48649

```

RESULT 4

AC122277/c

LOCUS

DEFINITION

AC122277

ACCESSION

AC122277.2

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

2 (bases 1 to 233378)

AUTHORS

TITLE

JOURNAL

REFERENCE

3 (bases 1 to 233378)

AUTHORS
TITLE
JOURNAL
COMMENT

McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 30, 2002 this sequence version replaced gi:21105133.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0231N07

----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100%
Assembly: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 229423 bases at least Q40
Consensus quality: 230099 bases at least Q30
Consensus quality: 230466 bases at least Q20
Insert size: 170000; agarose-fp
Quality coverage: 13.22 in Q20 bases; agarose-fp
Quality coverage: 10.03 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 71720: contig of 71720 bp in length
* 71721 71820: gap of unknown length
* 71821 134774: contig of 62954 bp in length
* 134775 134874: gap of unknown length
* 134875 136238: contig of 1364 bp in length
* 136239 136338: gap of unknown length
* 136339 138393: contig of 2055 bp in length
* 138394 138493: gap of unknown length
* 138494 140771: contig of 2278 bp in length
* 140772 140871: gap of unknown length
* 140872 182345: contig of 41473 bp in length
* 182345 182444: gap of unknown length
* 182445 233378: contig of 50934 bp in length.

FEATURES
source

1..233378
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-231N7"

misc_feature

1..71720
/note="assembly_name:Contig10"
71821..134774
/note="assembly_name:Contig11"
134875..136238
/note="assembly_name:Contigs"
136339..138393
/note="assembly_name:Contig6"
138494..140771
/note="assembly_name:Contig7"
140872..182344
/note="assembly_name:Contig8"
182445..233378
/note="assembly_name:Contig9"

ORIGIN

Query Match 41.4%; Score 30.2; DB 2; Length 233378;

Best Local Similarity 65.7%; Pred. No. 10;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 TTGCAGGATAGGTAACTACCTGTTGAAGCTTGACGAGTGGTTAACTATCTCTG 60
Db 218995 TTTCAGGGTATGAAGGACCTCTCTGTTGAACCTTAATAAGTAGTACTGTTGCTTCTG 218936
Qy 61 CTAACAG 67
Db 218935 CCAAAAG 218929

RESULT 5

AC151668 107660 bp DNA linear HTG 12-OCT-2004
LOCUS Medicago truncatula clone mth2-6e22, WORKING DRAFT SEQUENCE, 3
DEFINITION ordered pieces.
AC151668
ACCESSION AC151668.8 GI:54035640
VERSION HTG; HTGS PHAS82; HTGS DRAFT.
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.

TITLE
JOURNAL

Medicago truncatula BAC Clone mth2-6e22
Unpublished

REFERENCE

2 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.

TITLE
JOURNAL

Direct Submission
Submitted (23-SEP-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.

COMMENT

On Oct 12, 2004 this sequence version replaced gi:53984532.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 3048: contig of 3048 bp in length
* 3049 3148: gap of unknown length
* 3149 38700: contig of 35552 bp in length
* 38701 38800: gap of unknown length
* 38801 107660: contig of 68860 bp in length.

FEATURES
source

1..107660
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
/clone="mth2-6e22"
/clone_lib="Medicago truncatula BAC library H2"

ORIGIN

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Query Match      40.5%; Score 29.6; DB 2; Length 107660;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACTCTTGAAGCTTCAGAGGTTGTTAATCTATCTCTCTGCTTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 17664 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCITCTAACA 17723

RESULT 6
AC139709/c
LOCUS      AC139709
DEFINITION Medicago truncatula clone mth2-22d18, complete sequence.
VERSION    AC139709
KEYWORDS   HTG;
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 116983)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Medicago truncatula BAC Clone mth2-22d18
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 116983)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (11-FEB-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 116983)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (15-JUN-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  4 (bases 1 to 116983)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (31-JUL-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Jul 31, 2004 this sequence version replaced gi:48717554.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            -----
FEATURES             source
            Location/Qualifiers
            1. .116983
               /organism="Medicago truncatula"
               /mol_type="genomic DNA"
               /db_xref="taxon:3880"
               /clone="mth2-22d18"
               /clone_lib="Medicago truncatula BAC library H2"
               /notes="This is one of two clones in the same well from
               mth2-22d18"
ORIGIN
Query Match      40.5%; Score 29.6; DB 8; Length 116983;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACTCTTGAAGCTTCAGAGGTTGTTAATCTATCTCTCTGCTTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 103089 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCITCTAACA 103030

```

```

RESULT 7
AC141364/c
LOCUS      AC141364
DEFINITION Medicago truncatula clone mth2-8a2, WORKING DRAFT SEQUENCE, 2
            ordered pieces.
VERSION    AC141364
KEYWORDS   HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 120033)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Medicago truncatula BAC Clone mth2-8a2
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 120033)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (13-MAR-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 120033)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (05-OCT-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Oct 5, 2004 this sequence version replaced gi:47174786.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * been provided by the submitter.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            * 1 117025: contig of 117025 bp in length
            * 117026 117125: gap of unknown length
            * 117126 120033: contig of 2908 bp in length.
FEATURES             source
            Location/Qualifiers
            1. .120033
               /organism="Medicago truncatula"
               /mol_type="genomic DNA"
               /db_xref="taxon:3880"
               /clone="mth2-8a2"
               /clone_lib="Medicago truncatula BAC library H2"
ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 120033;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACTCTTGAAGCTTCAGAGGTTGTTAATCTATCTCTCTGCTTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 103131 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCITCTAACA 103072

RESULT 8
AC137835/c

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LOCUS      AC137835      122355 bp      DNA      linear      HTG 06-AUG-2004
DEFINITION Medicago truncatula clone mth2-29b14, WORKING DRAFT SEQUENCE, 2
AC137835
AC137835
AC137835.41 GI:51011171
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 122355)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Medicago truncatula BAC Clone mth2-29b14
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 122355)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (04-DEC-2002) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 122355)
AUTHORS   Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (06-AUG-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Aug 6, 2004 this sequence version replaced gi:50950328.
            -----
            Center: Genome Center
            Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 3645: contig of 3645 bp in length
            * 3646 3745: gap of unknown length
            * 3746 122355: contig of 118610 bp in length.
FEATURES   source
            location/Qualifiers
            1..122355
               /organism="Medicago truncatula"
               /mol_type="genomic DNA"
               /db_xref="taxon:3880"
               /clone="mth2-29b14"
               /clone_lib="Medicago truncatula BAC library H2"
ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 122355;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGACGAGGTGTTAACTATCTCTCTCTAACA 66
|||||
Db 107426 GGAAATAGGTAATTAAGTGGTATAGCATCTTATATGCTTAATCGATCTCTCTCTAACA 107367
|||||
RESULT 9
AC093544/c
LOCUS      AC093544      124033 bp      DNA      linear      PLN 11-MAR-2003
DEFINITION Medicago truncatula chloroplast, complete genome, complete
            sequence.
AC093544
VERSION    AC093544.8 GI:17149410

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KEYWORDS   HTG.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Medicago truncatula Variety Jema Long A-17 Chloroplast, Complete
            Sequence
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (31-AUG-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (19-SEP-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  4 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (19-OCT-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  5 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (03-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  6 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (07-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  7 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  8 (bases 1 to 124033)
AUTHORS   Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE     Direct Submission
JOURNAL   Submitted (11-MAR-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Nov 29, 2001 this sequence version replaced gi:16756257.
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            Center: Genome Center
            Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
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            Location/Qualifiers
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               /mol_type="genomic DNA"
               /strain="Variety Jema Long A-17"
FEATURES   source

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/db_xref="taxon:3880"
/clon="chloroplast"

ORIGIN
Query Match      40.5%; Score 29.6; DB 8; Length 124033;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6449 GGAATAAGGTAATTAGGTGGTATAGCATTTCTATATGCTTATATCGATCTCTCTTCTAACA 6390

RESULT 10
AC142142/c      124158 bp      DNA      linear      HTG 06-OCT-2004
LOCUS      Medicago truncatula clone mth2-31e20, WORKING DRAFT SEQUENCE, 4
DEFINITION      ordered pieces.
ACCESSION      AC142142
VERSION      AC142142.18 GI:53828773
KEYWORDS      HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM      Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE      1 (bases 1 to 124158)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Medicago truncatula BAC Clone mth2-31e20
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 124158)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (22-MAR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE      3 (bases 1 to 124158)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (06-OCT-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT      On Oct 6, 2004 this sequence version replaced gi:53793750.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 104141: contig of 104141 bp in length
* 104142 104241: gap of unknown length
* 104242 107695: contig of 3454 bp in length
* 107696 107795: gap of unknown length
* 107796 121925: contig of 14130 bp in length
* 121926 122025: gap of unknown length
* 122026 124158: contig of 2133 bp in length.
* Location/Qualifiers
FEATURES
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/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"

/clon="mth2-31e20"
/clon_lib="Medicago truncatula BAC library H2"
/notes="This is one of two clones in the same well from
mth2-31e20"

ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 124158;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89560 GGAATAAGGTAATTAGGTGGTATAGCATTTCTATATGCTTATATCGATCTCTCTTCTAACA 89501

RESULT 11
AC126018/c      124977 bp      DNA      linear      HTG 28-SEP-2004
LOCUS      Medicago truncatula clone mth2-14h13, WORKING DRAFT SEQUENCE, 4
DEFINITION      unordered pieces.
ACCESSION      AC126018
VERSION      AC126018.19 GI:52346226
KEYWORDS      HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM      Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE      1 (bases 1 to 124977)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Medicago truncatula BAC Clone mth2-14h13
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 124977)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE      3 (bases 1 to 124977)
AUTHORS      Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL      Submitted (28-SEP-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT      On Sep 19, 2004 this sequence version replaced gi:52318767.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2357: contig of 2357 bp in length
* 2358 2457: gap of unknown length
* 2458 4533: contig of 2076 bp in length
* 4534 4633: gap of unknown length
* 4634 6932: contig of 2299 bp in length
* 6933 7032: gap of unknown length
* 7033 124977: contig of 117945 bp in length.
* Location/Qualifiers
FEATURES
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1..124977
/organism="Medicago truncatula"
/mol_type="genomic DNA"

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/db_xref="taxon:3880"
/clone="mth2-14h13"
/clone_lib="Medicago truncatula BAC library H2"

ORIGIN
    Query Match      40.5%; Score 29.6; DB 2; Length 124977;
    Best Local Similarity 68.3%; Pred. No. 17;
    Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy  7  GGAGATAGTTAACTACCTGTTGAAGCTTGAGCAGGTGTTAACTATCTCTCTGCTAACA 66
    |||||
Db  110414  GGAAATAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCTTCTAACA 110355

RESULT 12
AC149573/c
LOCUS      AC149573              320731 bp      DNA      linear      HTG 06-OCT-2004
DEFINITION Medicago truncatula clone mth2-119g4, WORKING DRAFT SEQUENCE, 52
            unordered pieces.
ACCESSION  AC149573
VERSION    AC149573.8 GI:53828780
KEYWORDS   HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Medicago truncatula BAC Clone mth2-119g4
            Unpublished
REFERENCE  2 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Direct Submission
            Submitted (08-JUN-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Direct Submission
            Submitted (06-OCT-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Oct 6, 2004 this sequence version replaced gi:53793764.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 52 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
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            * 2120: contig of 2120 bp in length
            * 2121: gap of unknown length
            * 2221: contig of 2157 bp in length
            * 4378: gap of unknown length
            * 4478: contig of 2022 bp in length
            * 6500: gap of unknown length
            * 6509: contig of 2059 bp in length
            * 8658: gap of unknown length
            * 8759: contig of 2518 bp in length
            * 11276: gap of unknown length
            * 11377: contig of 2614 bp in length
            * 13991: gap of unknown length
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            * 14091: contig of 2242 bp in length
            * 16332: gap of unknown length
            * 16333: contig of 2068 bp in length
            * 18500: gap of unknown length
            * 18600: contig of 2551 bp in length
            * 21151: gap of unknown length
            * 21251: contig of 2238 bp in length
            * 23489: gap of unknown length
            * 26707: contig of 3118 bp in length
            * 26807: gap of unknown length
            * 30025: contig of 3218 bp in length
            * 30125: gap of unknown length
            * 30126: contig of 3008 bp in length
            * 32133: gap of unknown length
            * 35396: contig of 2163 bp in length
            * 35496: gap of unknown length
            * 38285: contig of 2789 bp in length
            * 38386: gap of unknown length
            * 42317: contig of 3832 bp in length
            * 42318: gap of unknown length
            * 44932: contig of 2615 bp in length
            * 45032: gap of unknown length
            * 48055: contig of 3023 bp in length
            * 48155: gap of unknown length
            * 50571: contig of 2416 bp in length
            * 50671: gap of unknown length
            * 52786: contig of 2115 bp in length
            * 52886: gap of unknown length
            * 55014: contig of 2128 bp in length
            * 55114: gap of unknown length
            * 58456: contig of 3342 bp in length
            * 58556: gap of unknown length
            * 60674: contig of 2018 bp in length
            * 64933: contig of 4259 bp in length
            * 65033: gap of unknown length
            * 68622: contig of 3589 bp in length
            * 68722: gap of unknown length
            * 73490: contig of 4768 bp in length
            * 73491: gap of unknown length
            * 77278: contig of 3688 bp in length
            * 77379: gap of unknown length
            * 80719: contig of 3341 bp in length
            * 80819: gap of unknown length
            * 85277: contig of 4458 bp in length
            * 85377: gap of unknown length
            * 92306: contig of 6929 bp in length
            * 92406: gap of unknown length
            * 92407: contig of 4830 bp in length
            * 97236: gap of unknown length
            * 102561: contig of 5225 bp in length
            * 102562: gap of unknown length
            * 106887: contig of 4226 bp in length
            * 106988: gap of unknown length
            * 112013: contig of 5026 bp in length
            * 112113: gap of unknown length
            * 116962: contig of 4849 bp in length
            * 116963: gap of unknown length
            * 117063: contig of 5181 bp in length
            * 122243: gap of unknown length
            * 122344: contig of 9312 bp in length
            * 131655: gap of unknown length
            * 131755: contig of 6082 bp in length
            * 137837: gap of unknown length
            * 137937: contig of 6174 bp in length
            * 144111: gap of unknown length
            * 144112: contig of 9300 bp in length
            * 153511: gap of unknown length
            * 153611: contig of 5872 bp in length
            * 159483: gap of unknown length
            * 159583: contig of 9115 bp in length
            * 168698: gap of unknown length
            * 168699: contig of 9662 bp in length
            * 178460:

```


* 178461 178560: gap of unknown length
 * 178561 189146: contig of 10586 bp in length
 * 189147 189246: gap of unknown length
 * 189247 205996: contig of 16750 bp in length
 * 205997 206096: gap of unknown length
 * 206097 221512: contig of 15416 bp in length
 * 221513 221612: gap of unknown length
 * 221613 235904: contig of 14292 bp in length
 * 235905 236005: gap of unknown length
 * 236006 248142: contig of 12138 bp in length
 * 248143 248242: gap of unknown length
 * 248243 263641: contig of 15399 bp in length
 * 263642 263741: gap of unknown length
 * 263742 280695: contig of 16954 bp in length
 * 280696 280796: gap of unknown length
 * 280797 301898: contig of 21103 bp in length
 * 301899 301999: gap of unknown length
 * 301999 320731: contig of 18733 bp in length.

FEATURES
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 /db_xref="taxon:3880"
 /clone_lib="mh2-11994"
 /clone_lib="Medicago truncatula BAC library H2"

ORIGIN
 Query Match 40.5%; Score 29.6; DB 2; Length 320731;
 Best Local Similarity 68.3%; Pred. No. 17;
 Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTATCTCTCGTAACA 66
 |||||
 Db 85884 GGAATAAGGTAATTAGTGGTATAGCATTCTATATGCTTAAATCGATCTCTCTTAACA 85825

RESULT 13
 AC019298
 LOCUS
 DEFINITION Homo sapiens clone RP11-30H20, WORKING DRAFT SEQUENCE, 24 unordered
 pieces.
 AC019298
 VERSION AC019298.3 GI:7382219
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 147552)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Aldred, E., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
 Boguslavsky, L., Bouckhalter, B., Brown, A., Burkett, G., Castle, A.,
 Chao, P., Collins, S., Collins, S., Collins, S., Collins, S., Collins, S.,
 DeArnell, K., Dewar, K., Domino, M., Doyle, M., Fenebor, J.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, T., Lechoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,
 MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
 McPheeters, R., Meldrum, J., Meneus, L., Morrow, J., Navlor, J.,
 Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
 Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
 Zimmer, A., and Zody, M.
 Direct Submission
 Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Apr 1, 2000 this sequence version replaced gi:6721285.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center.
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L4878
 Center Clone name: 30_H_20
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 134743 bases at least Q40
 Consensus quality: 140753 bases at least Q30
 Consensus quality: 142882 bases at least Q20
 Insert size: 150000; agarose-fp
 Quality coverage: 145252; sum-of-contigs
 Quality coverage: 3.6 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 24 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1112: contig of 1112 bp in length
 * 1113 1212: gap of 100 bp
 * 1213 2733: contig of 1521 bp in length
 * 2734 2833: gap of 100 bp
 * 2834 4679: contig of 1846 bp in length
 * 4680 4779: gap of 100 bp
 * 4780 7239: contig of 2460 bp in length
 * 7240 7339: gap of 100 bp
 * 7340 9564: contig of 2225 bp in length
 * 9565 9664: gap of 100 bp
 * 9665 13696: contig of 4032 bp in length
 * 13697 13796: gap of 100 bp
 * 13797 17531: contig of 3735 bp in length
 * 17532 17631: gap of 100 bp
 * 17632 21388: contig of 3657 bp in length
 * 21389 21388: gap of 100 bp
 * 21389 25895: contig of 4507 bp in length
 * 25896 25995: gap of 100 bp
 * 25996 31062: contig of 5067 bp in length
 * 31063 31162: gap of 100 bp
 * 31163 33753: contig of 2591 bp in length
 * 33754 33854: gap of 100 bp
 * 33854 38963: contig of 5110 bp in length
 * 38964 39064: gap of 100 bp
 * 39064 45861: contig of 6698 bp in length
 * 45862 45861: gap of 100 bp
 * 45862 52769: contig of 6908 bp in length
 * 52770 52869: gap of 100 bp
 * 52870 60905: contig of 8036 bp in length
 * 60906 61005: gap of 100 bp
 * 61006 66911: contig of 5906 bp in length
 * 66912 67011: gap of 100 bp
 * 67012 73602: contig of 6591 bp in length
 * 73603 73702: gap of 100 bp
 * 73703 80372: contig of 6670 bp in length
 * 80373 80472: gap of 100 bp
 * 80473 91073: contig of 10601 bp in length
 * 91074 91173: gap of 100 bp
 * 91174 99031: contig of 7858 bp in length
 * 99032 99331: gap of 100 bp
 * 99332 110237: contig of 11106 bp in length

ACCESSION AC079965
VERSION AC079965.5 GI:14547792
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154866)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone CTD-2649A9
Unpublished
2 (bases 1 to 154866)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bida,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepell,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
Lanazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisan,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 25, 2001 this sequence version replaced gi:14336470.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RN/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10817
Center clone name: 2649_A_9
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 153320 bases at least Q40
Consensus quality: 154086 bases at least Q30
Consensus quality: 154389 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 154566; sum-of-contigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 873: contig of 873 bp in length
* 874 973: gap of 100 bp
* 974 2323: contig of 1350 bp in length
* 2324 2423: gap of 100 bp

2424 56290: contig of 53867 bp in length
56291 56390: gap of 100 bp
56391 154866: contig of 98476 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="CTD-2649A9"
/clone_lib="CITD Human BAC"
1..873
/note="assembly_fragment"
974..2323
/note="assembly_fragment"
2424..56290
/note="assembly_fragment"
56391..154866
/note="assembly_fragment"
ORIGIN
Query Match 40.3%; Score 29.4; DB 2; Length 154866;
Best Local Similarity 70.9%; Pred. No. 20;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 15 GTTAACCTACTCTGTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTACAGTT 69
|||||
Db 150557 GTTAACCTAGCTGTGTGATCTTGGGCAGTTATTATCTCTCTGGGCTTACATTT 150611
Search completed: August 14, 2005, 20:53:49
Job time : 1929 secs

FEATURES
source
misc_feature
misc_feature
misc_feature
misc_feature

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 19:23:31 ; Search time 3242 Seconds
(without alignments)
857.092 Million cell updates/sec

Title: US-10-698-070-2
Perfect score: 73
Sequence: 1 ttggcaggagataggttaac.....tctcctgctaacagttttt 73

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	42.5	944	8	AZ673840 ENTIV66TR
2	30.4	41.6	768	5	BU333082 603500907
3	29.6	40.5	358	2	BE323297 NF005803P
4	29.6	40.5	390	4	EG456980 NF098609P
5	29.6	40.5	590	9	CR323291 Medicago
6	29.6	40.5	696	9	CR342420 Medicago
7	29.4	40.3	530	8	BH615508 BMBAC303A
8	29	39.7	559	8	BH765778 BMBAC357E
9	28.6	39.2	861	7	CK418262 AUF Ipint
10	28.4	38.9	662	8	BH462209 BOHA125TR
11	28	38.4	248	8	E04037
12	28	38.4	552	5	EX476471 DXF2p686F
13	27.6	37.8	662	9	AG177371 Pan trogl
14	27.6	37.8	722	5	BU476113 60384221A
15	27.6	37.8	775	7	CK312407 SB02011B2
16	27.4	37.5	660	4	BM682169
17	27.4	37.5	673	4	EM683036
18	27.2	37.3	456	9	CC689926
19	27.2	37.3	682	9	CE706471 tigr-g88
20	27	37.0	485	7	CK751301 eca01-8cs
21	27	37.0	595	8	AQ259536 nbxb0023C
22	27	37.0	759	9	CC869050 NDL.39P13
23	26.8	36.7	360	9	CL900263 abg59905
24	26.8	36.7	415	2	AW327602 dq01a04.y

c 98 25.8 35.3 425 2 AW450084 UT-H-BI3-
c 99 25.8 35.3 447 4 BM126223 i07e04.x
c 100 25.8 35.3 448 1 AI609071 tw29g01.x

ALIGNMENTS

RESULT 1
LOCUS AZ673840
DEFINITION ENTIV66TR Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000
genomic, genomic survey sequence.
ACCESSION AZ673840
VERSION AZ673840.1 GI:11810986
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE 1 (bases 1 to 944)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
JOURNAL
COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 78
High quality sequence stop: 811.

FEATURES

source
1..944
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHS1; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

ORIGIN

Query Match 42.5%; Score 31; DB 8; Length 944;
Best Local Similarity 68.3%; Pred. No. 5;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 10 GATAGTTACTACCTGGTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTAACAGTT 69
19 GTTAGGTTAGTTTTTTTTTGGTGTGCTGTAGTAGTCTAATCTCTGCTACAGAT 78
Db
QY 70 TTT 72
79 TGT 81
Db

RESULT 2

BU333082
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

FEATURES

source
1..768
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST418m1"
/tissue_type="whole embryo"
/dev_stage="10"
/lab_host="DH10B"
/clone_lib="CSEQCHM65"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 41.6%; Score 30.4; DB 5; Length 768;
Best Local Similarity 63.9%; Pred. No. 7.9;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGGTTAACTACCTGTGAGCTTGACGAGGTGGTTAATCTATCTCTG 60
378 TTGGCAAGGGCTATATTGCTCCCTGTTACCTCTCGAAACTGGGTAATGTCACCTG 437
QY 61 CTAACAGTTTTT 72
Db 438 GTCACCGGTGTT 449

RESULT 3

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

BU333082
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

FEATURES

source
1..768
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST418m1"
/tissue_type="whole embryo"
/dev_stage="10"
/lab_host="DH10B"
/clone_lib="CSEQCHM65"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 41.6%; Score 30.4; DB 5; Length 768;
Best Local Similarity 63.9%; Pred. No. 7.9;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGGTTAACTACCTGTGAGCTTGACGAGGTGGTTAATCTATCTCTG 60
378 TTGGCAAGGGCTATATTGCTCCCTGTTACCTCTCGAAACTGGGTAATGTCACCTG 437
QY 61 CTAACAGTTTTT 72
Db 438 GTCACCGGTGTT 449

RESULT 3

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

BE323297
LOCUS
DEFINITION
ACCESSION

```

VERSION BE323297.2 GI:11966701
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 358)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT On Jul 14, 2000 this sequence version replaced gi:9197074.
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Medicago Genome Initiative accession: MGI:S:19485
Insert Length: 808 Std Error: 0.00
Plate: 005 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES
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Location/Qualifiers
1..358
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF005E03PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/notes="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
ORIGIN
Query Match 40.5%; Score 29.6; DB 2; Length 358;
Best Local Similarity 68.3%; Pred. No. 13;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGAGATAGGTTAACTACCTGTTGAGCTTGAGCAGGTGTTATCTATCTATCTCTCTTAACA 66
Db 150 GGAATAAGGTAATTAGTGGTATAGCAATTTCTATATGCTTAATCGATCTCTCTTAACA 209

RESULT 4
BC456980
LOCUS NF098G09PL1F1070 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION clone NF098G09PL 5', mRNA sequence.
ACCESSION BC456980
VERSION BC456980.1 GI:13380305
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 390)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Medicago Genome Initiative accession: MGI:S:19485
Insert Length: 808 Std Error: 0.00
Plate: 005 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES
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1..390
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF098G09PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/notes="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
ORIGIN
Query Match 40.5%; Score 29.6; DB 2; Length 390;
Best Local Similarity 68.3%; Pred. No. 14;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGAGATAGGTTAACTACCTGTTGAGCTTGAGCAGGTGTTATCTATCTCTCTTAACA 66
Db 150 GGAATAAGGTAATTAGTGGTATAGCAATTTCTATATGCTTAATCGATCTCTCTTAACA 209

RESULT 5
CR312921/c
LOCUS CR312921 Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
DEFINITION truncatula, genomic survey sequence.
ACCESSION CR312921
VERSION CR312921.1 GI:44859065
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 590)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
FEATURES
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Location/Qualifiers
1..590
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/notes="Vector: pIndigoBAC ; Site 1: EcoRI ; Site 2: EcoRI
mtel-35B18FM1"
ORIGIN
Query Match 40.5%; Score 29.6; DB 9; Length 590;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGAGATAGGTTAACTACCTGTTGAGCTTGAGCAGGTGTTATCTATCTCTCTTAACA 66

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Db 478 GGAAATAGGTAATAGGTGGTATAGCATTTCTATATGATTAATCGATCTCTCTTAACA 419

RESULT 6
CR342420/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CR342420
Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.
CR342420
GSS.
CR342420.1 GI:44912755
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosid I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
1 (bases 1 to 696)
Genoscope.
Direct Submission
Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI ; Debelle F. and Chalhou B.-Genoscope sequence ID : mte1-75K21PM1"

FEATURES
source
Location/Qualifiers
1..696
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/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (l1)"
/notes="Vector: pBAC3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed with Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

ORIGIN
Query Match 40.5%; Score 29.6; DB 9; Length 696;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 7 GGAGTAGGTAACCTACCTGTTGAGCTTGAGCAGGTGTTAACTATCTCTCGTAAACA 66
Db 481 GGAAATAGGTAATAGGTGGTATAGCATTTCTATATGATTAATCGATCTCTCTTAACA 422

RESULT 7
BH615508/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH615508
BMBAC303A02T7_P5U Brugia malayi Genomic Bac Library 3 Brugia malayi genomic, genomic survey sequence.
BH615508
GSS.
BH615508.1 GI:18380196
Brugia malayi
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 530)
Whitton, C., Daub, J., Quail, M., Hall, N., Foster, J., Ware, J., Ganatra, M., Slatko, B., Barrell, B. and Blaxter, M.
A genome sequence survey of the filarial nematode Brugia malayi: repeats, gene discovery, and comparative genomics
Mol. Biochem. Parasitol. 137 (2), 215-227 (2004)
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.

collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
Seq primer: T7 (TAATACGACTCACTATAGG)
Class: BAC ends.
Location/Qualifiers
1..530
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"

collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
Seq primer: T7 (TAATACGACTCACTATAGG)
Class: BAC ends.
Location/Qualifiers
1..530
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"

collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
Seq primer: T7 (TAATACGACTCACTATAGG)
Class: BAC ends.
Location/Qualifiers
1..530
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"

/dev_stage="microfilaria (L1)"
 /clone lib="Brugia malayi Genomic Bac Library 3"
 /notes="Vector: pBACE3.6; Site 1: BamH I; Brugia malayi
 genomic DNA was partially cleaved with Sau3A I and size
 fractionated. 7,392 clones were generated with mean insert
 size ~48 kbp. The library was constructed by Claire
 Whitton, Blaxter Nematode Genetics Lab, University of
 Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
 Unit, The Sanger Centre, Cambridge, UK."

ORIGIN

Query Match 39.7%; Score 29; DB 8; Length 559;
 Best Local Similarity 71.7%; Pred. No. 24;
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 21 TACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTAACAGTCTTTT 73
 |||||
 Db 232 TACCTCTTGAACTTGGCTGGTAGTTAATTTATTACTGACAGAGTCTTTT 180
 |||||

RESULT 9

CK418262/c
 LOCUS 861 bp mRNA linear EST 05-JAN-2004
 DEFINITION AUF_ipint_58_m01 Intestine cDNA library Ictalurus punctatus cDNA
 5', mRNA sequence.

ACCESSION CK418262

VERSION CK418262

KEYWORDS EST.

SOURCE Ictalurus punctatus (channel catfish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 Ictaluridae; Ictalurus.

REFERENCE

1 (bases 1 to 861)

AUTHORS

Liu, Z., Li, P., Liu, L., He, C., Kucuktas, H., Peng, J., Chen, L.,
 Featman, E., Baopraeerukul, P., Simmons, M., Muir, W., Grizzle, J.,
 Dunham, R. and Brady, Y.

30,000 new catfish ESTs: new resources for functional analysis of
 genes involved in aquaculture performance traits

TITLE

Unpublished (2004)

JOURNAL

Contact: Liu ZJ

COMMENT

The Fish Molecular Genetics and Biotechnology Laboratory,
 Department of Fisheries and Allied Aquacultures and Program of Cell
 and Molecular Biosciences

Auburn University

203 Swingle Hall, Auburn University, Auburn, AL 36849, USA

Tel: 334 844 4054

Fax: 334 844 9208

Email: zliu@acesag.auburn.edu

Seq primer: T7.

FEATURES

source

1..861

/organism="Ictalurus punctatus"

/mol_type="mRNA"

/db_xref="taxon:7998"

/clone lib="Intestine cDNA library"

/notes="Organ: Intestine; Vector: pSport1; Site_1: NotI;
 Site_2: SalI"

ORIGIN

Query Match 39.2%; Score 28.6; DB 7; Length 861;
 Best Local Similarity 64.2%; Pred. No. 35;
 Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 6 AGAGATAGTTAACTACCTGTTGAGCTTGAGCTTGAGCAGGTGTTTATCTATCTCTGCTAAC 65
 |||||
 Db 222 AGCGATACAGAACCTACCTGTTGTTCTTCTGAGCTCCCTGCTCTCTCTGCTAAC 163
 |||||

QY 66 AGTTTTT 72

|||||

Db 162 TGTTTTT 156

RESULT 10

BH462209

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other_GSSs: BOHAI25TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..662

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHAI25"

/clone lib="BOHA"

/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

Query Match 38.9%; Score 28.4; DB 8; Length 662;
 Best Local Similarity 66.1%; Pred. No. 40;
 Matches 41; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 5 CAGGAGATAGTTAACTACCTGTTGAGCTTGAGCAGGTGGTGTATCTCTCTGCTAA 64
 |||||
 Db 265 CAGGAGTGGGATTACAACTCTGTTGAGCTTGAGCAGATGGGTATTGATATCTGCGAA 324
 |||||

QY 65 CA 66

325 GA 326

Db

RESULT 11

B04037/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Evans GA, Shane Probst

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RESULT 14
BU476113
LOCUS
DEFINITION 603842214f1 CSEQRBN22 Gallus gallus cdna clone CHEST82514 5', mRNA
ACCESSION BU476113
VERSION BU476113.1 GI:25969690
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..722
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST82514"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN22"
/notes="Vector: Bluescript II KS(+), Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
ORIGIN
Query Match 37.8%; Score 27.6; DB 5; Length 722;
Best Local Similarity 78.6%; Pred. No. 77;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 5 CAGGAGATAGGTTAACTACCTGTTGAAGCTTGACGAGGTGGT 46
|||||
DB 24 CAGGAGACAGGTTAACTACAGGTTTAGGCATCAGCAGGAGGT 65
|||||

RESULT 15
CK312407/c
LOCUS
DEFINITION SB02011B2D06.f1 normalized Kech-Tagu Library SB02 Taeniopygia
guttata cdna clone SB02011B2D06.f1 5, mRNA sequence.
ACCESSION CK312407
VERSION CK312407.1 GI:44821981

```

```

KEYWORDS EST.
SOURCE Taeniopygia guttata
ORGANISM Taeniopygia guttata
REFERENCE
AUTHORS Archosoria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosoria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
1 (bases 1 to 775)
Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogie,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.
TITLE The Songbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
JOURNAL Unpublished (2004)
COMMENT Contact: David F. Clayton
University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 3668
Fax: 217 244 1648
Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
Genome Center.
Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.
This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative,'
PCR Primers
FORWARD: TAATACGACTCACTATAGGG(T7)
BACKWARD: ATTAACCTCACTAAG(T73)
Insert length: 775 Std Error: 0.00
Plate: SB02011B2 row: D column: 06
Seq primer: TAATACGACTCACTATAGGG (T7)
High quality sequence stop: 775.
FEATURES
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/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="SB02011B2D06.f1"
/tissue_type="brain"
/dev_stage="late embryo, post-hatch days 1, 10, 20, 45,
and adult (pooled)"
/lab_host="DH10B"
/clone_lib="normalized Kech-Tagu Library SB02"
/notes="Organ: brain; Vector: pBS II SK(+); Site 1:
EcoRI(5' side of insert); Site 2: NotI (3' side of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identifying tag
was added at the 3'during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAATCGCA."
ORIGIN
Query Match 37.8%; Score 27.6; DB 7; Length 775;
Best Local Similarity 72.0%; Pred. No. 78;
Matches 36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 16 TTAACCTACCTGTTGAAGCTTGACGAGGTGGTAACTATCTCTCTGCTAAC 65
|||||
DB 723 TTAATACCTCTTGAAGCTTTATCATCTGCTTAACTGTACCATGATATC 674
|||||

Search completed: August 14, 2005, 21:48:05
Job time : 3257 secs

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